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*the plant journal*

**Plant-arthropod interactions: who is the winner?**

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12 5 Plant-arthropod interactions: who is the winner?  
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16 7 Elia Stahl, Olivier Hilfiker and Philippe Reymond\*  
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32 18 coevolution, arms race  
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4 22 **SUMMARY**  
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6 23 Herbivorous arthropods have interacted with plants for millions of years. During  
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8 24 feeding they release chemical cues that allow plants to detect the attack and mount an  
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10 25 efficient defense response. A signaling cascade triggers the expression of hundreds of  
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12 26 genes, which encode defensive proteins and enzymes for synthesis of toxic metabolites.  
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14 27 This direct defense is often complemented by emission of volatiles that attract  
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16 28 beneficial parasitoids. In return, arthropods have evolved strategies to interfere with  
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18 29 plant defenses, either by producing effectors to inhibit detection and downstream  
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20 30 signaling steps, or by adapting to their detrimental effect. In this review, we address the  
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22 31 current knowledge on the molecular and chemical dialogue between plants and  
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24 32 herbivores, with an emphasis on coevolutionary aspects.  
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## 34 INTRODUCTION

35 Plants and herbivorous arthropods have coevolved for millions of years and it is  
36 commonly believed that these interactions have generated the large variety of plant and  
37 arthropod species that inhabit our planet. Although a large fraction of arthropods  
38 provide service to plants in the form of pollination or protection against enemies, they  
39 also constitute a threat since they are generally herbivorous. Whether they chew leaf or  
40 root material, feed on cell content, mine mesophyll tissue or suck phloem, arthropods  
41 from different feeding guilds impose a stress that plants have to resist. Depending on the  
42 type of attack, plants have a battery of strategies that include preexisting constitutive  
43 defenses complemented by the induction of direct (toxic secondary metabolites and  
44 proteins) and indirect (emission of volatiles to attract predators) defenses (Fig. 1). These  
45 responses depend on precise perception of the aggressor, followed by a signal  
46 transduction cascade that culminates in a transcriptional reprogramming and synthesis  
47 of specific defense compounds. Efficient plant resistance imposes a selection pressure  
48 on herbivores, which in turn develop ways to interfere with defense mechanisms or  
49 adapt to the detrimental effect of toxins. In recent years, a wealth of information has  
50 accumulated on molecular components that control this on-going arms race. Several  
51 aspects of plant-arthropod interactions have been reviewed elsewhere (Schoonhoven *et*  
52 *al.*, 2005; Zhu-Salzman *et al.*, 2005; Will and van Bel, 2006; Howe and Jander, 2008;  
53 Wu and Baldwin, 2010; Hogenhout and Bos, 2011; Farmer, 2014; Jouannet *et al.*, 2014;  
54 Hilker and Fatouros, 2015; Schuman and Baldwin, 2016). In this review, we place  
55 emphasis on the molecular and chemical dialogue that underlies these interactions. We  
56 present the current knowledge on arthropods elicitors and effectors, provide examples  
57 of plant defense compounds and adaptations by arthropods, to illustrate a fascinating

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4 58 coevolution between organisms that are generally foes but can also engage in  
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6 59 mutualistic relationships.  
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## 10 61 **PERCEPTION OF FEEDING HERBIVORES**

11  
12 62 Plants have evolved exquisite ways to detect their enemies. When infected by bacterial  
13  
14 63 or fungal pathogens, hosts recognize pathogen-derived molecules from the attacker that  
15  
16 64 have been termed pathogen- or microbe-associated molecular patterns  
17  
18 65 (PAMPs/MAMPs). These PAMPs are highly conserved and are generally associated  
19  
20 66 with a class of attacker. PAMP perception is achieved by plasma membrane-bound  
21  
22 67 pattern recognition receptors (PRRs), which are either receptor-like kinases (RLKs) or  
23  
24 68 receptor-like proteins (RLPs) that lack a cytoplasmic kinase domain (Boller and Felix,  
25  
26 69 2009; Couto and Zipfel, 2016). Upon ligand binding, PRRs associate with regulatory  
27  
28 70 receptor kinases, including the well-studied BRI1-ASSOCIATED RECEPTOR  
29  
30 71 KINASE 1 (BAK1) (Couto and Zipfel, 2016). PAMP recognition leads to a  
31  
32 72 transcriptional defense program called pattern-triggered immunity (PTI), which restricts  
33  
34 73 growth of the invading pathogens through local and systemic production of defenses  
35  
36 74 proteins and metabolites (Li *et al.*, 2016). In analogy to plant-pathogen interactions,  
37  
38 75 scientists have identified herbivore-associated molecular patterns (HAMPs) (Mithöfer  
39  
40 76 and Boland, 2008; Bonaventure *et al.*, 2011; Hogenhout and Bos, 2011; Jouannet *et al.*,  
41  
42 77 2014; Acevedo *et al.* 2015) but knowledge about their corresponding PRRs is scarce.  
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## 49 79 **Arthropod-derived HAMPs**

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51 80 Initially termed "elicitors" because they elicited defense responses from the plant,  
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53 81 HAMPs have been found in a variety of sources, including saliva, oral secretions (OS),  
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4 82 reproductive glands, whole body or eggs (Table 1). HAMPs (like PAMPs) constitute  
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6 83 essential patterns, making it difficult for herbivores to eliminate them and hence avoid  
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8 84 recognition.  
9

10 85 One of the first and best-known example is volicitin, a fatty acid-amino acid  
11  
12 86 conjugate (FAC) purified from OS of the beet armyworm caterpillar *Spodoptera exigua*  
13  
14 87 (Alborn *et al.*, 1997). When applied to maize leaves, volicitin triggers the emission of a  
15  
16 88 bouquet of volatile terpenoids and indoles that attract parasitic wasps. Volicitin is  
17  
18 89 composed of 17-hydroxylinolenic acid coupled to glutamine. Interestingly, chemical  
19  
20 90 analysis established that linolenic acid originates from the plant and is further  
21  
22 91 hydroxylated and conjugated to glutamine by the insect (Lait *et al.*, 2003; Pare *et al.*,  
23  
24 92 1998). Volicitin and related FACs (fatty acids of different length and saturation coupled  
25  
26 93 to glutamine or glutamate) were further identified in OS from different Lepidoptera  
27  
28 94 (Pohnert *et al.*, 1999; Halitschke *et al.*, 2001; Mori *et al.*, 2003) and even in other  
29  
30 95 insects (Yoshinaga *et al.*, 2007). The physiological role of FACs is not yet clear but it  
31  
32 96 has been suggested that they are important for nitrogen assimilation in larvae  
33  
34 97 (Yoshinaga *et al.*, 2008). In addition, the amphiphilic nature of these molecules might  
35  
36 98 emulsify the ingested food.  
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42 99 Caeliferins are sulfated hydroxy fatty acids isolated from OS of the grasshopper  
43  
44 100 *Shistocera americana*. In maize, they elicit emission of volatiles similar to those  
45  
46 101 triggered by volicitin, although there is no evidence for natural enemies of grasshoppers  
47  
48 102 (Alborn *et al.*, 2007). 2-hydroxy octadecatrienoic acid (2-HOT) was detected in OS of  
49  
50 103 the tobacco hornworm *Manduca sexta* and triggers the emission of the sesquiterpene  
51  
52 104 trans- $\alpha$ -bergamotene in wild tobacco *Nicotiana attenuata*. In plants, 2-HOT is produced  
53  
54 105 from linolenic acid by the action of  $\alpha$ -dioxygenases. Occurrence of 2-HOT in *M. sexta*  
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4 106 OS may allow plants to sense herbivore feeding by the presence of a modified  
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6 107 membrane constituent (Gaquerel *et al.*, 2009). Bruchins are fatty acid derived long-  
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8 108 chain  $\alpha,\omega$ -diols, esterified at one or both ends with 3-hydroxypropanoic acid. They  
9  
10 109 were isolated from pea and cowpea weevil oviposition fluid and induce tumor-like  
11  
12 110 growth of undifferentiated cells (neoplasms) on pea pods, like naturally deposited eggs.  
13  
14 111 Neoplasms serve as direct defense by blocking larval entry (Doss *et al.*, 2000). Eggs of  
15  
16 112 the white backed planthopper *Sogatella furcifera* stimulate the production of the  
17  
18 113 ovicidal substance benzyl benzoate in certain rice varieties. Purification of female  
19  
20 114 extracts yielded active phospholipids, including phosphatidylcholine and  
21  
22 115 phosphatidylethanolamine (Yang *et al.*, 2014). Finally, oviposition by the large white  
23  
24 116 *Pieris brassicae* induces defense gene expression, local necrosis and production of  
25  
26 117 reactive oxygen species in Arabidopsis (Little *et al.*, 2007). The inducing activity is  
27  
28 118 found in egg extracts from different insects and is enriched in the lipid fraction  
29  
30 119 (Bruessow *et al.*, 2010).  
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35 120 All the above examples seem to indicate that lipid-derived HAMPs are prevalent  
36  
37 121 in OS from chewing herbivores. However, known HAMPs also include proteins,  
38  
39 122 peptides and small metabolites. A  $\beta$ -glucosidase in *P. brassicae* OS is responsible for  
40  
41 123 volatile emission in cabbage (Mattiacci *et al.*, 1995), a lipase in the grasshopper  
42  
43 124 *Schistocera gregaria* OS induces defense gene expression (Schäfer *et al.*, 2011), and an  
44  
45 125 uncharacterized 12kDa protein from oviduct secretions of the sawfly *Diprion pini*  
46  
47 126 induces volatile emission in pine (Hilker *et al.*, 2005). Inceptin is a peptide that  
48  
49 127 originates from the digestion of plant proteins, illustrating plants' ability to detect  
50  
51 128 feeding-dependent modification of self. This cyclic peptide of eleven amino acids was  
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53 129 purified from OS of the fall armyworm *S. frugiperda* and derives from proteolytic  
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4 130 cleavage of a plant chloroplastic ATPase in the insect midgut (Schmelz *et al.*, 2006).  
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6 131 When applied to cowpea (*Vigna unguiculata*) or maize, inceptin induces the production  
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8 132 of defense-related hormones, volatiles and defense compounds. Small metabolites  
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10 133 include for example benzyl cyanide and indole from reproductive accessory glands of *P.*  
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12 134 *brassicae* and *Pieris rapae*, respectively. They are associated with eggs and induce  
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14 135 indirect plant defense by arresting egg parasitoids at the oviposition site (Fatouros *et al.*,  
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16 136 2008; Fatouros *et al.*, 2009).

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19 137 The feeding mode and physiology of phloem-sucking aphids have rendered  
20  
21 138 HAMPs isolation difficult. Aphids deliver minute amounts of saliva with their syringe-  
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23 139 like stylet when probing and navigating through different cell layers to reach sieve  
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25 140 elements. Proteomic and genomic analyses of secreted proteins from the green peach  
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27 141 aphid *Myzus persicae* salivary glands have nevertheless identified candidate HAMPs  
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29 142 that induced defense gene expression or lowered aphid fecundity when overexpressed in  
30  
31 143 *Arabidopsis* (Table 1) (de Vos and Jander, 2009; Elzinga *et al.*, 2014). In addition,  
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33 144 Thrips and phytophagous mites have different feeding mode than chewing herbivores or  
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35 145 aphids. Although they belong to different classes (insects or arachnids), both pierce  
36  
37 146 plant tissues and feed on cell content. The Western flower thrips *Frankliniella*  
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39 147 *occidentalis* and the two-spotted spider mite *Tetranychus urticae* have been used as a  
40  
41 148 model to study *Arabidopsis* and tomato plant defenses. Whereas transcriptional changes  
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43 149 similar to those induced by lepidopteran herbivores were observed, the nature of the  
44  
45 150 eliciting activity is still unknown (de Vos *et al.*, 2005; Abe *et al.*, 2008; Kant *et al.*,  
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47 151 2008; Zhurov *et al.*, 2014).

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50 152 Interestingly, recognition can be mediated through bacterial PAMPs that are  
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52 153 present in OS. A porin-like protein from *Ralstonia* was purified from *S. littoralis* OS  
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4 154 and activated early defense responses, including channel formation and calcium fluxes  
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6 155 (Guo *et al.*, 2013). The bacterial chaperonin GroEL was identified in saliva of the potato  
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8 156 aphid *Macrosiphum euphorbiae*. This protein originated from the endosymbiont  
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10 157 *Buchnera aphidicola* and induced PTI responses that depended on BAK1 in  
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12 158 Arabidopsis (Chaudhary *et al.*, 2014). These two examples expand the range of  
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14 159 potential sources of HAMPs to the gut microbiome.  
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### 20 161 **HAMP recognition by potential PRRs**

21  
22 162 Strikingly, contrary to the case of bacterial and fungal PAMPs where direct binding to a  
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24 163 PRR has been demonstrated (Boller and Felix, 2009; Couto and Zipfel, 2016), there is  
25  
26 164 yet no evidence for a *bona fide* PRR that perceives a HAMP. However, *M. persicae*-  
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28 165 derived HAMPs were shown to elicit defenses characteristic of PTI responses in a  
29  
30 166 BAK1-dependent manner (Prince *et al.*, 2014; Vincent *et al.*, 2017). These studies  
31  
32 167 provide evidence for detection of aphid HAMPs by (unknown) PRRs that are distinct  
33  
34 168 from PRRs that detect bacterial and fungal PAMPs (Prince *et al.*, 2014). More than a  
35  
36 169 decade ago, a biochemical study using a radiolabelled form of volicitin reported binding  
37  
38 170 to a plasma-membrane protein from maize leaves (Truitt *et al.*, 2004). However, this  
39  
40 171 protein has not been further characterized and no gene has been cloned. A cluster of  
41  
42 172 three lectin receptor kinase (LecRK) genes conferred resistance to the brown  
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44 173 planthopper (BPH) in rice, but whether these LecRK bind to yet unknown HAMPs from  
45  
46 174 BPH or mediate downstream events is unknown (Liu *et al.*, 2015). Arabidopsis LecRK-  
47  
48 175 I.8 is involved in the perception of egg-derived HAMPs. Indeed, a *lecRK-I.8* mutant  
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50 176 displayed a significantly reduced expression of the defense gene *PR1* in response to egg  
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4 177 extract treatment (Gouhier-Darimont *et al.*, 2013). This interesting observation will  
5  
6 178 however await chemical identification of the lipid-derived HAMP and binding assays.  
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9 179 Recently, a LecRK receptor for extracellular ATP was discovered in  
10  
11 180 Arabidopsis. DORN1 (LecRK-I.9) bound ATP with high affinity and ectopic expression  
12  
13 181 triggered plant responses associated with wounding. It was concluded that DORN1 may  
14  
15 182 mediate perception of feeding herbivores by detecting ATP liberated from cell content  
16  
17 183 after physical damage (Choi *et al.*, 2014). Although ATP is not formerly a HAMP but  
18  
19 184 rather a damage-associated molecular pattern (DAMP), this finding reinforces the  
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21 185 hypothesis that LecRKs may be important components of HAMP perception.  
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#### 25 26 187 **Wound responses**

27  
28 188 It has long been recognized that wounding is an important component of plant responses  
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30 189 to chewing herbivores (Green and Ryan, 1972; Howe and Jander, 2008). Early work in  
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32 190 Solanaceae identified systemin, a 18-aa polypeptide wound signal that regulates the  
33  
34 191 production of anti-insect proteinase inhibitors (reviewed in Ryan and Pierce, 1998).  
35  
36 192 Although some early responses to herbivory are not or only partially mimicked by  
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38 193 mechanical damage (Bricchi *et al.*, 2010) and emission of volatiles is specifically  
39  
40 194 triggered by insect-derived cues (Alborn *et al.*, 1997), wounding and feeding activate  
41  
42 195 overlapping sets of genes (Reymond *et al.*, 2000; Major *et al.*, 2006). In addition,  
43  
44 196 jasmonic acid (JA), the main signal controlling defenses (see below), rapidly  
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46 197 accumulates in response to mechanical damage (Reymond *et al.*, 2000; Glauser *et al.*,  
47  
48 198 2008). For aphids, turgor changes associated with stylet penetration of the phloem may  
49  
50 199 also contribute to some defense responses, like for instance the rapid plugging of sieve  
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52 200 plates by callose or protein aggregates (reviewed in Will and van Bel, 2006).  
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4 201 Since many studies on the role of HAMPs involve exogenous application of OS  
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6 202 on wounded leaves, conclusions from such experiments have to be assessed critically.  
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8 203 Future experiments aiming at removing HAMPs genetically or physically from the  
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10 204 herbivore, as in the case of salivary gland ablation (Musser *et al.*, 2002), will be  
11  
12 205 necessary to demonstrate the specific role of these elicitors.  
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### 17 207 **Open questions**

18  
19 208 In several cases, the defense inducing activity of HAMPs is associated with crude  
20  
21 209 extracts or unknown proteins, but their exact chemical nature is unknown. For most  
22  
23 210 HAMPs, information on their role in arthropod biology is lacking and future work  
24  
25 211 should elucidate why they have been kept since they alert the plant about the attack. In  
26  
27 212 addition, genes responsible for HAMP synthesis need to be identified. Host specificity  
28  
29 213 and distribution in different arthropod taxa should also be addressed. For instance,  
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31 214 FACs have a broad-range activity but do not elicit volatile emission in lima bean and  
32  
33 215 cotton (Spiteller *et al.*, 2001; Schmelz *et al.*, 2009). Inceptin action is restricted to  
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35 216 Fabaceae while Arabidopsis only responds to caeliferins (Schmelz *et al.*, 2009). Finally,  
36  
37 217 there is a clear lack of knowledge on potential PRRs and efforts should be placed in  
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39 218 finding ligand/binding pairs and defining downstream steps to establish if plants use the  
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41 219 same molecular machinery to detect HAMPs and PAMPS.  
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### 48 221 **SIGNALING**

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50 222 Upon feeding, early signaling events include membrane depolarization, Ca<sup>2+</sup> influx,  
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52 223 production of reactive oxygen species (ROS), and activation of mitogen-activated  
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54 224 protein kinases (MAPK) (Howe and Jander, 2008; Wu and Baldwin, 2010; Vincent *et*

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4 225 *al.*, 2017). These fast responses have been observed in different plant species and thus  
5  
6 226 seem to constitute a general mechanism to transduce HAMP perception. Since Ca<sup>2+</sup>,  
7  
8 227 ROS, and MAPK are also involved in plant responses to pathogens, how they  
9  
10 228 specifically trigger anti-herbivore defense is currently unknown. For oviposition, there  
11  
12 229 is little information on early signaling steps, however ROS accumulation under eggs has  
13  
14 230 been reported (reviewed in Reymond, 2013; Hilker and Fatouros, 2015). Following  
15  
16 231 early responses to arthropods, alteration in hormonal profile plays a crucial role. JA is  
17  
18 232 the predominant signal that regulates downstream defense steps. Depending on the  
19  
20 233 attacker and on its developmental stage, a role for salicylic acid (SA), ethylene (ET),  
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22 234 and other plant hormones as primary signals or modulators has also been reported.  
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### 236 **JA pathway**

237 A large body of literature has detailed the importance of the JA pathway in response to  
238 necrotrophs and herbivores (Howe and Jander, 2008; Browse, 2009; Acosta and Farmer,  
239 2010; Wu and Baldwin, 2010; Pieterse *et al.*, 2012). In brief, upon damage fatty acids  
240 are released from plastidic galactolipids. 13-lipoxygenases oxygenate 18:3 and 16:3  
241 fatty acids to produce hydroperoxides, which are further converted by allene oxide  
242 synthase and allene oxide cyclase to 12-oxo-phytodienoic acid (OPDA) and dinor-oxo-  
243 phytodienoic acid (dnOPDA), respectively. OPDA and dnOPDA are transferred to  
244 peroxisomes where they are reduced by OPDA reductase 3 (OPR3) and subjected to a  
245 series of  $\beta$ -oxidation cycles to yield JA (Acosta and Farmer, 2010). Conjugation with  
246 Ile by the enzyme JAR1 in the cytosol generates the bioactive (+)-7-iso-JA-Ile (JA-Ile)  
247 (Staswick and Tiryaki, 2004; Fonseca *et al.*, 2009). After import in the nucleus, JA-Ile  
248 forms a complex with its receptor, the F-box CORONATINE INSENSITIVE 1 (COI1),

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4 249 and a JASMONATE-ZIM DOMAIN PROTEIN (JAZ). This leads to ubiquitination and  
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6 250 degradation of the JAZ proteins by the proteasome. JAZs are repressors of transcription  
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8 251 factors, including the Arabidopsis bHLH MYC2, MYC3 and MYC4, which control JA-  
9  
10 252 dependent responses additively (Chini *et al.*, 2007; Thines *et al.*, 2007; Browse, 2009;  
11  
12 253 Fernández-Calvo *et al.*, 2011) (Fig. 2). In Arabidopsis, transcriptome analyses revealed  
13  
14 254 that herbivory alters the expression of hundreds of genes and that a majority of these  
15  
16 255 genes are regulated by COI1 and MYC2/3/4 (Reymond *et al.*, 2004; de Vos *et al.*, 2005;  
17  
18 256 Schweizer *et al.*, 2013a; Schweizer *et al.*, 2013b). As a consequence, *coil-1* and *myc234*  
19  
20 257 mutants were significantly more susceptible to herbivory by the generalist herbivore *S.*  
21  
22 258 *littoralis* (Fernández-Calvo *et al.*, 2011; Schweizer *et al.*, 2013b). In addition, role of the  
23  
24 259 JAZ1/3/4/9/10-MYC2/3/4 Arabidopsis module in resistance against the generalist  
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26 260 *Trichoplusia ni* was recently demonstrated (Major *et al.*, 2017).

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31 261 That the JA pathway is central to resistance against arthropods in plants was  
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33 262 demonstrated using mutants. An original study using the Arabidopsis *fad3-2 fad7-2*  
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35 263 *fad8* triple mutant deficient in the jasmonate precursor linolenic acid showed that it was  
36  
37 264 highly susceptible to larvae of the saprophagous fungal gnat, *Bradysia impatiens*  
38  
39 265 (McConn *et al.*, 1997). Loss of function of the COI1 homologue in tomato increased  
40  
41 266 susceptibility to the two-spotted spider mite *T. urticae* (Li *et al.*, 2004b), and to the  
42  
43 267 lepidopteran herbivores *M. sexta* (Chen *et al.*, 2005) and *T. ni* (Herde and Howe, 2014).  
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45 268 Silencing COI1 in *N. attenuata* improved performance of *M. sexta*, and of the stem  
46  
47 269 weevil *Trichobaris mucorea* (Paschold *et al.*, 2007; Diezel *et al.*, 2011); the silverleaf  
48  
49 270 whitefly *B. tabaci* accelerated nymphal development on Arabidopsis *coil-1* (Zarate *et*  
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51 271 *al.*, 2007); the isopod crustacean *Porcellio scaber* completely devoured Arabidopsis *aos*  
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53 272 whereas wild-type plants remained intact (Farmer and Dubugnon, 2009); silencing LOX  
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4 273 and AOC in rice plants increased root herbivory by the generalist cucumber beetle  
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6 274 *Diabrotica balteata*, and the specialist rice water weevil *Lissorhoptrus oryzophilus* (Lu  
7  
8 275 *et al.*, 2015); in maize, mutants of *OPR7* and *OPR8*, two close homologues of *OPR3*,  
9  
10 276 were more susceptible to *S. exigua* (Yan *et al.*, 2012); the tomato jasmonate  
11  
12 277 biosynthesis mutant *def-1* that is impaired in volatile emission did not attract predatory  
13  
14 278 mites when infested with *T. urticae*, indicating that the JA pathway is also essential for  
15  
16 279 indirect defense (Ament *et al.*, 2004). For aphids, Ellis *et al.* (2002) showed that  
17  
18 280 Arabidopsis mutants with constitutive activation of JA-signaling were more resistant to  
19  
20 281 *M. persicae*.

282

### 283 **Other hormones**

284 The SA pathway is generally important to fend off biotrophic pathogens and plays a  
285 major role in PTI/ETI (Pieterse *et al.*, 2012). SA is a phenolic compound that is mainly  
286 synthesized from the precursor chorismate by ISOCHORISMATE SYNTHASE 1  
287 (ICS1/SID2). Activation of the lipase-like protein ENHANCED DISEASE  
288 SUSCEPTIBILITY 1 (EDS1) and its related interacting partner PHYTOALEXIN  
289 DEFICIENT 4 (PAD4) by biotrophic pathogens trigger SA accumulation (Vlot *et al.*,  
290 2009). Consequently, change in the redox state of the cell redirects the transcriptional  
291 coactivator NON EXPRESSOR OF *PR* GENES 1 (NPR1) from the cytosol to the  
292 nucleus, where it regulates expression of numerous defense genes, including the SA  
293 marker gene *PR-1* (Vlot *et al.*, 2009; Pieterse *et al.*, 2012).

294 The role of the SA pathway in resistance to arthropods has received some  
295 attention. Aphid feeding induced expression of SA-marker genes, but no SA  
296 accumulation was observed and studies with SA-pathway mutants in Arabidopsis

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4 297 generated contrasting data on arthropod performance (reviewed in Jaouannet *et al.*,  
5  
6 298 2014). For example, in one study (Mewis *et al.*, 2005) *npr1* and NahG were less  
7  
8 299 susceptible to the green peach aphid *M. persicae*, whereas this difference was not found  
9  
10 300 by Pegadaraju *et al.* (2005). However, *pad4* showed increased performance to *M.*  
11  
12 301 *persicae* but this effect was independent on EDS1 (Pegadaraju *et al.*, 2005, 2007). By  
13  
14 302 suppressing *PAD4* expression, *BOTRYTIS*-INDUCED KINASE1 (BIK1) was also  
15  
16 303 shown to confer enhanced susceptibility to *M. persicae*, indicating that this PTI  
17  
18 304 modulator and target of BAK1 acted as a negative regulator of the plant defense to  
19  
20 305 aphids (Lei *et al.*, 2014). Finally, *M. persicae* infestation triggered a transient trehalose  
21  
22 306 accumulation in Arabidopsis, which was shown to enhance PAD4 expression (Singh *et*  
23  
24 307 *al.*, 2011). PAD4 seems thus to constitute an important component mediating defense  
25  
26 308 against aphids but its connection to the SA pathway remains elusive (Shah and Louis,  
27  
28 309 2015).

29  
30  
31  
32  
33 310 For chewing herbivores, *S. littoralis* larvae were smaller when feeding on *ics1*  
34  
35 311 and *npr1-1*, implying a negative role of SA (Stotz *et al.*, 2002; Bodenhausen and  
36  
37 312 Reymond, 2007). Since the SA pathway is known to antagonize the JA pathway  
38  
39 313 (Pieterse *et al.*, 2012), these findings suggest that the enhanced resistance of the mutants  
40  
41 314 is due to a lack of inhibition of the JA pathway rather than a direct effect of SA  
42  
43 315 (Koorneef and Pieterse, 2008). Spider mite performance was higher on SA-deficient  
44  
45 316 tomato line NahG than on wild type (Villarroel *et al.*, 2016). When the brown  
46  
47 317 planthopper *Nilaparvata lugens* infested a rice line that overexpresses the resistance  
48  
49 318 gene *Bph14*, there was an induced expression of SA-related genes (Du *et al.*, 2009).  
50  
51 319 Finally, SA accumulated in resistant willow genotypes when attacked by the gall midge  
52  
53 320 *Dasineura marginemtorquens* (Ollerstam and Larsson, 2003).  
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4 321 *P. brassicae* oviposition on Arabidopsis triggered SA accumulation and  
5  
6 322 expression of SA-responsive genes (Little *et al.*, 2007). Follow-up studies using SA-  
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8 323 signaling mutants indicated that Arabidopsis responses to egg extract, including defense  
9  
10 324 gene expression, ROS accumulation and local cell death, share similarities with PTI and  
11  
12 325 requires a functional SA pathway (Gouhier-Darimont *et al.*, 2013) (Fig. 2).

13  
14  
15 326 ET is a modulator of SA and JA pathways. For instance, the ET pathway has a  
16  
17 327 synergistic effect on the JA pathway to fight necrotrophic pathogens or acts with NPR1  
18  
19 328 to enable SA antagonistic action on the JA pathway (reviewed in Pieterse *et al.*, 2012).  
20  
21 329 Information on the role of ET against arthropods is however incomplete or inconclusive.  
22  
23 330 The ET-insensitive Arabidopsis mutant *ein2-1* is more resistant to *S. littoralis* feeding  
24  
25 331 (Bodenhausen and Reymond, 2007; Stotz *et al.*, 2000). On the contrary, inhibition of  
26  
27 332 ET perception in maize enhances feeding by *S. frugiperda* (Harfouche *et al.*, 2006).  
28  
29 333 Treatment with HAMPs induced ET production in different plant species (Schmelz *et*  
30  
31 334 *al.*, 2009). Similarly, FACs elicited ET burst in *N. attenuata* and this prevented SA  
32  
33 335 accumulation, hence reducing a potential inhibitory effect of SA on the JA pathway  
34  
35 336 (Diezel *et al.*, 2009). Whitefly-induced interference of parasitoid attraction triggered by  
36  
37 337 *Plutella xylostella* feeding was abolished in *ein2-1* (Zhang *et al.*, 2013). Finally,  
38  
39 338 inhibition of the JA pathway after *P. brassicae* oviposition-induced SA accumulation in  
40  
41 339 Arabidopsis is dependent on both NPR1 and EIN2 (Schmiesing *et al.*, 2016).

42  
43  
44 340 Involvement of abscisic acid (ABA), auxin, gibberellins, brassinosteroids and  
45  
46 341 cytokinins in response to herbivory has been addressed in several studies (reviewed in  
47  
48 342 Erb *et al.*, 2012). The emerging picture is that these hormones primarily act as  
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50 343 modulators of the JA pathway and thus do not play a direct role in defense (reviewed in  
51  
52 344 Erb *et al.*, 2012).

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4 3455  
6 346 **Systemic responses**

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8 347 Evidence for a long-distance activation of defenses in response to herbivory has  
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10 348 accumulated over years. It requires activation of the JA pathway in local and distal  
11  
12 349 tissues but the nature of the systemic signal (hydraulic, chemical or electrical) has been  
13  
14 350 the subject of controversy (reviewed in Farmer *et al.*, 2014; Huber and Bauerle, 2016).  
15  
16 351 That JA or a precursor is the mobile signal was postulated but not demonstrated (Li *et*  
17  
18 352 *al.*, 2002a; Stratmann, 2003; Koo *et al.*, 2009). On the other hand, rapid voltage changes  
19  
20 353 in local and distal Arabidopsis leaves in response to *S. littoralis* feeding were recently  
21  
22 354 reported and depended on *GLUTAMATE RECEPTOR-LIKE (GLR)* genes *GLR3.3* and  
23  
24 355 *GLR3.6* (Mousavi *et al.*, 2013; Salvador-Recatalà *et al.*, 2014). Implanting platinum  
25  
26 356 wires in the petiole of a leaf and injecting current triggered JA and JA-Ile accumulation,  
27  
28 357 and defense gene expression in the leaf lamina distal to the treatment site, providing  
29  
30 358 strong evidence for the role of electrical signaling in systemic response to herbivory  
31  
32 359 (Mousavi *et al.*, 2013). Similar electrophysiological changes were further observed in  
33  
34 360 monocotyledonous and dicotyledonous species after challenge with *S. littoralis* and *M.*  
35  
36 361 *sexta* (Zimmermann *et al.*, 2016). Interestingly, aphid-induced Ca<sup>2+</sup> accumulation in  
37  
38 362 Arabidopsis was shown to depend on *GLR3.3* and *GLR3.6*, but here a role in long-  
39  
40 363 distance signaling is unlikely (Vincent *et al.*, 2017). In contrast, systemic responses  
41  
42 364 from wounded Arabidopsis cotyledons to roots was shown to be independent of GLRs  
43  
44 365 and electrical signaling but more probably due to JA transport (Gasperini *et al.*, 2015).  
45  
46 366 Similarly, JA but not JA-Ile was identified as a long-distance transmissible signal in *N.*  
47  
48 367 *attenuata* response to *M. sexta* using stem-to-stem grafted plants (Bozorov *et al.*, 2017).  
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50 368 In tomato, application of isotope-labeled precursors in wounded leaves indicated that  
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4 369 JA-Ile may be a mobile signal (Matsuura et al., 2012). It thus appears that a  
5  
6 370 combination of electrical signaling and hormone transport may be responsible for  
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8 371 systemic induction of JA-related defenses, but that the contribution of each signal may  
9  
10 372 depend on the organ or plant species considered (Fig. 3).

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13 373 Oviposition also triggers changes in distal leaves. Egg deposition by the elm leaf  
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15 374 beetle *Xanthogaleruca luteola*, the sawfly *D. pini*, and the stemborer moth *Chilo*  
16  
17 375 *partellus* induced the release of volatiles in local and distal leaves of *Ulmus minor*,  
18  
19 376 *Pinus sylvestris*, and maize respectively (Meiners and Hilker, 2000; Hilker et al., 2002;  
20  
21 377 Tamiru et al., 2011). Recently, *P. brassicae* oviposition on Arabidopsis leaves inhibited  
22  
23 378 infection by the bacterial pathogen *Pseudomonas syringae*, both in local and distal  
24  
25 379 leaves (Hilfiker et al., 2014). This systemic acquired resistance (SAR) depended on the  
26  
27 380 metabolic SAR signal pipecolic acid. Indeed, pipecolic acid accumulated in local and  
28  
29 381 distal leaves after oviposition and mutation in the biosynthesis gene *ALDI* abolished  
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31 382 egg-induced SAR (Hilfiker et al., 2014). For all these examples, the nature of the  
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33 383 systemic signal is however unknown (Fig. 3).

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### 38 385 **Open questions**

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41 386 The precise connection between detection of herbivory or egg deposition and the  
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43 387 following activation of different signaling pathways is currently unknown. Although the  
44  
45 388 JA pathway is crucial to fend off a majority of herbivores, which downstream defenses  
46  
47 389 genes are critical for resistance is still unresolved in most plant species. The SA  
48  
49 390 pathway may be important in some plant-arthropod interactions, but further experiments  
50  
51 391 should demonstrate SA accumulation and altered performance on SA mutants.  
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53 392 Similarly, more work will be necessary to understand the exact molecular contribution  
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4 393 of the ET pathway. Modulation of defenses against herbivory by other plant hormones  
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6 394 will also have to be better explored (Erb *et al.*, 2012). Finally, a better knowledge on the  
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8 395 nature of systemic signals that activate defenses in distal tissues is needed.  
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## 11 397 **DEFENSE COMPOUNDS**

### 12 398 **Metabolites**

13 399 The plant multilayered immune system is accompanied by the endogenous production  
14  
15 400 of metabolites with direct antimicrobial or/and insecticidal activity, whereas some  
16  
17 401 metabolites act as signals and contribute to plant immunity by regulatory means  
18  
19 402 (Mithöfer and Boland, 2012). Examples of plant-derived metabolites with a direct  
20  
21 403 insecticidal activity are given in Table 2.  
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24 404 Plants produce non-protein amino acids that function in response to herbivory  
25  
26 405 (reviewed in Huang *et al.*, 2011). One of the best-studied example is L-canavanine, a  
27  
28 406 major nitrogen storage compound in seeds of many species of Leguminosae and a  
29  
30 407 structural analog of L-arginine. L-canavanine is integrated in proteins, which results in  
31  
32 408 the synthesis of dysfunctional proteins and poor larval development (Rosenthal *et al.*,  
33  
34 409 1976, Rosenthal, 2001). Tobacco and soybean plants respond rapidly to herbivore attack  
35  
36 410 with a production of  $\gamma$ -aminobutyric acid (GABA) (Bown *et al.*, 2002). Larvae of the  
37  
38 411 oblique-banded leafroller *Choristoneura rosaceana* raised on GABA-containing  
39  
40 412 artificial diets showed decreased growth and survival rates, indicating that GABA  
41  
42 413 possess direct insecticidal activity (Bown *et al.*, 2006). This insecticidal activity could  
43  
44 414 result from inhibition of neurotransmission via GABA-regulated fast-acting chloride  
45  
46 415 channels (Hosie *et al.*, 1997, Bown *et al.*, 2006).  
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4 416 Terpenoid-based compounds with insecticidal properties are widely spread in the  
5  
6 417 plant kingdom. Azadirachtin is synthesized by the neem tree *Azadirachta indica* and  
7  
8 418 reduces growth of *Spodoptera littoralis*, *Spodoptera frugiperda*, and *Schistocerca*  
9  
10 419 *gregaria* by negatively influencing cell division and disruption of the endocrine system  
11  
12 420 (Mordue Luntz *et al.*, 1998). Pyrethrin from *Chrysanthemum cinerariifolium* inactivates  
13  
14 421 sodium channels along nerve cells and thereby harm insects from different orders and  
15  
16 422 families, including Tetranychidae, Pseudococcidae, Auchenorrhyncha, Coleoptera,  
17  
18 423 Caelifera, and Aleyrodidae (Casida *et al.*, 1983). In response to JA, ET, and attack by  
19  
20 424 the European corn borer *Ostrinia nubilalis*, *Zea mays* produces *ent*-kaurane-related  
21  
22 425 diterpenoids, collectively termed kauralexins, which exhibit antifeedant activity on *O.*  
23  
24 426 *nubilalis* (Schmelz *et al.*, 2011). Moreover, the lactone taraxinic acid  $\beta$ -D-  
25  
26 427 glucopyranosyl ester (TA-G) in latex protects the dandelion *Taraxacum officinale*  
27  
28 428 against its major root herbivore, the cockchafer *Melolontha melolontha*. Silencing of the  
29  
30 429 germacrene A synthase ToGAS1 resulted in decreased levels of TA-G in *T. officinale*  
31  
32 430 and in increased *M. melolontha* feeding (Huber *et al.*, 2016).

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37 431 Nicotine is one of the best-studied plant-derived alkaloid with insecticidal  
38  
39 432 activity and is produced by native tobacco species, such as *N. attenuata* and *Nicotiana*  
40  
41 433 *sylvestris*. It is structurally related to acetylcholine and can thereby target acetylcholine  
42  
43 434 receptors in the nervous system of insects (Gepner *et al.*, 1978). Silencing putrescine N-  
44  
45 435 methyltransferase (PMT), which is involved in nicotine biosynthesis, results in  
46  
47 436 decreased constitutive and inducible nicotine levels in *N. attenuata*. Consequently,  
48  
49 437 IR<sub>pmt</sub> plants grown in field experiments were more frequently attacked by the *S. exigua*  
50  
51 438 and *Trimerotropis* spp. grasshoppers (Steppuhn *et al.*, 2004). The medicinal plant  
52  
53 439 *Catharanthus roseus* produces more than a hundred different monoterpene indole  
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4 440 alkaloids (MIAs), which are well described as anticancer drugs in chemotherapy.  
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6 441 Catharanthine accumulates in leaf wax exudates and exhibits insect toxicity on *Bombyx*  
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8 442 *mori* larvae when included in artificial diet (Roepke *et al.*, 2010). Furthermore,  
9  
10 443 transcriptomic and metabolic analysis showed that *C. roseus* respond to *M. sexta*  
11  
12 444 feeding with the biosynthesis of specific MIAs. Interestingly, *C. roseus* leaf  
13  
14 445 consumption resulted in a rapid death of *M. sexta* larvae, which could be linked to MIA  
15  
16 446 generation and dimerization (Dugé de Bernonville *et al.*, 2017). Other examples of  
17  
18 447 insecticidal alkaloids include caffeine, colchicine, strychnine, and swainsonine (Wink *et*  
19  
20 448 *al.*, 1998, Mithöfer and Boland, 2012).

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22  
23  
24 449 Flavonoids, derived from the phenylpropanoid metabolism, are a diverse group  
25  
26 450 of plant secondary metabolites found in all plant species and they display some  
27  
28 451 antiherbivore effects (Ververidis *et al.*, 2007). Rotenone is produced in roots of tropical  
29  
30 452 legumes, such as *Derris elliptica* and *Lonchocarpus*, and is a mitochondrial poison that  
31  
32 453 blocks the electron transport chain and disrupts energy production (Isman *et al.*, 2006).  
33  
34 454 Kaempferol-3,7-dirhamnoside (KRR) accumulates in *Arabidopsis* in response to *P.*  
35  
36 455 *brassicae* feeding (Onkokesung *et al.*, 2016). Overexpression of *MYB75*, a transcription  
37  
38 456 factor that activates the anthocyanin pathway, resulted in decreased KRR levels in  
39  
40 457 *Arabidopsis* plants and increased susceptibility to *P. brassicae*. Furthermore, *P.*  
41  
42 458 *brassicae* gained less weight when reared on artificial diet containing KRR  
43  
44 459 (Onkokesung *et al.*, 2014).

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47  
48 460 Aliphatic- and indole-glucosinolates (GS) belong to the best-studied insecticidal  
49  
50 461 metabolites in Brassicaceae, including the model plant *Arabidopsis*. Aliphatic-GS and  
51  
52 462 indole-GS are derived from methionine and tryptophan, respectively. They are produced  
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54 463 in leaves constitutively and act as phytoanticipins in basal immunity against arthropods,  
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4 464 but their synthesis can also be induced in response to various pathogen attacks. Thereby,  
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6 465 GS biosynthesis relies on a complex regulatory network, controlled by several MYB  
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8 466 and MYC transcription factors (Schweizer *et al.*, 2013b; Frerigmann, 2016). Upon  
9  
10 467 plant-tissue disruption,  $\beta$ -thioglucoside glucohydrolase-dependent GS hydrolysis leads  
11  
12 468 to the generation of chemically unstable aglycones, such as toxic nitriles, thiocyanates,  
13  
14 469 and isothiocyanates. These aglycones can react spontaneously with biological  
15  
16 470 nucleophiles and modify proteins and nucleic acids (reviewed Pastorczyk and Bednarek,  
17  
18 471 2016). Strikingly, GS-deficient *Arabidopsis* mutants are highly susceptible to arthropod  
19  
20 472 feeding, including chewing larvae, spider mites, and aphids (Mewis *et al.*, 2005;  
21  
22 473 Beekwilder *et al.*, 2008; Schlaeppi *et al.*, 2008; Schweizer *et al.*, 2013b; Zhurov *et al.*,  
23  
24 474 2014; Madsen *et al.*, 2015). Tryptophan can also serve as a precursor for several indolic  
25  
26 475 alkaloids, which act as defense-related metabolites in *Arabidopsis*. Camalexin is  
27  
28 476 produced in *Arabidopsis* upon infestation by the phloem feeding green peach aphid *M.*  
29  
30 477 *persicae*. Consequently, *M. persicae* grows more successfully on camalexin-deficient  
31  
32 478 *pad3* mutant, indicating that camalexin functions in defense against phloem sap sucking  
33  
34 479 insects (Kettles *et al.*, 2013). Similarly, camalexin accumulated in response to  
35  
36 480 infestation by the cabbage aphid *Brevicoryne brassicae* and aphid performance was  
37  
38 481 augmented on *pad3* (Kusnierczyk *et al.*, 2008).

44 482 Many defense compounds are stored in developmental structures, including  
45  
46 483 glandular trichomes, laticifers, resin ducts, and specialized cell types or tissues  
47  
48 484 (Mithöfer and Boland, 2012). Genetic evidence for the role of trichomes as a source of  
49  
50 485 defense against herbivores was provided for tomato (Kang *et al.*, 2010; Bleeker *et al.*,  
51  
52 486 2012), *Arabidopsis* (Mauricio, 1998), *Arabidopsis lyrata* (Kivimäki *et al.*, 2007) and  
53  
54 487 *Nicotiana attenuata* (Luu *et al.*, 2017). Induction of terpene-containing traumatic resin  
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4 488 ducts by JA in Norway spruce provides support for a defensive role of these structures  
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6 489 against conifer pests (Martin *et al.*, 2002).  
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8  
9 490 In addition to ingested defense metabolites that target physiological processes in  
10  
11 491 arthropods, plants produce metabolites that harm feeding herbivores physically. In the  
12  
13 492 barrel medic *Medicago truncatula*, calcium oxalate crystals accumulate around  
14  
15 493 secondary veins and act as physical abrasive of *S. exigua* mandibles. Consistent with  
16  
17 494 this, larvae showed a feeding preference for the calcium oxalate-defective mutants *cod5*  
18  
19 495 and *cod6* (Korth *et al.*, 2006). Silica constitutes another important physical defense  
20  
21 496 compound, particularly in grasses (reviewed in Hartley and DeGrabriel, 2016). For  
22  
23 497 example, *Spodoptera exempta* larvae exposed to silica-rich diet displayed mandible  
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25 498 wear and reduced growth (Massey and Hartley, 2009).  
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### 30 500 **Proteins and peptides**

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33 501 Besides toxic metabolites, plants produce numerous proteins and peptides with direct  
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35 502 insecticidal activity (Table 3). Acrelin-1 is a 60 kDa dimeric glycoprotein found in  
36  
37 503 seeds of the wild kidney bean *Phaseolus vulgaris*. Acrelin-1 is highly resistant to  
38  
39 504 proteolytic degradation and binds to complex glycans, which leads to disruption of the  
40  
41 505 epithelial structure in the midgut of the Mexican bean weevil *Zabrotes subfasciatus*  
42  
43 506 (Fabre *et al.*, 1998). Plant-derived lectins are a heterogenous group of proteins found in  
44  
45 507 many members of Leguminosae. They can bind to specific carbohydrate structures in  
46  
47 508 the insect digestive tract, which leads to harmful effects in the whole insect body.  
48  
49 509 Insecticidal activity of lectins was reported against members of Coleoptera,  
50  
51 510 Lepidoptera, and Homoptera (Vandenborre *et al.*, 2011).  
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4 511 Cyclotides represent a group of small peptides found in Rubiaceae and  
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6 512 Violaceae. A cyclic peptide backbone in combination with a cysteine knot confer strong  
7  
8 513 chemical and biological stability. Cyclotides inhibit larval growth and development of  
9  
10 514 the native budworm *Helicoverpa punctigera* and leads to disruption of microvilli and  
11  
12 515 cellular rupture in the gut epithelium of *H. armigera* larvae (Jennings *et al.*, 2001;  
13  
14 516 Barbeta *et al.*, 2008). Canatoxin (CNTX) is an urease found in seeds of the jack bean  
15  
16 517 *Canavalia ensiformis*. Proteolytic activation of CNTX releases a 10 Kda peptide that  
17  
18 518 interferes with serotine-related processes in *Callosobruchus maculatus* and *Rhodnius*  
19  
20 519 *prolixus* (Stanisçuaski and Carlini, 2012). In tomato, threonine deaminase TD2 has  
21  
22 520 insecticidal properties by depriving herbivores from the essential Thr. Proteolytic  
23  
24 521 activation of TD2 is catalyzed by chymotrypsin in the gut of lepidopteran herbivores,  
25  
26 522 such as *S. exigua*, but not in coleopteran herbivores. Consequently, *S. exigua* larvae  
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28 523 performed better on TD2-deficient tomato plants (Gonzales-Vigil *et al.*, 2011).

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32 524 Arthropod digestion and nutrient acquisition relies on enzymes such as  $\alpha$ -  
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34 525 amylases, cysteine proteases, and serine proteases. So far, numerous plant protease and  
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36 526 amylase inhibitors have been reported that inhibit digestive enzymes and thereby  
37  
38 527 interfere with larval development. For instance, expression of an Arabidopsis cysteine  
39  
40 528 protease inhibitor (*Atcys*) in transgenic white poplar plants is sufficient to inhibit most  
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42 529 of the digestive proteinase activity of the leaf beetle *Chrysomela populi* and confers  
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44 530 resistance to this insect (Delledonne *et al.*, 2001).

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### 50 532 **Open questions**

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52 533 Numerous plant-derived insecticides have been identified and some of them are of great  
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54 534 interest in agriculture for plant protection. However, activity of most of them has just  
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4 535 been studied in artificial diets. We need better knowledge of biosynthetic pathways and  
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6 536 generation of knock-out mutants to test their role *in vivo*. Moreover, target sites for  
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8 537 many of the known insecticides are poorly characterized.  
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### 11 539 **SUPPRESSION OF DEFENSES**

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13 540 Effective plant PTI exerts as strong selection pressure on aggressors. Bacterial and  
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15 541 fungal pathogens have thus evolved numerous effectors to interfere with PTI (Dodds *et*  
16  
17 542 *al.*, 2009; Deslandes and Rivas, 2012;). These effectors are secreted and transferred or  
18  
19 543 directly injected into plant cells. In return, plants have developed strategies to directly or  
20  
21 544 indirectly detect effectors by intracellular nucleotide-binding, leucine-rich-repeat  
22  
23 545 receptors (NB-LRRs) that trigger an enhanced defense response called effector-  
24  
25 546 triggered immunity (ETI)(Jones and Dangl, 2006). This process illustrates the on-going  
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27 547 arms race that has been the driving force for generating a multitude of effectors and  
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29 548 defense proteins during plant-pathogen coevolution. Similarly, plant defense  
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31 549 suppression by arthropods has been reported in several studies (Table 1).  
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### 38 551 **Arthropod-derived effectors**

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40 552 A seminal discovery by Musser *et al.* (2002) reported that glucose oxidase (GOX) in *H.*  
41  
42 553 *zea* salivary glands inhibited nicotine production in tobacco. Elegant experiments using  
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44 554 ablation of the secretory apparatus, the spinneret, and ectopic application of active or  
45  
46 555 inactive GOX demonstrated that this enzyme is responsible for a lower accumulation of  
47  
48 556 nicotine upon feeding. Since GOX generates H<sub>2</sub>O<sub>2</sub> from D-Glucose, it was further  
49  
50 557 shown that this ROS may interfere with plant defense signaling (Bede *et al.*, 2006;  
51  
52 558 Diezel *et al.*, 2009). An ATP-hydrolyzing apyrase activity was found in *H. zea* saliva.  
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4 559 Tomato plants treated with this enzyme showed reduced defense gene expression (Wu  
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6 560 *et al.*, 2012). Since ATP can be perceived as a DAMP by plant PRRs, it is tempting to  
7  
8 561 speculate that some insects have evolved a way to reduce ATP levels in their host.  
9  
10 562 Unknown proteins or peptides from lepidopteran OS inhibited wound-induced defense  
11  
12 563 gene expression in *Arabidopsis* and tomato, and this was correlated with enhanced  
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14 564 insect performance in the case of *Arabidopsis* (Lawrence *et al.*, 2007; Consales *et al.*,  
15  
16 565 2012).

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19 566 Although they act as HAMPs in several insects, FACs may have dual roles.  
20  
21 567 Emission of some volatiles was reduced when *M. sexta* FACs were applied to *N.*  
22  
23 568 *attenuata* plants. Whether this interfered with parasitoid attraction was however not  
24  
25 569 tested (Gaquerel *et al.*, 2009). Heat-stable components of *M. sexta* OS suppressed  
26  
27 570 wound-induced accumulation of *N. attenuata* transcripts but their chemical nature was  
28  
29 571 not studied (Schittko *et al.*, 2001). Another striking example of a modified HAMP  
30  
31 572 activity is found in the legume-specialist velvetbean caterpillar *Anticarsia gemmatalis*.  
32  
33 573 OS of this insect contain a modified inceptin that does not induce plant defenses and  
34  
35 574 furthermore acts as an antagonist of the normally active inceptin, probably by  
36  
37 575 competing with inceptin-PRR binding (Schmelz *et al.*, 2012).

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40 576 For spider mites and aphids, examples of effective suppression of defenses exist.  
41  
42 577 In the spider-mite *T. urticae*, two proteins of unknown function suppressed defenses and  
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44 578 increased mite performance when expressed in *N. benthamiana* (Villaruel *et al.*, 2016).  
45  
46 579 A salivary component with high homology to human macrophage migration inhibitory  
47  
48 580 factor (MIF) was identified in the pea aphid *Acyrtosiphon pisum* (Naessens *et al.*,  
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50 581 2015). MIFs are important pro-inflammatory cytokines modulating immunity and  
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52 582 inflammation in vertebrates. Interestingly, RNAi of *ApMIF1* reduced survival and  
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5 583 fecundity of *A. pisum*. In addition, ectopic expression of MIF1 reduced plant defenses in  
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7 584 *N. benthamiana* (Naessens *et al.*, 2015). Since MIFs form heterocomplexes and  
8  
9 585 homologues have been recently identified in plant genomes (Panstruga *et al.*, 2015),  
10  
11 586 aphid MIF may interfere with endogenous MIFs to alter plant defenses (Naessens *et al.*,  
12  
13 587 2015; Reymond and Calandra, 2015). A salivary calcium-binding protein from  
14  
15 588 *Megoura viciae* prevented sieve plate occlusion, a known defense mechanism against  
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17 589 phloem-feeding that is triggered by calcium release (Will and van Bel, 2006; Will *et al.*,  
18  
19 590 2007). *A. pisum*, in which expression of the salivary protein C002 was reduced by  
20  
21 591 RNAi, was impaired in phloem feeding (Mutti *et al.*, 2008). Attempts to identify more  
22  
23 592 aphid effectors have relied on the same proteomic and genomic approaches that  
24  
25 593 successfully isolated secreted HAMPs. A series of proteins of unknown function have  
26  
27 594 been tested and were shown to suppress PTI responses and increase aphid performance  
28  
29 595 when expressed *in planta* (Bos *et al.*, 2010; Atamian *et al.*, 2013; Elzinga *et al.*, 2014).  
30  
31 596 For example, the *M. persicae* Mp10 effector suppressed flg22-induced but not chitin-  
32  
33 597 induced ROS production (Bos *et al.*, 2010). Furthermore, Mp10 was shown to act in the  
34  
35 598 BAK1 pathway (Drurey *et al.*, 2017). *M. persicae* Mp1 promoted aphid virulence by  
36  
37 599 targeting a vacuolar sorting protein (VSP52) from its preferred host plants Arabidopsis  
38  
39 600 and potato, but not with VSP52 from poor-host barley and *Medicago truncatula*  
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41 601 (Rodriguez *et al.*, 2017). Similarly, a comparative study on aphid effectors revealed that  
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43 602 they act in a plant-specific way and that sequences displayed high nonsynonymous  
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45 603 substitution rates, indicative of positive selection (Pitino and Hohenhout; 2013).  
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51 604 The Hessian fly *Mayetiola destructor* is an economically important pest of  
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53 605 wheat and a well-studied member of the plant parasitic gall midges (Stuart *et al.*, 2012).  
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55 606 The Hessian fly genome revealed a large family of secreted proteins (SSGP-71) that  
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4 607 resemble ubiquitin E3 ligases in plants (Zhao *et al.*, 2015). They contain a F-box  
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6 608 domain and variable leucine-rich repeats (LRR). In plants, the F box interacts with Skp,  
7  
8 609 a component of the SCF-E3-ubiquitin-ligase complex that targets proteins for  
9  
10 610 degradation. Interestingly, two Hessian fly F-box-LRR effectors were shown to directly  
11  
12 611 bind to wheat Skp proteins, suggesting that the role of these effectors is to hijack the  
13  
14 612 plant proteasome in order to block defenses (Zhao *et al.*, 2015). As further evidence that  
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16 613 F-box-LRRs are true effectors that can be recognized by NB-LRRs and trigger ETI,  
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18 614 mutations in two SSGP-71 genes were associated with regained virulence on wheat  
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20 615 cultivars containing the respective *H* resistance genes (Zhao *et al.*, 2015).  
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24 616 As discussed above, JA and SA signaling pathways generally modulate plant  
25  
26 617 defenses against arthropods and pathogens, respectively. These pathways are  
27  
28 618 antagonistic to each other and this property has been hijacked by bacterial effectors to  
29  
30 619 effectively suppress SA-dependent defenses (Pieterse *et al.*, 2012; Zheng *et al.*, 2012;  
31  
32 620 Gimenez-Ibanez *et al.*, 2014). Interestingly, effectors from arthropods also exploit  
33  
34 621 antagonism between SA and JA pathways. In *Arabidopsis*, defense gene expression and  
35  
36 622 JA levels were lower in response to *S. exigua* larvae with intact salivary glands  
37  
38 623 compared to larvae with ablated spinneret. This effect was lost in a mutant that does not  
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40 624 accumulate SA, implying a role for SA in inhibiting JA accumulation (Weech *et al.*,  
41  
42 625 2008). Silverleaf whitefly induced SA defenses while suppressing JA defenses in  
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44 626 *Arabidopsis* and lima bean (Zarate *et al.*, 2007; Zhang *et al.*, 2009). Similarly, the  
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46 627 mealybug *Phenacoccus solenopsis* inhibited JA accumulation and JA-dependent  
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48 628 defenses in tomato and this suppression was due to SA accumulation (Zhang *et al.*,  
49  
50 629 2015). A somewhat twisted example comes from the Colorado potato beetle (CPB)  
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52 630 *Leptinotarsa decemlineata* that uses microbe-derived flagellin to trigger SA-dependent  
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4 631 inhibition of the JA pathway in tomato. Indeed, bacteria in CPB OS decreased JA-  
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6 632 responsive defenses and increased SA and SA-related gene expression. These responses  
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8 633 were lost when using antibiotic-treated larvae and a SA-mutant (Chung *et al.*, 2013).  
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10 634 The observation that chitinase in larval frass of the fall armyworm *S. frugiperda*  
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12 635 suppress maize defenses through induction of the SA-dependent gene expression  
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14 636 provides another intriguing evidence of indirect effector-like activity. Finally, *P.*  
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16 637 *brassicae* oviposition or egg extract-treatment triggered SA accumulation, suppressed  
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18 638 larval-induced JA-dependent gene expression, and enhanced larval performance in  
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20 639 *Arabidopsis* (Little *et al.*, 2007; Bruessow *et al.*, 2010). This egg-induced inhibition of  
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22 640 the JA pathway is achieved through SA-dependent destruction of MYC2, MYC3 and  
23  
24 641 MYC4 transcription factors that control JA defense gene expression (Schmiesing *et al.*,  
25  
26 642 2016). Intriguingly, *P. brassicae* oviposition also triggers a SAR against bacterial  
27  
28 643 pathogens, a response that may benefit hatching larvae (Hilfiker *et al.*, 2014). This latter  
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30 644 phenomenon does not seem to be strictly related to suppression of defenses but  
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32 645 illustrates a manipulation of plant signaling pathways by an egg-derived effector, to the  
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34 646 potential benefit of the attacker.

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#### 648 **Defense suppression by insect-vectorized viruses and phytoplasma**

649 Plant pathogens like viruses and phytoplasma are often transmitted by arthropods and  
650 thus engage in mutualistic interactions with their vector to ensure dispersal and survival.  
651 Improved performance and reproduction of the carrier is thus crucial for the pathogen  
652 and consequently compromising plant defenses has obvious advantages. The  
653 pathogenesis protein  $\beta$ C1 of *Tomato yellow leaf curl China virus* (TYLCCNV), a  
654 begomovirus transmitted by the whitefly *B. tabaci*, binds to the plant transcription

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4 655 factor AS1, triggering a reduced expression of JA-responsive genes (Yang *et al.*, 2008).  
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6 656  $\beta$ C1 interacted with MYC2 and interfered with expression of TPS genes, which are  
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8 657 responsible for biosynthesis of defensive terpenoids (Li *et al.*, 2014). Consequently,  
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10 658 virus-infected whiteflies displayed a significantly higher survival and reproduction on  
11  
12 659 tobacco plants than non-infected ones (Luan *et al.*, 2013). The C2 protein from the  
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14 660 *Tomato yellow leaf curl Sardinia virus* (TYLCSV) and *Tomato yellow leaf curl virus*  
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16 661 (TYLCV) was shown to interfere with the activity of COP9 signalosome complex,  
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18 662 which subsequently compromised the function of several CUL1-based SCF ubiquitin  
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20 663 E3 ligases. Jasmonate responses were altered in *Arabidopsis* expressing C2 from  
21  
22 664 TYLCSV or TYLCV, suggesting that SCF<sup>COI1</sup> is one target of this virulence factor  
23  
24 665 (Lozano-Durán *et al.* 2011; Rosas-Díaz *et al.*, 2016). The 2b protein of aphid-  
25  
26 666 transmitted *Cucumber mosaic virus* inhibited expression of JA-regulated genes  
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28 667 downstream of JA production (Lewsey *et al.*, 2010). *M. persicae* aphid fecundity was  
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30 668 enhanced by *Turnip mosaic virus* infection of *Arabidopsis*, which showed increased  
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32 669 callose deposition. This effect depended on ET-signaling and was caused by the Nuclear  
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34 670 Inclusion a-Protease domain (Casteel *et al.*, 2015).

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39 671 Phytoplasma are obligate bacterial pathogens that develop in plant phloem. The  
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41 672 Aster Yellows phytoplasma strain Witches' Broom (AY-WB) secretes the SAP11  
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43 673 protein that destabilizes class II CIN-TCP transcription factors, some of which are  
44  
45 674 positive regulators of the JA-biosynthesis enzyme LOX2. As a consequence,  
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47 675 *Arabidopsis* lines expressing SP11 or AY-WB infected plants produced less JA and  
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49 676 allowed enhanced performance of the leafhopper vector *Macrostelus quadrilineatus*  
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51 677 (Sugio *et al.*, 2011).  
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679 **Arthropod resistance genes**

680 ETI triggered by pathogen or fungal effectors is driven by NB-LRRs. These resistance  
681 proteins usually contain a Toll-Interleukin-1 receptor-Resistance protein (TIR) or a  
682 coiled-coil (CC) domain at the amino terminus. They are encoded by numerous  
683 resistance (*R*) genes usually clustered in plant genomes, allowing recombination-based  
684 diversification to respond to the evolution of pathogen effectors (Jones and Dangl,  
685 2006; McHale *et al.*, 2006). In contrast to *R* genes associated with bacterial and fungal  
686 pathogens, only a few arthropod-directed *R* genes have been cloned and characterized  
687 (Gururani *et al.*, 2012). *Mi-1.2* from tomato encodes a CC-NB-LRR and confers  
688 resistance to the potato aphid, the whitefly *B. tabaci*, the psyllid *Bactericerca cockerelli*,  
689 and the root-knot nematode *Meloidogyne incognita*, illustrating the first example of a  
690 resistance gene acting against distantly related pests (Milligan *et al.*, 1998; Rossi *et al.*,  
691 1998; Nombela *et al.*, 2003; Casteel *et al.*, 2006). In the presence of potato aphid saliva  
692 *Mi-1.2* was shown to interact with *SISERK1*, a receptor kinase related to Arabidopsis  
693 BAK1, and this complex formation is suggested to confer aphid resistance (Peng *et al.*,  
694 2016). *Vat* from melon is also a CC-NB-LRR and, interestingly, provides dual  
695 resistance against the aphid *Aphis gossypii* and viruses transmitted by this vector  
696 (Dogimont *et al.*, 2014). Resistance to the brown planthopper (BPH) *Nilaparvata*  
697 *lugens*, a sucking insect attacking rice plants, is conferred by two CC-NB-LRR genes,  
698 *Bph14* and *Bph16* (Du *et al.*, 2009; Tamura *et al.*, 2014). In lettuce, *Ra* is part of a large  
699 CC-NB-LRR gene cluster and provides resistance against the root aphid *Pemphigus*  
700 *bursarius* (Wroblewski *et al.*, 2007). The *AIN* locus in *M. truncatula* is associated with  
701 resistance against the bluegreen aphid *Acyrtosiphon kondoi* and resides in a cluster of  
702 CC-NB-LRR genes (Klingler *et al.*, 2009). Similarly, *Hdic* is embedded in a family of



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4 703 NB-LRR *H* resistance genes that are active against the Hessian fly *M. destructor* (Stuart  
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6 704 *et al.*, 2012).  
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11 706 **Open questions**

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13 707 Chemical identity, mode of action, and molecular target(s) of several effectors are  
14  
15 708 poorly characterized. Whether each type of effector represents an evolutionary response  
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17 709 to PTI and appears in only a subset of related arthropod species or biotypes, similar to  
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19 710 bacterial or fungal effectors, remains an open question. When effectors inhibit defenses  
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21 711 via SA-dependent inhibition of the JA pathway, it is unclear whether activation of the  
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23 712 SA pathway by arthropod-derived cues illustrates a strategy evolved by the attacker to  
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25 713 indirectly target the JA pathway or whether this is a trade-off, since the SA pathway  
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27 714 may be needed for defense.  
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31 715 Strikingly, all examples of cloned resistance genes are CC-NB-LRRs that target  
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33 716 phloem-feeding insects. Whether there is a mechanistic reason for such specificity or  
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35 717 whether this is explained by a lack of success in cloning resistance genes against  
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37 718 members of other feeding guilds will await future experiments. Indeed, many loci  
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39 719 providing resistance against different orders of arthropods have been identified in  
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41 720 different crop species and need to be characterized (Smith and Clement, 2011; Gururani  
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43 721 *et al.*, 2012). Alternatively, other feeding guilds that rapidly consume leaf material may  
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45 722 avoid recognition by "eating the evidence". Also, besides F-box-LRR effectors and H  
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47 723 resistance proteins in Hessian fly/wheat interaction, information about the nature of  
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49 724 effectors interacting with known arthropod NB-LRRs is currently lacking.  
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55 726 **PLANT-ARTHROPOD COEVOLUTION**  
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4 727 Plants and herbivores are engaged in a continuous battle for survival and rely on  
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6 728 different strategies to counteract the evolution of resistance or adaptation to defense  
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8 729 compounds. In addition to PTI and ETI immunity responses, which are based on HAMP  
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10 730 recognition and inhibition of HAMP-triggered defenses by arthropod effectors (see  
11  
12 731 previous sections), there are numerous examples of behavioral or metabolic responses  
13  
14 732 that overcome plant defenses (Table 4). In a few cases, a successive appearance of  
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16 733 defense and counterdefense mechanisms can be observed and nicely illustrates  
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18 734 coevolutionary processes that underlie plant-arthropod interactions.  
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### 736 **Behavioral adaptations**

737 Capability of arthropods to circumvent plant defenses by specialized feeding behavior  
738 has been documented (reviewed in Dussourd, 2017). Cardenolides are toxic cardiac  
739 glycosides that inhibit Na/K-ATPase and are stored in latex from several plant families.  
740 Larvae of the queen butterfly *Danaus gilippus* cut trenches on leaves of the milkweed  
741 *Asclepias syriaca*, releasing a flow of cardenolide-containing latex and thus rendering  
742 the plant more palatable (Dussourd and Eisner, 1987). In some *Bursera* species,  
743 terpene-containing resin is stored under pressure in leaf canals. Upon feeding, the toxic  
744 resin is ejected and solidifies around small herbivores. Adapted members of  
745 chrysomelid beetles of the genus *Blepharida* puncture leaf veins to stop the flow before  
746 feeding (Becerra, 2003). Leaf vein severing or trench cutting is frequent and found in  
747 several arthropod families (Dussourd, 2017).

748 To avoid defensive trichomes in *Solanum* sp., larvae of the ithomiid butterfly  
749 *Mechanitis isthmia* spin a fine silk fabric over spines, allowing them to move and feed  
750 safely (Rathcke and Poole, 1975). Another behavioral adaptation is to minimize contact

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4 751 with induced plant defenses. When carefully studying movement of *H. armigera*  
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6 752 caterpillars feeding on Arabidopsis, Perkins *et al.* (2013) noticed that larvae moved  
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8 753 away from elicited and closely connected leaves, suggesting that they are capable of  
9  
10 754 detecting a signal that triggers this response. The nature of the warning signal is  
11  
12 755 unknown but depends on activation of the JA pathway (Perkins *et al.*, 2013). There are  
13  
14 756 also examples of behaviors that reduce attraction of parasitoids. Larvae of *Heliothis*  
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16 757 *subflexa* have specialized on their host plant *Physalis angulata* by feeding exclusively  
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18 758 on fruits, which lack linolenic acid. As a consequence, no volicitin is produced in *H.*  
19  
20 759 *subflexa* OS and feeding does not trigger volatile emission (De Moraes and Mescher,  
21  
22 760 2004). Since linolenic acid is required for development of most insect larvae, this  
23  
24 761 physiological adaptation is remarkable and provides both a protection against  
25  
26 762 parasitoids and an exclusive access to a food source. Interestingly, linolenic acid is also  
27  
28 763 a precursor for JA and there is the possibility that *P. angulata* fruits are unable to trigger  
29  
30 764 JA-dependent defenses against herbivores. This hypothesis was however not tested in  
31  
32 765 the study. Recently, the first evidence of insect resistance against an introduced  
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34 766 parasitoid wasp was reported (Tomasetto *et al.*, 2017). The Argentine stem weevil  
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36 767 *Listronotus bonariensis* was discovered in New Zealand in 1927 and cause intensive  
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38 768 damage to pasture grass. Since the introduction of a natural parasitoid of the stem  
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40 769 weevil in the 90's there has been a gradual decline in parasitism rate from 80-90% to 10-  
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42 770 20%. This sharp reduction is attributed to a host shift from *Lolium multiflorum* to the  
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44 771 more widely cultivated *Lolium perenne*, which is potentially impaired in herbivore-  
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46 772 induced volatile emission (Tomasetto *et al.*, 2017).  
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55 774 **Metabolic resistance**  
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4 775 Target modification and metabolism of plant toxins are the main strategies to overcome  
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6 776 plant defenses and have been the subject of numerous studies, which in some instances  
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8 777 have revealed the molecular mechanism (reviewed in Després *et al.*, 2007; Li *et al.*,  
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10 778 2007; Heidel-Fischer and Vogel, 2015).

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13 779 Insensitivity of the monarch butterfly *Danaus plexxipus* to cardenolides was  
14  
15 780 attributed to an amino acid substitution in the binding site of a Na/K-ATPase (Holzinger  
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17 781 and Wink, 1996). The same substitution was found in four species that span four insect  
18  
19 782 orders and 300 million years of divergence, providing a stunning example of convergent  
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21 783 evolution (Dobler *et al.*, 2012). *H. zea* evolved a structural modification in the binding  
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23 784 site of a carboxypeptidase to evade inhibition of the potato carboxypeptidase inhibitor  
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25 785 (Bayés *et al.*, 2005). Similarly, a single amino acid substitution in chymotrypsin from  
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27 786 *Helicoverpa* larvae removes a binding contact to a tobacco proteinase inhibitor (Dunse  
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29 787 *et al.*, 2010). As described above, L-canavanine from legumes is a L-Arg analog with  
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31 788 insecticidal properties. Larvae of the bruchid beetle *Caryedes brasiliensis* have evolved  
32  
33 789 a discriminating arginyl-tRNA synthetase that does not accept L-canavanine as  
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35 790 substrate and thus are protected against the toxic effect of this analog (Rosenthal *et al.*,  
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37 791 1976).

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40 792 Detoxification of cyanogenic glycosides from *Passiflora* sp. by larvae of the  
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42 793 butterfly *Heliconius* is carried out by sequestration and replacement of a nitrile by a  
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44 794 thiol group that prevents cyanide release (Engler *et al.*, 2000). However, the enzyme  
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46 795 responsible for this reaction has not been identified yet. Another way to avoid cyanide  
47  
48 796 poisoning is to metabolize HCN. Remarkably, the spider mite *T. urticae* has acquired a  
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50 797 bacterial gene encoding a  $\beta$ -cyanoalanine synthase (CAS) that can detoxify HCN to  $\beta$ -  
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52 798 cyanoalanine (Wybouw *et al.*, 2014). The same activity was found in the lepidopteran  
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4 799 herbivore *P. rapae* where CAS genes are also predicted to originate from bacteria  
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6 800 through horizontal gene transfer (van Ohlen *et al.*, 2016). Excretion of the alkaloid  
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8 801 nicotine by the specialist tobacco hornworm *M. sexta* is thought to be the main method  
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10 802 by which this insect can thrive on Solanaceae (Self *et al.*, 1964; Maddrell and Gardiner,  
11  
12 803 1976). Interestingly, it was recently shown that part of the ingested nicotine is  
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14 804 transported from *M. sexta* midgut to the hemolymph, from where it is actively exhaled  
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16 805 and used as a defensive signal against the spider predator *Camptocosa parallela* (Kumar  
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18 806 *et al.*, 2014).

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22 807 Arthropod adaptation to the GS-myrosinase system of Brassicaceae has been  
23  
24 808 extensively studied (Winde and Wittstock, 2011). In larvae of *P. rapae* and *P.*  
25  
26 809 *brassicae*, midgut nitrile-specifier proteins (NSPs) favor GS hydrolysis to less toxic  
27  
28 810 nitriles, instead of isothiocyanates (ITC) (Wittstock *et al.*, 2004). In contrast, the  
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30 811 diamondback moth *P. xylostella* and the desert locust *S. gregaria* detoxify intact GS  
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32 812 with a sulfatase, preventing formation of hydrolysis products (Ratzka *et al.*, 2002; Falk  
33  
34 813 and Gershenzon, 2007). Remarkably, the cabbage aphid *B. brassicae* sequesters intact  
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36 814 GS from its host plants in the haemolymph and produces a myrosinase in microbodies.  
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38 815 Upon attack by predators, aphids use this "mustard-oil bomb" to generate bioactive  
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40 816 compounds and defend themselves (Bridges *et al.*, 2002; Kazana *et al.*, 2007). Similarly,  
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42 817 the crucifer specialist flea beetle *Phyllotreta striolata* accumulates GS when feeding and  
43  
44 818 has acquired a myrosinase gene (Beran *et al.*, 2014).

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49 819 Major detoxification gene families from arthropods include cytochrome P450  
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51 820 monooxygenases (CYP450s), glutathione-S-transferases (GSTs), UDP-  
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53 821 glycosyltransferases (UGTs), carboxyl/cholinesterases (CCEs) and ABC transporters  
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55 822 (ABCs) (Li *et al.*, 2007; Heidel-Fischer and Vogel, 2015). These enzymes have  
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4 823 relatively broad substrate specificity and are generally important for generalist  
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6 824 herbivores that face a variety of plant toxins. Using the polyphagous *T. ni* and defense  
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8 825 or signaling mutants, Herde and Howe (2014) were the first to demonstrate  
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10 826 transcriptional reprogramming and altered expression of detoxification genes in  
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12 827 response to GS in *Arabidopsis*. Similarly, a comparative transcriptomic analysis of  
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14 828 larvae of the generalist *Heliothis virescens* and the specialist *P. brassicae* feeding on  
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16 829 *Arabidopsis* genotypes with contrasting GS levels revealed a significant upregulation of  
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18 830 detoxification genes from all the above-mentioned families in the generalist, whereas  
19  
20 831 there was a much-reduced transcriptional activation in the specialist (Schweizer *et al.*,  
21  
22 832 2017). Furanocoumarins are DNA-interfering agents primarily found in Apiaceae and  
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24 833 Rutaceae. Species of the genus *Papilio*, including the black swallowtail *P. polyxenes*,  
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26 834 induce the expression of CYP450s from the CYP6B class upon feeding on  
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28 835 furanocoumarin-containing plants. CYP6B proteins were shown to metabolize  
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30 836 furanocoumarins and were more active in the specialist *P. polyxenes* than in the  
31  
32 837 generalist *H. zea* (Hung *et al.*, 1997; Li *et al.*, 2004a; Li *et al.*, 2007). The fly genus  
33  
34 838 *Scaptomyza* is closely related to the genus *Drosophila* and has acquired the ability to  
35  
36 839 feed on Brassicaceae. A duplication in the GST gene *GstD1* in *S. nigra* is responsible  
37  
38 840 for an enhanced detoxification activity against isothiocyanates, toxic breakdown  
39  
40 841 products of GS, and is postulated to be linked to the evolutionary transition to herbivory  
41  
42 842 in Drosophilidae (Gloss *et al.*, 2014). Gossypol is a major sesquiterpene defensive  
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44 843 compound in cotton. Larvae of the generalist Heliothine moth *H. armigera* can develop  
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46 844 on cotton plants and are equipped with two UGTs, UGT41B3 and UGT40D1, which are  
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48 845 capable of glycosylating gossypol (Krempel *et al.*, 2016).  
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4 846 Although CCEs have been clearly associated with resistance to synthetic  
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6 847 insecticides and CCE gene expression is induced after feeding (Li *et al.*, 2007; Teese *et*  
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8 848 *al.*, 2010), there is limited information on their role against plant allelochemicals. In  
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10 849 different strains of the gypsy moth *Lymantria dispar*, larval survival on artificial diet  
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12 850 containing phenolic glycosides was positively correlated with CCE activity (Lindroth  
13  
14 851 and Weisbrod, 1991). Similarly, ABC transporters have been associated with insecticide  
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16 852 resistance, including *Bacillus thuringiensis* insecticidal toxins (Bt). There is an  
17  
18 853 expansion of ABC genes in the *T. urticae* genome and expression of ABC genes is  
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20 854 enhanced upon switching to a different host plant or feeding on artificial diet containing  
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22 855 plant secondary metabolites (Grbic *et al.*, 2011; Dermauw *et al.*, 2013a; Dermauw *et al.*,  
23  
24 856 2013b; Dermauw and Van Leeuwen, 2014; Tay *et al.*, 2015; Bretschneider *et al.*, 2016).  
25  
26 857 However, direct evidence for a role of ABCs in resistance to plant allelochemicals is  
27  
28 858 scarce. In the only known example, the *CpMRP* transporter of the Chrysomelid leaf  
29  
30 859 beetle *Chrysomela populi* is involved in the sequestration of salicin, a toxic phenolic  
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32 860 glucoside found in willow and poplar leaves. *CpMRP* shuttles salicin from the  
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34 861 hemolymph into specialized defensive glands, which play a role against predators.  
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36 862 Reduction of *CpRMP* expression by RNAi abolished salicin excretion and rendered leaf  
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38 863 beetles defenseless (Strauss *et al.*, 2013).  
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#### 46 **Escaping detection or anticipating defenses**

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48 866 As a striking example of adaptation, larvae of the velvetbean caterpillar produce a  
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50 867 modified form of the cyclic peptide inceptin, a HAMP found in OS of the generalist Fall  
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52 868 armyworm (see section on HAMPs). Through yet unknown modification of a gut  
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54 869 protease, digestion of chloroplastic ATP synthase of the host plant cowpea generates a  
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4 870 peptide lacking the C-terminal amino acid, *Vu-In<sup>-A</sup>* (Schmelz *et al.*, 2012). Velvetbean  
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6 871 OS induced a significantly weaker ET production and volatile emission in cowpea  
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8 872 leaves, suggesting that the truncated inceptin evades recognition by a (unknown) plant  
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10 873 receptor (Schmelz *et al.*, 2012).  
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12  
13 874 A lag phase between ingestion/perception of plant toxins and transcriptional  
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15 875 activation of detoxification genes may be detrimental to optimal larval development. An  
16  
17 876 interesting study reported that treatment of *H. zea* larvae with the plant defense signals  
18  
19 877 JA and SA induced the expression of four CYP450s that metabolize furanocoumarins  
20  
21 878 and other toxins (Li *et al.*, 2002b). This induction was shown to provide an advantage to  
22  
23 879 larvae, which performed better on furanocoumarin-containing plants or diets.  
24  
25 880 "Eavesdropping" on defense signals seems thus an effective way of anticipating the  
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27 881 production of defense compounds but the generality of this phenomenon amongst  
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29 882 arthropods has yet to be established.  
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### 34 35 884 **Coevolution**

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37 885 The seminal publication by Ehrlich and Raven (1964) stressed the importance of  
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39 886 reciprocal relationship between butterflies and plant hosts in shaping the evolution and  
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41 887 diversification of each group, and by extension supported the notion that plant-enemy  
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43 888 interactions are responsible for much of global biological diversity. This has stimulated  
44  
45 889 decades of research to test these predictions and provide experimental data for such  
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47 890 scenario. Evidence is however scarce, because evolution is such a slow process that it is  
48  
49 891 difficult to catch it in action and because several environmental, biogeographical and  
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51 892 ecological factors may confound interpretations (reviewed in Futuyma and Agrawal,  
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53 893 2009). For example, removal of herbivore pressure in replicate fields of the evening  
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4 894 primrose *Oenothera biennis* caused a rapid evolutionary divergence (Agrawal *et al.*,  
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6 895 2012). Phylogenetic reconstructions of plant and arthropods lineages have however  
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8 896 generated useful hints that evolution of defense chemistry responds to herbivore  
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10 897 pressure and that counteradaptation drives arthropod diversity. A convincing example is  
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12 898 the stepwise evolution of GS complexity in Brassicales, mirrored with the radiation of  
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14 899 Pierinae butterfly species (Wheat *et al.*, 2007; Edger *et al.*, 2015). A robust  
15  
16 900 phylogenetic analysis of 14 families from the Brassicales revealed that this order  
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18 901 originated ~90 million years ago (Ma) and that plants only synthesized aromatic Phe-  
19  
20 902 GS. Indole-GS appeared after a whole-genome duplication (WGD) ~77 Ma, followed  
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22 903 by the occurrence and diversification of aliphatic-GS-containing families ~60 Ma.  
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24 904 Finally, after a second WGD, Brassicaceae appeared ~30 Ma and coincided with the  
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26 905 greatest GS and species diversification (Edger *et al.*, 2015). Pierinae colonized  
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28 906 Brassicales 68 Ma, approximately 10 million years after indole-GS appearance, and  
29  
30 907 radiated through the acquisition of NSPs. Again, shortly after occurrence of  
31  
32 908 Brassicaceae, new lineages of Pierinae evolved and diversified. Strikingly, independent  
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34 909 nitrile-specifier gene lineages could be associated with independent colonization of  
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36 910 Brassicaceae by two Pierinae lineages (Edger *et al.*, 2015).

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41 911 Comparative phylogenies of *Bursera* sp. and *Blepharida* sp. indicated that both  
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43 912 groups diversified synchronously, showing that plant lineages possessing the defensive  
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45 913 trait (resin under high pressure) coevolved with beetles lineages equipped with vein  
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47 914 severing ability (Becerra, 2003). In addition, escalation of species and chemical  
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49 915 diversity through time was observed in *Bursera*, providing support for herbivore-plant  
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51 916 coevolution theory (Becerra *et al.*, 2009). Similarly, diversification of milkweeds was  
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53 917 correlated with increased phenolic production (Agrawal *et al.*, 2009). For evolution of  
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4 918 herbivores, a phylogenetic study of the leaf miner fly *Phytomyza* provided evidence that  
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6 919 repeated shifts to host plants with different chemistry during 40 million years of  
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8 920 evolution led to elevated diversification (Winkler *et al.*, 2009). Remarkably, beak length  
9  
10 921 of the seed-eater soapberry bug *Jadera haemotoloma* has adapted within 40-150  
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12 922 generations after shifting to novel host species of Sapindaceae from North America  
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14 923 (Carroll, 1992).

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16  
17 924 Although adaptation of specialist arthropods to plant defenses is well  
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19 925 documented, evidence for plant resistance to specialists is less frequent. Interestingly,  
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21 926 some Brassicaceae contain other defense compounds besides GS, including alkaloids  
22  
23 927 (camalexin in *Arabidopsis* and cochlearine in *Cochlera* sp.) and the steroid cucurbitacin  
24  
25 928 in *Iberis amara* (Tsuji *et al.*, 1992; Sachdev-Gupta *et al.*, 1993; Brock *et al.*, 2006).  
26  
27 929 Cucurbitacin has some antifeedant activity on *P. rapae* (Sachdev-Gupta *et al.*, 1993)  
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29 930 and a study on natural variation in resistance to *P. brassicae* in *Arabidopsis* accessions  
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31 931 identified QTLs that are not linked to GS biosynthesis (Pfalz *et al.*, 2007). In a beautiful  
32  
33 932 example of coevolution, some cyanogenic glycoside-containing species of *Passiflora*  
34  
35 933 have counteradapted to the specialist *Heliconius* butterfly by the development of egg  
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37 934 mimics that repel oviposition (Williams and Gilbert, 1981). Egg mimics have also  
38  
39 935 evolved in the GS-containing crucifer *Streptanthus breweri* to fend off the specialist  
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41 936 *Pieris sisymbrii* (Shapiro, 1981). Many plants face the problem of attracting pollinators  
42  
43 937 without being a target for herbivory. *N. attenuata* is a night-flowering tobacco whose  
44  
45 938 flowers emit benzyl acetone that attracts pollinators, including the adapted herbivore  
46  
47 939 moth *M. sexta*. In response to *M. sexta* feeding, *N. attenuata* shows a striking change of  
48  
49 940 phenology by generating flowers that produce low levels of benzyl acetone and open  
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51 941 during the day, attracting hummingbird as novel pollinators (Kessler *et al.*, 2010).  
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4 9425  
6 943 **Open questions**

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8 944 Although many assumptions still rely on correlative evidence, progress has been made  
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10 945 in the understanding of evolutionary forces that drive escalation of chemical defenses  
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12 946 and arthropod adaptations to these chemicals. A recurring issue is to know the exact  
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14 947 chain of events and causative agents that result in apparent defense-adaptation-  
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16 948 counterdefense scenarios. Improved and additional plant/arthropod phylogenies are  
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18 949 needed as well as experimental evolution experiments.  
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24 951 **PLANT-ARTHROPOD COLLABORATIONS**

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26 952 Interactions between plants and arthropods are not always antagonistic. Insects pollinate  
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28 953 about two-third of flowering plant species. In reward of nutrient-rich pollen and nectar,  
29  
30 954 insects offer this service as a mutualistic engagement (Schoonhoven *et al.*, 2005). Seed  
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32 955 dispersal by arthropods, mainly ants, helps colonization while providing food for the  
33  
34 956 carrier (Howe and Smallwood, 1982). However, the most sophisticated collaboration is  
35  
36 957 the association of plants with beneficial arthropods to fend off herbivores. Plants have  
37  
38 958 evolved exquisite ways to "cry for help", which rely on offering refuge or food for  
39  
40 959 guarding predatory mites and ants, or on emitting complex volatiles to attract carnivores  
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42 960 (reviewed in Romero and Benson, 2005; Heil, 2008; Stam *et al.*, 2014; Heil, 2015;  
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44 961 Hilker and Fatouros, 2015).

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48 962 Leaf domatia are cavities or hair tufts on the lower surface of leaves and create  
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50 963 shelter for mites that are predators of phytophagous mites. Several studies have proven  
51  
52 964 that these structures benefit plants by decreasing herbivore pressure (reviewed in  
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54 965 Romero and Benson, 2005). Extrafloral nectar, food bodies on leaflets and hollow  
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4 966 thorns are attributes found in certain acacia trees that host ants, providing nutrition and  
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6 967 housing (Heil, 2008). This intimate association is maintained because ants constantly  
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8 968 patrol trees and aggressively remove unwanted herbivores. Extrafloral nectar production  
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10 969 is induced in response to herbivory, showing that plants keep control of this energy  
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12 970 demanding process. In an elegant and long-term experiment in an African savanna,  
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14 971 removing large herbivores for 10 years reduced nectar production and thorns by *Acacia*  
15  
16 972 *drepanolobium*, and increased antagonistic behavior of the ant mutualist *Crematogaster*  
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18 973 *mimosae*, which ultimately led to a decreased tree defense and growth (Palmer *et al.*,  
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20 974 2008).

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24 975       Upon herbivory and detection of HAMPs in OS, plants emit a complex blend of  
25  
26 976 volatiles that attract parasitic wasps or predators (reviewed in Dicke and Loon, 2000;  
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28 977 Stam *et al.*, 2014). Volatiles generally consist of terpenes,  
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30 978 phenylpropanoids/benzenoids, and fatty acid derivatives (green leaf volatiles) (Pare and  
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32 979 (Tumlinson, 1999; Dudareva *et al.*, 2004). This tritrophic interaction is an efficient  
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34 980 defense mechanism since carnivores either kill their prey directly or parasitize them,  
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36 981 therefore dramatically reduce feeding activity (Dicke and Loon, 2000). Qualitative and  
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38 982 quantitative differences in volatile emission explain the specific attraction of parasitoids  
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40 983 to their host. For instance, the specialist parasitic wasp *Cardiochiles nigriceps* was  
41  
42 984 significantly more attracted by the volatile blend produced by tobacco and cotton plants  
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44 985 infested with his host *H. virescens* than by volatiles produced by plants infested with *H.*  
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46 986 *zea* (De Moraes *et al.*, 1998). Similarly, oviposition triggers volatile release and  
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48 987 attraction of egg parasitoids, illustrating the specificity of the emitted blend (Hilker and  
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50 988 Fatouros, 2015). Strikingly, indirect defense was also discovered belowground. Upon  
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52 989 feeding by the rootworm *Diabrotica virgifera virgifera*, maize roots emit the  
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4 990 sesquiterpene (*E*)- $\beta$ -caryophyllene. However, this response not attract arthropods but  
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6 991 entomopathogenic nematodes (Fig.1) (Rasmann *et al.*, 2005).  
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### 10 993 **Open questions**

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12 994 One of the fascinating yet poorly studied question about plant-arthropod mutualism is  
13  
14 995 how indirect defense evolved. Evidence that plants benefit from attraction of parasitoids  
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16 996 suggests that genes involved in volatile biosynthesis are under positive selection.  
17  
18 997 Comparative genomic analyses of biosynthesis pathways across plant taxa and their  
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20 998 correlation with associated parasitoids will be necessary to have a better understanding  
21  
22 999 of how indirect defense appeared and was maintained. Whether roots attract beneficial  
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24 1000 arthropods is another unsolved question. On the parasitoid side, advent of more  
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26 1001 sequenced genomes may offer a resource for identifying genes important for volatile  
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28 1002 recognition and association with the host. Finally, the contribution of parasitoids to  
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30 1003 plant-arthropod coevolution is also a question that deserves more research.  
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### 36 1005 **CONCLUSIONS AND OUTLOOK**

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38 1006 Decades of research on plant-arthropod interactions have revealed that these organisms  
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40 1007 are engaged in a battle for survival that rely on sophisticated mechanisms of perception,  
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42 1008 signaling and defense activation on the plant side, and on effective suppression of  
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44 1009 defenses and chemical/behavioral adaptations on the arthropod side. Although it appears  
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46 1010 that nature has reached an equilibrium, since both plants and arthropods are abundant,  
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48 1011 evidence has accumulated that there is constant innovation to generate novel plant  
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50 1012 defenses strategies and that this exerts a selection pressure on arthropods to evolve  
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4 1013 novel effectors or detoxification solutions. This arms race has thus no winner and the  
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6 1014 coevolution process may continue for millions of years.  
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9 1015 Although substantial progress has been made in identifying genes and molecules  
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11 1016 involved in the molecular dialogue between plants and arthropods, as well as some  
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13 1017 evolutionary processes that underlie their coevolution, we have identified open  
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15 1018 questions that deserve further research. In addition, root herbivory (Johnson and  
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17 1019 Rasmann, 2015), insect galls (Stone, 2003), the role of leaf and arthropod microbiomes  
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19 1020 (Pineda *et al.*, 2010; Sugio *et al.*, 2015), and the outcome of multiple biotic interactions  
20  
21 1021 (Pieterse and Dicke, 2007) are clearly understudied. In times when stability of  
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23 1022 ecosystems, emergence of invasive species and sustainable control of insect pests in  
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25 1023 agriculture provide challenges to a growing human population, future research on plant-  
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27 1024 arthropod interactions may contribute viable solutions to these problems.  
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### 47 1033 **AUTHOR CONTRIBUTION**

48  
49  
50 1034 ES and PR wrote the paper. OH provided feedback on the text and designed the figures.  
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### 54 1036 **CONFLICT OF INTEREST**

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1037 The authors declare that they have no conflict of interest.

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## TABLES

**Table 1.** HAMPs and effectors from arthropods

Name	Origin	Response	Reference
<b>HAMPs</b>			
FAC (volicitin)	<i>Spodoptera exigua</i> OS	Volatiles attract parasitoids	Alborn <i>et al.</i> , 1997
2-HOT	<i>Manduca sexta</i> OS	Volatiles attract parasitoids	Gaquereel <i>et al.</i> , 2009
Caeliferins	<i>Schistocera americana</i> OS	Volatiles attract parasitoids	Alborn <i>et al.</i> , 2007
$\beta$ -glucosidase	<i>Pieris brassicae</i> OS	Volatiles attract parasitoids	Mattiacci <i>et al.</i> , 1995
Inceptin	<i>Spodoptera frugiperda</i> OS	Volatile and defense gene induction	Schmelz <i>et al.</i> , 2006
Lipase	<i>Schistocera gregaria</i> OS	Release of esterified OPDA	Schäfer <i>et al.</i> , 2011
$\beta$ -galactofuranose polysaccharide	<i>Spodoptera littoralis</i> OS	Plasma membrane depolarization	Bricchi <i>et al.</i> , 2013
Bacterial porin-like	<i>Spodoptera littoralis</i> OS	Channel-forming activity	Guo <i>et al.</i> , 2013
Protein (<10 kDa)	<i>Myzus persicae</i> saliva	Defense gene induction	De Vos and Jander, 2009
Mp56, Mp57, Mp58	<i>Myzus persicae</i> saliva	Lower aphid fecundity	Elzinga <i>et al.</i> , 2014
Bacterial GroEL	<i>Macrosiphum euphorbiae</i> OS	Lower aphid fecundity	Chaudhary <i>et al.</i> , 2014
Phosphatidylcholine	<i>Sogatella furcifera</i> female	Production of ovicidal compound	Yang <i>et al.</i> , 2014
12 kDa protein	<i>Diprion pini</i> oviduct secretion	Egg parasitoids attraction	Hilker <i>et al.</i> , 2005
Benzyl cyanide	<i>Pieris brassicae</i> ARG	Arrest of egg parasitoids	Fatouros <i>et al.</i> , 2008
Indole	<i>Pieris rapae</i> ARG	Arrest of egg parasitoids	Fatouros <i>et al.</i> , 2009
Lipid extract	<i>Pieris brassicae</i> eggs	Defense gene induction, necrosis	Bruessow <i>et al.</i> , 2010
Bruchin	<i>Callosobruchus maculatus</i> female	Neoplasm formation under eggs	Doss <i>et al.</i> , 2000
<b>Effectors</b>			
Modified inceptin	<i>Anticarsia gemmatilis</i> OS	Plant defense suppression	Schmelz <i>et al.</i> , 2012
Bacteria (flagellin)	<i>Leptinotarsa decemlineata</i> OS	Inhibition of the JA pathway	Chung <i>et al.</i> , 2013
Apyrase	<i>Helicoverpa zea</i> saliva	Lower defense gene expression	Wu <i>et al.</i> , 2012
Glucose oxidase	<i>Helicoverpa zea</i> saliva	Lower nicotine production	Musser <i>et al.</i> , 2002
Unknown (<3 kDa)	<i>Spodoptera littoralis</i> , <i>Pieris rapae</i> OS	Reduced defense gene expression	Consales <i>et al.</i> , 2012
Unknown (10-30 kDa)	<i>Leptinotarsa decemlineata</i> OS	Reduced defense gene expression	Lawrence <i>et al.</i> , 2007
Unknown	<i>Manduca sexta</i> OS	Reduced gene expression	Schittko <i>et al.</i> , 2001
FACs	<i>Manduca sexta</i> OS	Reduced volatile emission	Gaquereel <i>et al.</i> , 2009
Chitinases	<i>Spodoptera exigua</i> frass	Increased larval performance	Ray <i>et al.</i> , 2016
MIF (cytokine)	<i>Acyrtosiphon pisum</i> saliva	Plant defense suppression	Naessens <i>et al.</i> , 2015
Ca <sup>++</sup> -binding protein	<i>Megoura viciae</i> saliva	Inhibition of sieve tube plugging	Will <i>et al.</i> , 2007
Me23, Me10 (unknown)	<i>Megoura euphorbiae</i> saliva	Higher aphid fecundity	Atamian <i>et al.</i> , 2013
Mp1 (unknown)	<i>Myzus persicae</i> saliva	Higher aphid fecundity, targets VSP52	Rodriguez <i>et al.</i> , 2017
Mp10 (CSP)	<i>Myzus persicae</i> saliva	Suppress ROS production	Bos <i>et al.</i> , 2010
MpC002 (unknown)	<i>Acyrtosiphon pisum</i> saliva	Higher aphid performance	Mutti <i>et al.</i> , 2008
Mp55 (unknown)	<i>Myzus persicae</i> saliva	Higher aphid fecundity	Elzinga <i>et al.</i> , 2014
Tu28, Tu84 (unknown)	<i>Tetranychus urticae</i> heads	Higher mite performance	Villarroel <i>et al.</i> , 2016
F-box-LRR proteins	<i>Mayetiola destructor</i> saliva	Induce ETI in HF-resistant wheat	Zhao <i>et al.</i> , 2015
Lipid extract	<i>Pieris brassicae</i> eggs	Inhibition of the JA pathway	Bruessow <i>et al.</i> , 2010

ARG, accessory reproductive gland secretion; CSP, chemosensory protein; ETI, effector-triggered immunity; FAC, fatty acid-amino acid conjugate; GmSubPep, Glycine max subtilase peptide; GPX, glutathione peroxidase; GroEL, chaperone; HAMP, herbivore-associated molecular pattern; HF, Hessian fly; 2-HOT, 2-hydroxy-octadecatrienic acid; MIF, migration inhibitory factor; OS, oral secretions; SAR, systemic acquired resistance; VSP52, Vacuolar Protein Sorting Associated Protein52.

**Table 2.** Plant-derived metabolites with direct insecticidal activity

Metabolite	Plant species	Arthropod species	Mode of action (mutant lines)	Reference
Glucosinolates	Brassicaceae	<i>Mamestra brassicae</i> , <i>Trichoplusia ni</i> , <i>Manduca sexta</i> , <i>Spodoptera littoralis</i>	Myrosinase-dependent hydrolysis generates nitriles, thiocyanates, and isothiocyanates (ITC) that react with biological nucleophiles and modify proteins and nucleic acids. ( <i>tgg1/tgg2</i> , <i>quadGS</i> , <i>myc234</i> )	Beekwilder et al., 2008 Barth and Jander, 2006 Brown and Hampton, 2011 Schweizer et al., 2013b
Azadirachtin <sup>1</sup>	<i>Azadirachta indica</i>	<i>Spodoptera littoralis</i> , <i>Spodoptera frugiperda</i> , <i>Schistocerca gregaria</i>	Disruption of the endocrine system and inhibition of cell division.	Mordue Luntz et al., 1998
Benzoxazinoids <sup>7</sup>	<i>Zea mays</i>	<i>Rhopalosiphum maidis</i>	Unknown ( <i>Bx13NIL-Oh43</i> )	Handrick et al., 2016
Benzyl benzoate	<i>Oryza sativa</i>	<i>Sogatella furcifera</i>	Egg-killing substance.	Seino et al., 1996
Calcium Oxalate	<i>Medicago truncatula</i>	<i>Spodoptera exigua</i>	Physical abrasion of mandibles. Ingested calcium oxalate interferes with larval development ( <i>cod5</i> , <i>cod6</i> )	Korth et al., 2006.
Camalexin <sup>3</sup>	<i>Arabidopsis thaliana</i>	<i>Myzus persicae</i>	Unknown ( <i>pad3</i> , <i>cyp79b2/cyp79b3</i> )	Kettles et al., 2013
GABA <sup>2</sup>	All plant species	<i>Choristoneura rosaceana</i> , <i>Meloidogyne hapla</i> , <i>Heliothis virescens</i>	Suppression of neurotransmission	Hosie et al., 1997 Bown et al., 2002, 2006
Hydrogen cyanide (HCN)	<i>Trifolium repens</i> , <i>Lotus corniculatus</i> <i>Hypera postica</i>	<i>Capnodis tenebrionis</i> , <i>Heterobostrychus brunneus</i> ,	Inhibition of mitochondrial respiration	Vetter, 2000
Kaempferol <sup>4</sup>	<i>Arabidopsis thaliana</i>	<i>Pieris brassicae</i> <i>Nicotiana tabacum</i>	Unknown ( <i>oxMYB75</i> )	Onkokesung et al., 2014
Kauralexins <sup>1</sup>	<i>Zea mays</i>	<i>Ostrinia nubilalis</i>	Unknown	Schmelz et al., 2011
Lactone taraxinic acid <sup>1</sup>	<i>Taraxacum officinale</i>	<i>Melolontha melolontha</i>	Unknown ( <i>ToGAS1</i> )	Huber et al., 2016.
L-Canavanine <sup>2</sup>	Fabaceae	<i>Manduca sexta</i>	Integration of L-canavanine into proteins	Rosenthal et al., 1976 Rosenthal, 2001
Nicotine <sup>5</sup>	<i>Nicotiana tabacum</i> <i>Nicotiana attenuata</i>	<i>Spodoptera exigua</i> , <i>Trimerotropis spp.</i> , <i>Diabrotica undecimpunctata</i>	Agonist for acetylcholine receptors, disruption of nervous system ( <i>IRpmt</i> , <i>nic1</i> , <i>nic2</i> , <i>nic1/nic2</i> )	Gepner et al., 1978 Steppuhn et al., 2004 Katoh et al., 2005
Pyrethrin <sup>1</sup>	<i>Chrysanthemum cinerariifolium</i>	Tetranychidae, Pseudococcidae, Auchenorrhyncha, Coleoptera, Caelifera, Aleyrodidae	Inactivation of sodium channels along nerve cells	Casida et al., 1983
Rotenone <sup>4</sup>	<i>Derris eliptica</i> , <i>Pachyrrhizus erosus</i>	Brought spectrum insecticide	Inhibition of mitochondrial respiration	Dayan et al., 2009
Scopoletin <sup>6</sup>	<i>Artemisia annua</i>	<i>Spilartia obliqua</i>	Unknown	Tripathi et al., 2011
Teucrein <sup>1</sup>	<i>Teucrium marum</i>	<i>Monomorium pharaonis</i> , <i>Phormia regina</i> , <i>Periplaneta americana</i>	Unknown	Eisner et al., 2000

<sup>1</sup> Terpenoid, <sup>2</sup> Amino acid, <sup>3</sup> Indole, <sup>4</sup> Flavonoid, <sup>5</sup> Alkaloid, <sup>6</sup> Coumarin, <sup>7</sup> Hydroxamic acid,

**Table 3.** Plant-derived proteins with direct insecticidal activity

Protein	Plant species	Arthropod species	Mode of action (mutant lines )	Reference
$\alpha$ -Amylase inhibitors	Fabaceae, Poaceae, Caryophyllales	Coleoptera, Hemiptera, Blattidae	Inhibition of digestive $\alpha$ -amylases	Franco et al., 2002
Acrelins	<i>Phaseolus vulgaris</i>	<i>Zabrotes subfasciatus</i>	Binding to complex glycans disrupts midgut epithelial structure	Fabre et al., 1998
Canatoxins	<i>Canavalia ensiformis</i>	<i>Callosobruchus chinensis</i> , <i>Rhodnius prolixus</i> , <i>Nezara viridula</i> , <i>Dysdercus peruvianus</i>	Interfere with serotonin processes and disrupt fluid transport across anterior midgut epithelium	Carlini et al., 1997 Stanisçuaski and Carlini, 2012
Cyclotides	<i>Oldenlandia affinis</i> Rubiaceae, Violaceae	<i>Helicoverpa punctigera</i> , <i>Helicoverpa armigera</i>	Disrupt larval midgut membranes	Jennings et al., 2001 Barbeta et al., 2008
Cysteine protease	<i>Zea mays</i> L.	<i>Spodoptera frugiperda</i>	Disrupts caterpillar peritrophic matrix	Pechan et al., 2002
Cysteine protease inhibitors	<i>Oryza sativa</i> <i>Glycine max</i> <i>Arabidopsis thaliana</i>	Coleoptera, Hemiptera	Inhibition of digestive gut proteases	Kuroda et al., 1996 Koiwa et al., 1998 Delledonne et al., 2001
Lectins	Leguminosae	Coleoptera, Lepidoptera, Homoptera	Binding to glycosyl groups attached to digestive tract	Vandenborre et al., 2011
Ribosome-inactivating proteins (RIPs)	Fabaceae, Asparagaceae, Passifloraceae	<i>Anthomonus grandis</i> <i>Callosobruchus maculatus</i> <i>Anthomonus grandis</i>	Inactivation of 60S ribosomal subunit	Olsnes et al., 1974 Carlini and Grossi-de-Sá, 2002
Serine protease inhibitors	Solanaceae	<i>Spodoptera exigua</i>	Inhibition of digestive gut proteases	Green and Ryan, 1972 Hartl et al., 2010
Threonine deaminase	<i>Solanum lycopersicum</i>	<i>Spodoptera exigua</i>	Deprivation of essential Thr (TDAs15, TDAs7)	Gonzales-Vigil et al., 2011
Vegetative Storage Protein 2 (VSP2)	<i>Arabidopsis thaliana</i>	<i>Diabrotica undecimpunctata howardi</i> <i>Callosobruchus maculatus</i> , <i>Drosophila melanogaster</i>	Insecticidal activity correlated with acid phosphatase activity ( <i>vsp2</i> )	Liu et al., 2005

**Table 4.** Coevolution between plants and arthropods

Plant defense	Arthropod adaptation	Plant counterdefense	Reference
Cardenolides <i>Asclepias syriaca</i>	Leaf vein cutting <i>Danaus gilippus</i> and others		Dussourd and Eisner, 1987
High-pressure resin <i>Bursera sp.</i>	Leaf vein severing <i>Blepharida sp.</i>		Becerra, 2003
JA-dependent defenses Arabidopsis	Avoiding induced tissue <i>Helicoverpa armigera</i>		Perkins <i>et al.</i> , 2013
Trichomes <i>Solanum hirtum</i>	Silk threads over spines <i>Mechanitis isthmia</i>		Rathcke and Poole, 1975
Attraction of parasitoids <i>Lolium multiflorum</i>	Host shift, escape behavior (?) <i>Listronotus bonariensis</i>		Tomasetto <i>et al.</i> , 2017
Attraction of parasitoids <i>Physalis angulata</i>	Eating fruit, no volicitin in OS <i>Heliothis subflexa</i>		De Moraes and Mescher, 2004
Cardenolides Apocynaceae	ATPase N122H substitution <i>Danaus plexippus</i> and others		Dobler <i>et al.</i> , 2012
Protease inhibitors (PI) potato	PI-insensitive protease <i>Helicoverpa zea</i>		Bayés <i>et al.</i> , 2005
L-canavanine (Arg analog) <i>Dioclea megacarpa</i>	Discriminating tRNA synthetase <i>Caryedes brasiliensis</i>		Rosenthal <i>et al.</i> , 1976
Cyanogenic glycoside <i>Passiflora sp.</i>	Detoxification <i>Heliconius cydno</i>	Egg mimicry <i>Passiflora cyanea</i>	Williams and Gilbert, 1981
Cyanogenic glycoside <i>Phaseolus lunatus</i>	Bacterial $\beta$ -cyanoalanine synthase <i>Tetranychus urticae</i>		Wybouw <i>et al.</i> , 2014
Alkaloid <i>Nicotiana attenuata</i>	Nicotine excretion and metabolism <i>Manduca sexta</i>	Altered flower phenology <i>Nicotiana attenuata</i>	Kessler <i>et al.</i> , 2010
Glucosinolates Brassicales	Nitrile-specifier proteins <i>Pieris rapae</i> and other Pierinae	GS diversification Brassicales	Edger <i>et al.</i> , 2015
Glucosinolates Brassicales	Nitrile-specifier protein (?) <i>Pieris sysimbrii</i>	Egg mimicry <i>Streptanthus brewerii</i>	Shapiro, 1981
Glucosinolates Arabidopsis	Induction of detoxification genes <i>Heliothis virescens</i>		Schweizer <i>et al.</i> , 2017
Furanocoumarins Apiaceae	Detoxification by CYP6B1 <i>Papilio polyxenes</i>		Hung <i>et al.</i> , 1997
HAMP detection (inceptin) <i>Vigna unguiculata</i>	Inceptin modification <i>Anticarsia gemmatalis</i>		Schmelz <i>et al.</i> , 2012
Defense signaling <i>Apium graveolens</i>	Induction of CYP450s by JA, SA <i>Helicoverpa zea</i>		Li <i>et al.</i> , 2002b

Arg, arginine; GS, glucosinolates; HAMP, herbivore-associated molecular pattern. Question marks indicate no experimental evidence for the adaptation.

**FIGURE LEGENDS**

**Figure 1.** Overview of plant responses to herbivory.

Upon perception of herbivorous larvae or eggs, plants activate direct defenses (synthesis of toxic metabolites and proteins, localized cell death (HR)) and indirect defenses (emission of volatiles to attract larval or egg parasitoids and root nematodes). These responses occur both above- and belowground. HIPVs, herbivore-induced plant volatiles; EIPVs, egg-induced plant volatiles; HR, hypersensitive-response.

**Figure 2.** Signaling of plant responses to herbivory in Arabidopsis.

Current model for signaling steps activated by feeding larvae (a) and oviposition (b). (a) Upon recognition of HAMPs from larval oral secretions by yet unknown receptors, a signal transduction cascade generates the bioactive hormone JA-Ile. JA-Ile induces the interaction of SCF<sup>COI1</sup> with JAZs transcriptional repressors, which are further ubiquitinated and degraded. MYC2,3,4 can then regulate the transcription of numerous genes, including glucosinolate biosynthesis genes. (b) Egg-derived HAMPs are perceived by yet unknown receptors, which trigger both reactive oxygen species accumulation and activation of SA-biosynthesis enzyme ICS1 through lipase-related EDS1 and PAD4. SA accumulation provokes a redox change that leads to monomerization of NPR1, entry in the nucleus and activation of transcription factors. Expression of *PR-1* is associated with a HR-like response that culminates in localized cell death, presumed to inhibit egg development. In addition, local and distal accumulation of Pip is mediated by the biosynthesis enzyme ALD1 and triggers inhibition of infection by biotroph pathogens in local and distal tissues through SAR. There is evidence for a general conservation of both models in other plant species.



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4 HAMPs, herbivore-associated molecular patterns; RLK, receptor-like kinase; LOX,  
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6 lipoxygenases; AOS, allene oxide synthase; AOC, allene oxide cyclase; OPDA, 12-oxo-  
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8 oxophytodienoic acid; OPR3, OPDA-reductase 3;  $\square$ -ox.,  $\square$ -oxidation; JA, jasmonic  
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10 acid; JAR1, Jasmonate-resistant 1; JA-Ile, jasmonate-isoleucine; SCF<sup>CO11</sup>, SCF complex  
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12 with F-box Coronatine-insensitive 1 receptor for JA-Ile; JAZs, Jasmonate-ZIM domain  
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14 proteins; MYC2,3,4, MYC2, MYC3, MYC4 bHLH transcription factors; EDS1,  
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16 Enhanced-disease susceptibility 1; PAD4, Phytoalexin-deficient 4; ICS1, Isochorismate  
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18 synthase 1; SA, salicylic acid; NPR1, Non-expressor of pathogenesis-related genes1,  
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20 TFs, transcription factors; HR, hypersensitive response; *PR-1*, pathogenesis-related 1;  
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24 Pip, pipecolic acid; SAR, systemic acquired resistance.  
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31 **Figure 3.** Systemic responses to herbivory.

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33 (a) Current model of long-distance signaling in response to herbivory. Both GLR-  
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35 dependent electrical signaling and JA/JA-Ile movement have been shown to trigger JA-  
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37 dependent defenses in systemic leaves in response to local feeding. (b) Oviposition  
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39 triggers release of HIPVs in local and systemic leaves from several plant species,  
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41 although the nature of the systemic signal is unknown. ALD1-dependent Pip  
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43 accumulation in local and systemic leaves triggers a SAR against plant pathogens.  
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45 Whether Pip is the mobile SAR signal has not been demonstrated. JA, jasmonic acid;  
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47 JA-Ile, JA-isoleucine; GLR, Glutamate receptor-like; ALD1, AGD2-like defense  
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49 response protein 1; Pip, pipecolic acid; SAR, systemic acquired resistance; HIPVs,  
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51 herbivore-induced plant volatiles.  
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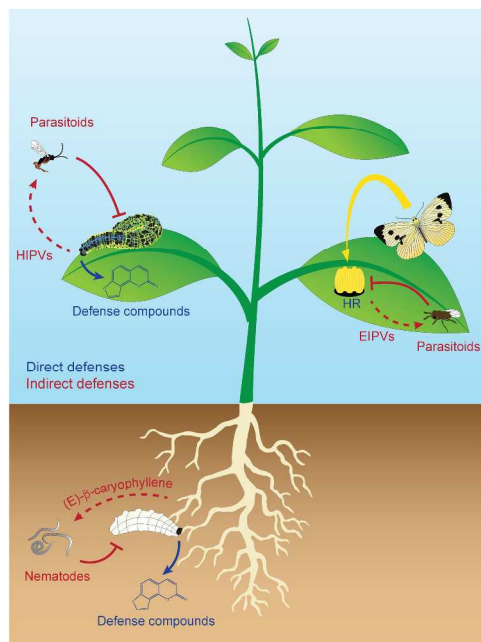


Figure 1

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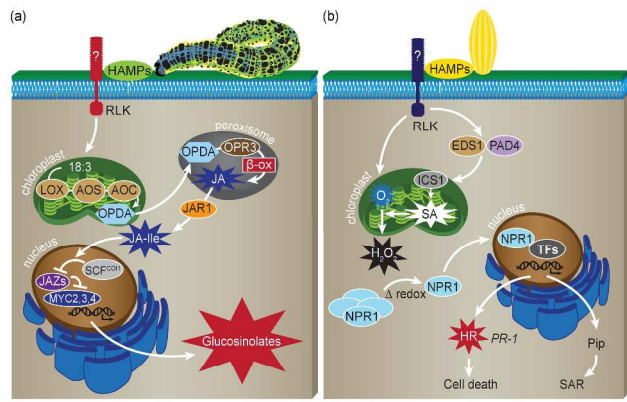


Figure 2

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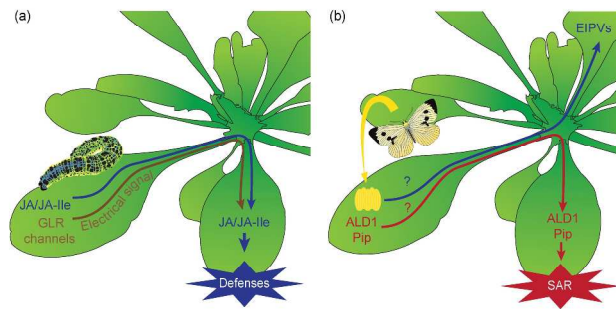


Figure 3

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