Annual Review of Phytopathology

Recognition and Response in Plant–Nematode Interactions

Shahid Siddique,[1] Alison Coomer,[2] Thomas Baum,[3] and Valerie Moroz Williamson[2]

[1]Department of Entomology and Nematology, University of California, Davis, California, USA; email: ssiddique@ucdavis.edu

[2]Department of Plant Pathology, University of California, Davis, California, USA

[3]Department of Plant Pathology and Microbiology, Iowa State University, Ames, Iowa, USA

Annu. Rev. Phytopathol. 2022. 60:143–62

First published as a Review in Advance on April 18, 2022

The *Annual Review of Phytopathology* is online at phyto.annualreviews.org

https://doi.org/10.1146/annurev-phyto-020620-102355

Keywords

plant-parasitic nematodes, nematode behavior, pattern-triggered immunity, root exudates, effectors, nematode attractant

Abstract

Plant-parasitic nematodes spend much of their lives inside or in contact with host tissue, and molecular interactions constantly occur and shape the outcome of parasitism. Eggs of these parasites generally hatch in the soil, and the juveniles must locate and infect an appropriate host before their stored energy is exhausted. Components of host exudate are evaluated by the nematode and direct its migration to its infection site. Host plants recognize approaching nematodes before physical contact through molecules released by the nematodes and launch a defense response. In turn, nematodes deploy numerous mechanisms to counteract plant defenses. This review focuses on these early stages of the interaction between plants and nematodes. We discuss how nematodes perceive and find suitable hosts, how plants perceive and mount a defense response against the approaching parasites, and how nematodes fight back against host defenses.

1. INTRODUCTION

Plant-parasitic nematodes (PPNs) are microscopic, soil-dwelling organisms that parasitize numerous plant species globally. PPNs have been estimated to cause $80 billion in worldwide crop damage per year, but the true figure is likely even higher (56, 81). There are more than 4,000 PPN species, and different species of nematodes feed on different plant tissues, including flowers, stems, leaves, and roots (26). Based on their feeding habits, PPNs can be broadly categorized as ectoparasitic or endoparasitic. Ectoparasitic nematodes spend their entire life cycles outside of the plant. By contrast, endoparasitic nematodes enter their hosts (either fully or partially) and feed on and reproduce within the plant tissue. Nearly all PPNs are obligate parasites that feed on the cytoplasm of living plant tissue (32).

All PPNs possess a hollow, protrusible spear known as a stylet that serves multiple purposes. The stylet can be used to probe and penetrate the plant cell wall and to deliver secretions containing enzymes and other effectors that induce cell wall degradation, suppress plant immune responses, and otherwise facilitate successful parasitism. Nematodes also utilize their stylets to withdraw nutrients from plant cells during feeding. This review focuses on two groups of endoparasitic PPNs: cyst nematodes (CNs; *Heterodera* spp. and *Globodera* spp.) and root-knot nematodes (RKNs; *Meloidogyne* spp.). These two groups are generally considered to be the most economically important PPNs and have been the most extensively studied (56). RKNs and CNs are both sedentary endoparasites; that is, they induce the formation of highly modified feeding cells and lose the ability to move during development in the host. However, they are thought to have evolved this lifestyle independently (48), and there are dramatic differences in their invasion strategy and feeding site development (99).

Both CNs and RKNs hatch from eggs as second-stage juveniles (J2s). This stage is nonfeeding, and juveniles must locate and invade a host to initiate feeding before their reserves are depleted. Upon finding a site to enter the host's root, the J2s perforate the walls of epidermal cells using their stylets (119, 120). Once inside the root, CNs migrate toward the vascular tissue, moving through different tissue layers by cutting slits and entering individual cells in a sequential manner. By contrast, RKNs migrate between cells until they reach the vascular tissue (119). The movement of nematodes inside the root is facilitated by the release of a wide array of cell wall–degrading and –modifying enzymes (1, 22, 24, 53, 95, 102, 111). Upon reaching the vascular cylinder, both CNs and RKNs become immobile and induce the formation of elaborate feeding sites, which enable them to withdraw large amounts of nutrients from the plant. For both groups, the nematode develops into an adult that derives nutrition from the feeding site.

PPNs spend considerable portions of their lives in close proximity to their host plants, and as biotrophic organisms, they completely depend on their living hosts for nourishment. During the prolonged process of parasitism, the host sustains damage and yield losses. This is an ancient and highly evolved interaction, a millennia-old conflict that reveals fundamental differences between how plants and animals perceive and respond to their environments. Plants are sessile and utilize a range of defenses, including both chemical and structural components. Nematodes have evolved strategies for perceiving and responding to threats through their neurosystem to avoid, escape, or inactivate plant defense mechanisms. Here, we review what is known about the early steps in the interaction between these organisms. We summarize progress in understanding how nematodes find their hosts and how the hosts perceive nematodes precontact and at their surfaces as well as which host defense responses are elicited upon perception. Finally, we discuss effectors that nematodes produce and secrete to combat host defenses.

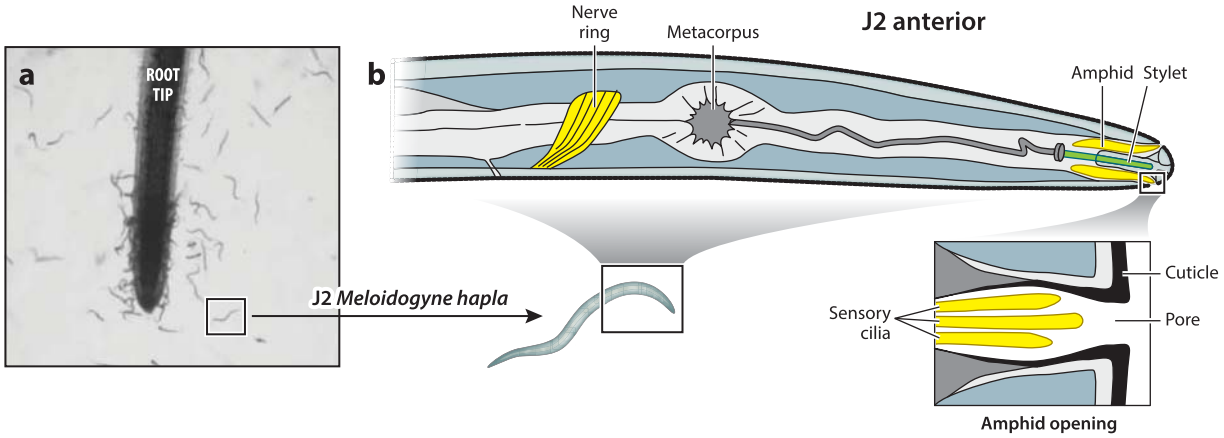

Figure 1

Perception of and responses to root exudates by plant-parasitic second-stage juveniles (J2). (*a*) Attraction of *Meloidogyne hapla* second-stage juveniles to a tomato seedling root tip in Pluronic gel. Panel *a* adapted from Wang et al. (114). (*b*) Location of amphids and nerve ring of root-knot nematode J2 and expanded view of amphid opening showing ends of sensory cilia, which are exposed to the environment via a pore in the cuticle. Components of panel *b* adapted from Eisenback (31).

2. HOW PLANT-PARASITIC NEMATODES FIND A SUITABLE HOST

In the race to establish feeding sites before starvation, root exudates serve as a primary guide for orienting nematodes to their destination (18, 19, 88). Volatile compounds are considered to direct the chemo-orientation and movement of nematodes over relatively long distances to locate roots, whereas water-soluble signals are thought to be utilized over shorter distances, possibly directing nematodes to appropriate entry sites in the root. The attraction of RKNs is strongest to regions containing growing root tips (**Figure 1*a***), and for both RKNs and CNs, infection generally occurs near root tips. Root exudates can also repel or be toxic to infective juveniles, possibly reflecting the suitability of the host and/or the plant's defense response.

In addition to directing migration, root exudates can induce other changes in nematode behavior, such as stimulating stylet thrusting, altering gene expression, and changing the cuticle surface (18, 29, 104). Plant parts other than roots have been shown to attract or immobilize infective juveniles, perhaps positioning them for infection when favorable entry sites become available. For example, Tsai et al. (108) found that RKNs are attracted to and accumulate around imbibing *Arabidopsis thaliana* seeds. Mutant analysis indicated that seeds are attractive to nematodes only when they synthesize seed-coat mucilage. However, once the radicals emerge from the seeds, nematodes seem to be attracted independent of the presence of mucilage, suggesting that different attractants direct them to root infection sites. Similarly, Hubbard et al. (52) found that root-cap exudates of several but not all plant species induced the quiescence of RKNs and that root penetration was enhanced following recovery from quiescence. Root exudates of host species also promote hatching of CN eggs, which in the absence of a host can remain dormant within cysts for many years (84, 100). The effects of root exudates on the hatching of RKNs, which generally have a much broader host range, are limited.

Here, we focus on what is known about how chemical signals are perceived and processed by nematodes. We discuss recent efforts aimed at identifying plant semiochemicals (signaling compounds) that direct nematode behaviors prior to host contact and infection.

2.1. Molecular Basis for Sensory Perception and Response in Nematodes

Nematodes have a compact and highly interconnected nervous system that has been extensively studied in the free-living species *Caenorhabditis elegans* (4). The connections among more than 300 neurons of this model organism have been mapped, facilitating the identification of microcircuits connecting sensory neuron components to interneurons and motor neurons (93). Although neuronal interconnections have been much less studied in PPNs, the general neuroanatomy is similar (91, 93). For all nematodes, the primary chemosensory organs are the two anterior, bilaterally symmetrical amphids located in the head region (**Figure 1*b***). Sensory organs in the tail region known as phasmids are also thought to be involved in chemo-orientation (4). Each amphid contains sensory cilia, dendritic processes of chemosensory neurons, that are exposed to the environment via a pore in the cuticle (**Figure 1*b***). Axonal processes from these neurons project into the circumpharyngeal nerve ring, where much of the sensory integration takes place. Signals from the environment are perceived and transmitted to other neurons to direct the nematode's responses.

Nematodes utilize a large repertoire of receptors and ion channels to detect small molecules (environmental signals and neurotransmitters) and transmit signals. The major receptors, G-protein coupled receptors (GPCRs), induce cellular responses primarily by coupling with intracellular heterotrimeric G proteins (44), which engage with a variety of molecular signals to mediate downstream responses. In contrast to more complex animals, individual sensory neurons in nematodes coexpress multiple GPCRs and as many as six receptor guanylate cyclases (rGCs) (46, 113). Members of both the GPCRs and rGC superfamilies function as targets for chemicals that trigger chemotaxis behavior (4). Although there are more than 1,000 GPCR genes in *C. elegans*, only 147 were annotated in the *Meloidogyne hapla* genome (86). This may reflect the more defined life cycle of the parasite compared to that of the free-living hunter species (7). Stage-specific transcriptome studies of RKNs and CNs showed the highest expression of GPCR and neuropeptide signaling pathway genes in preparasitic J2s, which is consistent with a major role for these pathways during the mobile, host-searching phase of the life cycle (15, 20).

PPNs encode proteins with sequence similarity to proteins that have been determined to have key roles in olfaction and neurotransmission in *C. elegans* (7, 8, 98). Recent work has supported the functional equivalence of some of these components. The putative *Meloidogyne incognita* homologs of four core *C. elegans* genes encoding components required for chemotaxis to both water-soluble and volatile chemicals were characterized, including *odr-1* (encoding a rGC), *odr-3* (encoding a GPCR component), and *tax-2/tax-4* (encoding components of a heteromeric cyclic nucleotide-gated ion channel required for downstream signaling) (98). Compared with other stages of the life cycle, these genes were most highly expressed in infective juveniles. Indeed, RNAi-mediated knockdown of their expression altered chemotaxis to root exudates and other aspects of nematode behavior (98). In situ hybridization indicated that *odr-1* is expressed in the cell bodies of amphidal neurons and phasmids. A similar expression pattern was observed for guanylate cyclase homologs in soybean CNs (*Heterodera glycines*) (121).

There is considerable overlap in the repertoire of neurotransmitters and neuromodulators between PPNs and *C. elegans* (47). Crisford et al. (17) demonstrated that the plant alkaloid reserpine, which depletes the neurotransmitter serotonin and other biogenic amines in animals, including mammals, inhibits activation of stylet thrusting and host infection by the potato CN *Globodera pallida*. The phenotypes of *C. elegans* mutants impaired in serotonin biosynthesis and signaling, including the GPCR SER-7 and the serotonin-gated chloride channel MOD-1, were complemented by homologous genes from *G. pallida*, supporting the existence of a conserved serotonergic signaling pathway in these nematodes (17). Serotonin and other biogenic amines have also been demonstrated to affect the behavior of other PPNs (40, 74).

Nematodes, like other animals, encode a diverse range of neuropeptides (47, 66). These neuropeptides play roles in many, if not all, behaviors of *C. elegans*. FMRFamide-like peptides (FLPs), which make up the largest neuropeptide family, modulate diverse sensory and motor processes. These peptides are characterized by a C- to N-terminal gradient of decreasing sequence conservation and a C-terminal Arg-Phe NH2 (28). *C. elegans* contains at least 31 *flp* genes, many of which encode multiple peptides that are processed posttranslationally. Most FLP receptors are GPCRs, which can bind to and be activated by multiple FLPs. PPNs encode and express an array of *flp* genes, many of which correspond to those in *C. elegans* (47). Kimber et al. (61) successfully used RNAi to silence each of the five neuronally expressed *flp* genes in *G. pallida* J2s, which compromised locomotory behavior. In situ hybridization revealed the expression of these genes in the neurons of infective juveniles (61). Modulating the level of FLPs and other neuropeptides by host-induced gene silencing, the exogenous application of these peptides, or other techniques represents promising approaches for nematode control (38, 64, 116).

2.2. Recent Progress Toward Identifying Plant Molecules that Modulate Nematode Behavior

Plants exude a large and diverse collection of metabolites into the rhizosphere (75). These exudates comprise a multitude of primary and secondary metabolites that likely include host-specific and general attractants as well as repellents for root-parasitic nematode species. However, the identification of biologically relevant molecules has been difficult. A recently compiled list of water-soluble and volatile compounds/fractions from root exudates that affect PPNs can be found in Sikder & Vestergard (100). In a recent addition to this list, Oota et al. (85) screened a chemical library of natural products for their ability to attract *M. incognita* and identified cadaverine and other diamines and polyamines as potential attractants. However, for most chemicals identified as attractants, it is not clear whether the nematode, in its quest for a host, is exposed to the concentrations of compounds tested in the laboratory. Additionally, for many chemicals, low concentrations are attractive, whereas higher concentrations are repellent (93). Here, we discuss the difficulties in identifying exudate components that contribute to the location of a suitable host as well as some recent progress in this area.

Observing and quantifying the responses of nematodes to their hosts are quite challenging, and the diversity of assays used has made it difficult to compare results between studies. These tiny animals cannot propel themselves through water and require a solid matrix through which to maneuver. Although assays in sand or soil may best simulate the natural environment, nematodes cannot be seen in these opaque substrates as they respond to their hosts but must instead be extracted to monitor migration. By contrast, when assays are conducted in transparent media, the nematodes can be observed microscopically as they respond to their host, but such conditions are less natural. On agar plates, nematodes generally move in two dimensions along the surface of the agar, although modifications have been devised to better resemble the natural situation (5, 21, 115). Pluronic F-127, a nontoxic, thermo-reversible copolymer that forms a gel at room temperature, is a popular alternative matrix, as it supports the formation of stable chemical gradients and is highly transparent, facilitating detailed observation of behavior (10, 85). Attraction assays vary widely in terms of the parameters measured and the time frame during which the response is assessed. The reported responses of PPNs to root exudates range from highly attractive to repellent depending on the study (10, 30, 114). The wide range of responses observed is likely due to differences in the preparation, treatment, and concentration of root exudate. For example, nonspecific signals such as pH, salts, CO_2, and chemicals produced by microbes can act as attractants or repellants or otherwise modulate behavior (51, 54, 88).

Comparing nematode responses to roots of wild-type and mutant plants or hosts in which specific genes have been downregulated has provided insights into factors/pathways that contribute to host location. For example, roots of *Arabidopsis*, tomato, and *Medicago truncatula* mutants defective in ethylene synthesis or signaling were found to be more attractive to RKNs than wild-type roots (10). The soybean CN *H. glycines* is also more attracted to both nonhost (*Arabidopsis*) and host (soybean) roots compromised in ethylene signaling (50). The ethylene signaling response is a complex, highly regulated network involving cross talk with other hormone-signaling pathways. Thus, the enhanced attraction of hosts defective in ethylene signaling could be due to higher levels of attractants or lower levels of repellents. In another example, silencing genes involved in the sugar transporter genes *STP1* and *STP2* in tomato resulted in reduced infectivity and stylet thrusting for the RKN *M. incognita* but not the CN *G. pallida* (115). This work also found that *M. incognita* was attracted to glucose but *G. pallida* was not. A more recent work using a different assay and different concentrations found that both *M. incognita* and *G. pallida* were attracted to glucose (6).

Measuring migration of RKNs toward different hosts through sand in dual-choice assays has provided insight into the identity of volatile attractants. In a dual olfactometer assay, *M. incognita* was attracted to moist sand with *Capsicum annum* plants compared to moist sand without a plant (60). Volatiles collected from sand containing *C. annum* plants were analyzed and 18 components were identified by gas chromatography–mass spectrometry (GC-MS). Dual-choice assays with five chemically synthesized components identified methyl salicylate as the strongest attractant. Consistent with this finding, earlier work using a six-armed olfactometer found that maize Mu-insertional *lox3–4* mutants, which are predicted to have elevated levels of salicylic acid (and multiple other phytohormones), were more attractive to *M. incognita* than were the wild type (33). Other potential volatile attractants were identified in this and other work, but methyl salicylate remains the strongest candidate for an important cue for long-distance host location (78). However, many volatile components released from roots are not available synthetically and others have not yet been identified.

Activity-guided fractionation of root exudates has advanced progress toward identification of soluble attractants. In this approach, the exudate is chemically fractionated using an activity assay as a guide. Fractionation of collected and concentrated exudate from 4- to 5-week-old tomato roots by high-pressure liquid chromatography fractionation coupled with activity assays found the highest attraction to the most polar fraction (45). LC-QTOF-MS (liquid chromatography quadrupole time-of-flight mass spectrometry) analysis of this fraction revealed a complex blend of metabolites. Synthetic versions of five identified compounds (zeatin, luteolin, quercetin, tomatidine, and solasodine) were tested for their ability to stimulate stylet thrusting and nematode attraction. Although all five compounds stimulated stylet thrusting, the results for attraction were more complex. Zeatin was an attractant at all concentrations examined, whereas the alkaloids tomatidine and solasodine were not attractants. The flavonoid quercetin was attractive at lower concentrations but repellent at higher concentrations, whereas the structurally similar flavonoid luteolin was repellent at all concentrations tested. However, the synthetic compounds were not tested at biologically relevant levels, and numerous other potentially active components present in the exudate were not tested.

To identify a biologically relevant attractant for RKNs, Cepulyte et al. (10) collected exudate from the root tips of 6-day-old tomato seedlings. Root tips of rapidly growing seedlings were previously shown to be highly attractive to J2s, and cell-free exudate collected from root tips retained the activity. The amount of exudate equivalent to 1% of that produced by a single seedling in 24 h displayed clear attraction activity for RKN J2s in a Pluronic gel assay. Activity-coupled deionization and size-exclusion chromatography were consistent with the attractant being a nonionic compound with an apparent mass of ~400 Daltons (10). Fractionation of exudate from *Medicago*

truncatula root tips identified an attractive fraction with similar properties. However, the chemical identity of the attractant(s) from these exudates was not determined due to the limited amount of available material.

Using a similar approach, Tsai et al. (109) investigated flaxseed mucilage, which was highly attractive to *M. incognita* J2s. Activity-guided fractionation of this water-soluble material using reverse-phase and size-exclusion chromatography revealed that the attractive component resembled the pectic polysaccharide rhamnogalacturonan-1. Chemical analysis showed that L-galactose side chains were required for attraction activity. Furthermore, the disaccharide α-L-galactosyl-1,3-liter-rhamnose was sufficient to attract J2s, but the corresponding disaccharide with a D-rhamnose linkage was not an attractant, illustrating the capability of nematodes to respond differentially to molecules that differ only in a single chiral center. However, L-galactose linkages are not found in the mucilage of most other plants, including many RKN hosts, suggesting that this linkage is not the universal signal used by RKN to identify its hosts.

2.3. Emerging Picture of Nematode Targeting to Host Infection Sites

Soil-dwelling nematodes and other animals are generally exposed to multiple sensory cues simultaneously and must process these inputs to determine how to react. In *C. elegans*, the neuronal basis for the integration of simultaneous cues with behavioral response is beginning to be understood (41). The perception of host exudates by PPNs is likely a highly evolved process that is fine-tuned to assess the condition of candidate hosts and optimize successful parasitism and reproductive success. The composition of plant metabolites exuded by roots differs based on the root tissue examined, its condition and age, the rhizosphere composition, and other factors (75). An enticing finding by Reynolds et al. (94) is that in a modified Y-chamber filled with Pluronic gel, RKN J2s moved in a direct path to the roots of the host seedlings but in a nondirect path to the roots of seedlings that are poor hosts or nonhosts of these parasites. This observation suggests that exudates contain a complex of signals and that the nematode can assess this information and orient its response accordingly. Conceivably, attractants and repellents released from the root surface in a topologically specific manner could guide PPN to sites for efficient penetration.

3. HOW PLANTS RECOGNIZE PARASITIC NEMATODES

Plants recognize pathogen- or microbe-associated molecular patterns (PAMPs or MAMPs, hereafter collectively referred to as PAMPs) and activate a plethora of defense responses collectively known as pattern-triggered immunity (PTI). PAMPs are molecules that are evolutionarily conserved throughout specific pathogen classes and contribute to the general fitness of the infectious organism's life cycle. The PAMPs identified to date range from structural components of various pathogens to biomacromolecules, such as nucleic acids and proteins (37). Virulent pathogens overcome PTI responses by releasing effectors into the host plants (see Section 4). These effectors interfere with the activation of PTI responses, promote nutrient acquisition, and alter plant metabolism, thereby reducing or eliminating the efficacy of the plant's defense responses. The second tier of pathogen recognition involves intracellular nucleotide-binding domain leucine-rich repeat (LRR) proteins [encoded by Resistance (*R*) genes], which perceive effectors leading to a robust defense response also known as effector-triggered immunity (55, 69). Effector-triggered immunity often culminates in a form of programmed cell death known as the hypersensitive response.

Recognition of PAMPs by plants is mediated by germline-encoded pattern recognition receptors (PRRs). With one exception among those characterized so far, plant PRRs involved in the activation of PTI are membrane-located receptor-like kinases (RKs) or receptor-like proteins (16). The exception is an extracellular protein that binds to the heptaglucoside from the oomycete

Phytophthora sojae (110). Structurally, RKs consist of an extracellular ligand-binding domain, a single membrane-spanning domain, and a cytoplasmic kinase domain. Plant PRRs are subclassified on the basis of the structural features of their extracellular domains: LRR-RKs, lysine-motif RKs, lectin-RKs (LeC-RKs), and epidermal growth factor RKs. Some PRRs can perceive host-derived molecules that are released from damaged cells undergoing pathogen attack, i.e., so-called damage-associated molecular patterns (DAMPs) (129).

Most, if not all, PRRs function as parts of multiprotein complexes at the plasma membrane. One such partner of PRRs is brassinosteroid-associated kinase 1 (BAK1), a member of the LRR-RK family. BAK1 forms receptor complexes with LRR-type PRRs, including FLS2 (flagellin sensing 2), which detects the PAMP flg22, a fragment of bacterial flagellin. FLS2 and BAK1 form heterodimers almost instantly upon flg22 perception. Crystallization studies suggest that the C terminus of flg22 binds to FLS2 and closely interacts with BAK1 to stabilize the FLS2-BAK1 association (103). Several recent reviews have summarized the sensing of various viral, bacterial, fungal, and oomycete patterns via the actions of different types of plant PRRs (9, 37, 92). Upon detection of PAMPs or DAMPs, PRRs mediate the activation of a broad range of downstream signaling events, including the rapid generation of reactive oxygen species, activation of mitogen-associated protein kinases (MAPKs) and calcium-dependent protein kinases, reinforcement of the cell wall, and the expression of immunity-related genes (16, 69). Collectively, these events restrict pathogen growth and development.

Extensive studies over the past two decades have identified numerous PAMPs that bind to PRRs to activate PTI, providing protection against infection in a wide range of plants (27, 69, 92). However, information on PAMPs and receptors that underlie the activation of PTI in plant–nematode interactions remains limited. Notable challenges include nematodes' obligate biotrophic lifestyle, their nonsynchronized infection, and the lack of methodology for nematode transformation. The general activation of plant immune responses and the roles of resistance genes in plant–nematode interaction are discussed in previous reviews (118, 126). Here, we summarize the progress in understanding PRR-based recognition of nematodes by plants.

3.1. Progress Toward Identifying Pathogen-Associated Molecular Patterns and Pattern Recognition Receptors Involved in Plant–Nematode Interaction

BAK1 is a coreceptor that forms complexes with LRR-type PRRs and is required for PTI induction. Silencing the expression of BAK1 orthologs (*SlSERK3A* and *SlSERK3B*) in tomato resulted in enhanced susceptibility to RKN because of defects in the activation of defense responses (87). Subsequently, Teixeira et al. (105) determined that PTI-compromised *Arabidopsis* plants (including the *bak1-5* mutant) have enhanced susceptibility to RKNs. This study also demonstrated that the invasion of roots by nematodes activates camalexin and glucosinolate pathways, both of which function in plant resistance against nematodes. Interestingly, the activation of the glucosinolate biosynthetic pathway is dependent on BAK1, whereas the camalexin biosynthetic pathway is mostly independent of this protein (105).

Although the analysis of *bak1* mutants established the relevance of PTI-like responses in plant resistance against nematodes, it did not make clear whether the induction of PTI occurs due to the direct recognition of nematode-associated PAMPs or whether it results from mechanical damage caused by nematode contact or invasion. Mendy et al. (77) found that NemaWater, a solution produced when J2 nematodes were incubated in water for 24 h and subsequently removed, triggered PTI responses in *Arabidopsis* that were dependent on the presence of BAK1. Although these experiments were conducted in *Arabidopsis*, two recent studies demonstrated that NemaWater could also induce PTI responses in tomato and rice (25, 106). These experiments indicate that nematode contact or invasion is not required for the host to trigger a PTI response. Zhou et al.

(127) recently performed a reverse genetic screen for *Arabidopsis* mutants with enhanced resistance or sensitivity to nematodes and identified a G-lectin receptor kinase (ERN1) that acts as a negative regulator of PTI. Interestingly, *ern1* mutants displayed stronger activation of PTI responses upon NemaWater treatment than did the wild type, further supporting a role for a factor present in NemaWater in nematode-mediated PTI responses (127). Although the identity of the elicitor in NemaWater remains unknown, heating NemaWater or preincubating it with proteinase K abolished its PTI-inducing capacity, suggesting that its eliciting activity requires the presence of a heat-sensitive protein. An intriguing possibility is that this protein is a nematode-derived enzyme that catalyzes release of a DAMP from the host cell wall.

A screen of *Arabidopsis* mutants identified two previously uncharacterized LRR-RKs (NILR1 and NILR2) that altered NemaWater-induced PTI responses (77). Although NemaWater-induced PTI responses were lost in the NILR1 loss-of-function mutant *nilr1*, they were only slightly reduced in *nilr2*. NILR1 is a 1,106 amino acid LRR-RK that is closely related to BRI1 (brassinosteroid insensitive 1). NILR1 is localized to the plasma membrane, and its extracellular domain consists of 22 tandem LRRs that are interrupted by a 76 amino acid island located between LRR17 and LRR18. The extracellular domain of NILR1 is followed by a transmembrane domain and a cytoplasmic kinase domain. A BLAST search using extracellular domain as a query revealed that orthologs of NILR1 are conserved across a wide range of dicotyledonous and monocotyledonous plants. Nevertheless, sequence homology does not imply functional conservation, and some of these orthologs may well represent BRI1 and other similar receptors. Functional characterization is required to establish the conservation of NILR1 in different plant species (77).

Recent work has identified an ascaroside as a potential nematode-specific PAMP. Ascarosides are nematode pheromones that are derivates of 3,6-dideoxy-L-sugar ascarylose modified with a fatty acid–derived side chain and in some cases other moieties (13). In several PPN species, the most abundant ascaroside is ascr#18, featuring an 11-carbon fatty acid side chain (59). Exogenous application of ascr#18 induced defense responses in *Arabidopsis*, including the expression of genes associated with PTI and activation of MAPKs (72). Application of ascr#18 in vitro reduced susceptibility of *Arabidopsis* to the CN *Heterodera schachtii* and the RKN *M. incognita* and inhibited *M. hapla* reproduction on tomato in a greenhouse assay (62, 72). Additionally, the application of ascr#18 to a range of crop species (including both monocots and dicots) increased resistance to diverse viral, bacterial, and fungal pathogens (62, 72). Although these observations support the notion that ascr#18 is a nematode-derived PAMP, these studies are not complete. So far, no plant receptors for ascarosides have been identified. Additionally, Manohar et al. (71) recently demonstrated that ascr#18 is metabolized to shorter side-chained ascarosides, predominantly ascr#9, by both monocot and dicot plants. Attraction assays with RKN J2s showed that although ascr#18 was an attractant, ascr#9, or the combination of ascr#9 and ascr#18, was repellent to nematodes. This raises the possibility that the reduced susceptibility of plants to PPNs following exposure to ascr#18 may (at least partially) be due to this repellent effect.

3.2. Perception of Nematode-Associated Damage by the Host Plant

Nematode invasion causes substantial physical damage to root tissues, releasing cell components that could act as DAMPs and activate PTI-like defense responses. High-resolution video-enhanced microscopy of nematode behavior inside roots suggested that DAMPs can be produced by two distinct nematode-associated activities: stylet thrusts and nematode body movements. CNs have been shown to migrate intracellularly inside roots, causing severe damage to root cells. By contrast, RKNs move intercellularly and cause less apparent tissue damage. However, these observations were made in the roots of *Arabidopsis* and other cruciferous plants, and it may be that

behavior differs in other hosts. In addition, PPNs secrete a range of cell wall–degrading enzymes that appear to have been obtained by ancient horizontal gene transfer from soil microbes, including cellulases (24, 102), pectate lyases (23, 111), and polygalacturonases (53). Products produced from host components by the action of such enzymes could potentially be recognized as DAMPs (20). Several DAMP–PRR pairs have been identified in plants (129). Here, we discuss current evidence suggesting that nematode damage produces DAMPs that are recognized by the host and that the host's response to DAMPs contributes to effective defense against PPNs.

Oligogalacturonides (OGs) are small cell wall fragments that are produced by the partial hydrolysis of homogalacturonan, the main component of pectin. Homogalacturonan is degraded by microbial polygalacturonases (PGs) during infection or by plant-endogenous PGs during mechanical damage. PG-inhibiting proteins (PGIPs) are a group of cell wall proteins that inhibit pectin-depolymerizing activity of PGs favoring the accumulation of partial degradation products that function as elicitor-active OGs. These OGs can act as DAMPs and activate PTI-like responses via pectin receptors such as wall-associated kinases (WAKs). Veronico et al. (112) studied the role of PGIPs in susceptible and resistant genotypes of pea (*Pisum sativum* L.) in response to *Heterodera goettingiana* infection. *PsPGIP1* was shown to be differentially expressed between susceptible and resistant genotypes. In situ hybridization revealed that *PsPGIP1* is localized to the syncytium of a resistant pea genotype (112). *Arabidopsis* harbors two PGIP genes: *AtPGIP* and *AtPGIP2*. Shah et al. (96) showed that CN migration inside roots induces the expression of both *AtPGIP* and *AtPGIP2*. Interestingly, although RKNs have been shown to harbor PGs (53), the expression of *PGIP* genes was not induced during the migratory stage of RKN infection (96). Experiments with mutants and overexpression lines revealed that *PGIP* expression reduces the infection of host roots by CNs but not by RKNs (96).

Proline-rich extensin-like receptor kinases (PERKs) are a family of RKs comprising 15 members in *Arabidopsis*. The extracellular domain of PERKs shares similarities with plant cell wall–associated proteins. Although little is known about the biological function of PERKs, their expression is strongly induced by various wounding stimuli, suggesting that they play a role in the perception of cell wall damage (80). Interestingly, PERK genes were recently shown to be induced by both CN and RKN infection (107). Experiments with *perk* mutants revealed that the induction of PERK genes attenuates the infection of host roots by both CNs and RKNs. Notably, immune responses mediated by PERKs involve binding of their extracellular domains to OGs, suggesting that PERKs function as damage-triggered immune receptors in plant–nematode interactions (107).

Plant elicitor peptides (PEPs) are small (23–29 amino acids long) peptides derived from the C termini of precursor proteins, PROPEPs. PEPs are perceived by membrane-bound RKs known as PEP receptors (PEPRs). PROPEP genes are induced by mechanical stimulation as well as pathogen-induced wounding. Experiments with reporter lines and loss-of-function mutants in *Arabidopsis* showed that the PEP–PEPR system contributes to plant defense against CNs (S Siddique, unpublished results). This system does not appear to function in defense against RKNs (105). Interestingly, treatment of soybean seeds with PEPs led to a significant reduction in both CN and RKN infection (65).

Adenosine triphosphate (ATP) acts as a universal energy currency in all organisms. ATP can also act as an extracellular signaling molecule. In plants, ATP is released into the extracellular space in response to physical damage, where it is then recognized by the LeC-RK DORN1 (does not respond to nucleotides 1). Considering that nematodes cause significant damage during migration, extracellular ATP could function as a DAMP. Interestingly, however, *dorn1* mutants and DORN overexpression lines did not show changes in susceptibility to CNs or RKNs, calling into question the role of DORN1 in plant–nematode interactions (105).

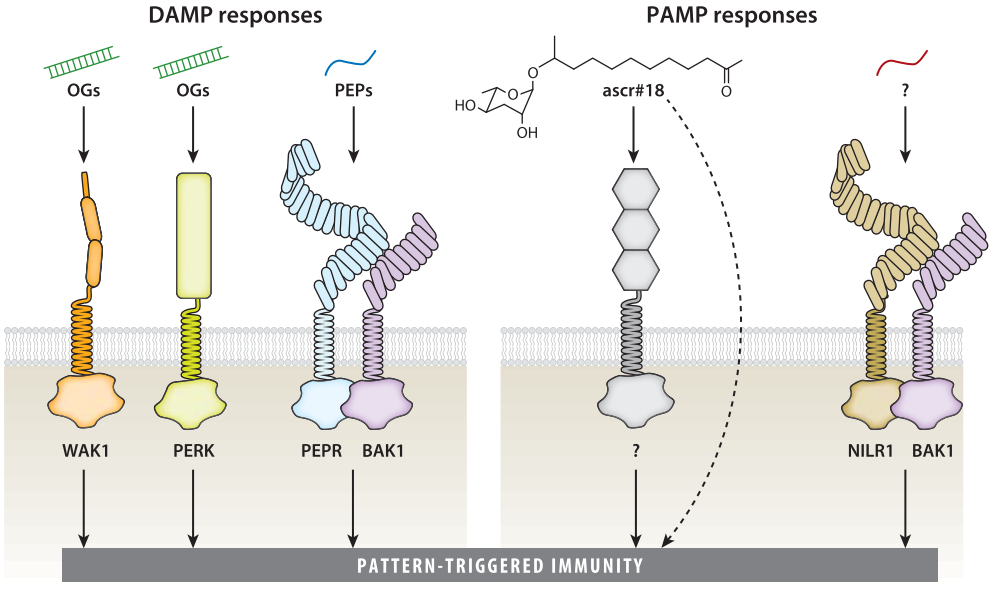

Figure 2

Model for cell surface perception of parasitic nematodes and defense induction by plants. Abbreviations: BAK1, brassinosteroid-associated kinase 1; DAMP, damage-associated molecular pattern; NILR1, nematode-induced LRR-RK1; OGs, oligogalacturonides; PAMP, pathogen-associated molecular pattern; PEP, plant elicitor peptide; PEPR, PEP receptor; PERK, proline-rich extension-like receptor protein kinase; WAK1, wall-associated kinase 1.

3.3. Current View of Plant Perception of Nematodes

Although evidence indicates that PAMP- and DAMP-triggered PTI contributes to reduced susceptibility to PPNs, many specifics remain unclear. The identities of PRR–ligand pairs and the downstream signaling cascades are largely unknown. A model for predicted interactions that could potentially trigger PTI is presented in **Figure 2**. NemaWater, which contains material exuded from intact infective juveniles, may contain proteins that act as PAMPs and/or catalyze the release of DAMPs such as cell wall fragments (77). One or more of these components could be recognized by NILR1, which then recruits BAK1 to form a heterodimeric complex. The activation of this NILR1–BAK1 complex induces PTI responses, including the production of reactive oxygen species bursts (77), the accumulation of defense hormones (59), and transcriptional reprogramming (77). The identification of NILR1 expands the paradigm of PRR-based immune recognition to plant–animal interactions. However, additional research is required to gain a full understanding of the role of the NILR1-containing PRR complexes in the activation of PTI. Ascarosides may also be recognized by an as-yet-unidentified PRR to trigger PTI responses. Cell wall fragments produced by nematode enzymes or physical damage may trigger DAMP responses via WAK1, PERK, PEPR, or other PRRs. Although it is clear that PTI is effective in reducing nematode infection, additional research is required to confirm the molecules and receptors responsible for perception and defense induction.

4. SUPPRESSION OF PLANT DEFENSES BY NEMATODE EFFECTORS

PPNs release molecules into the plant interaction space that facilitate their ability to navigate hostile plant environments. Among these molecules, effector proteins play particularly important roles. Most nematode effectors are delivered through the stylet into or around the plant tissue

and cells that mount defense responses against the parasitizing nematode. With the advent of genomic resources, an ever-increasing arsenal of nematode effectors is being uncovered. Once effectors have been functionally characterized, it has become evident that a large portion functions to modulate PTI responses such as defense gene expression, ROS production and MAPK activation.

A picture of diverse mechanisms targeting plant defenses is beginning to unfold. Plant proteins with clear defense functions are, not surprisingly, targeted by nematode effectors. These targeted proteins include those involved in the signal recognition and transduction processes leading to the triggering of defenses. For example, kinases and proteases with signal transduction roles are modulated by nematode effectors. Other nematode effectors bind, and presumably inactivate, proteins directly delivering the defense mechanisms, such as certain pathogenesis-related proteins. Finally, there are numerous reports of effectors interfering with the manifestation of known defense mechanisms, like cell death or other defense hallmarks, albeit without yet revealing the exact effector mode of action.

Some of the early discoveries of effectors with defense-suppression functions have been reviewed in detail in several publications (34, 35, 42, 73, 101). This current report provides diverse examples of defense-suppressing effectors, emphasizing recent and novel findings that have not previously been covered in review articles.

4.1. Functional Characterization and Novel Mechanisms of Defense-Suppressing Effectors

Secreted venom allergen-like proteins (VAPs) are ubiquitous among parasitic nematodes (117), and their function as defense-suppressing effectors is well understood in CNs. There, VAPs have been shown to modulate basal plant immunity by selectively targeting plant surface–localized immune receptors of immunogenic breakdown products of damaged host tissues (70, 117). A recent study reports that RKNs produce ligand mimic effectors that specifically target the FERONIA receptor-like kinase to interfere with the activation of PTI (123). Also, a secreted subset of SPRY domain–containing proteins, so-called SPRYSECs, has been shown in *Globodera* to interfere with the functions of both PTI and effector-triggered immunity (3, 90), and this function has been shown for one such effector to be mediated by targeting microtubule-associated proteins of the cytoskeleton (76). An intriguing example of defense suppression by a *Heterodera* effector is HgGland18. This protein is synthesized throughout the parasitic phase of the life cycle and is translocated to soybean cell nuclei after infection. A strong and persistent immunosuppressive ability of this effector was documented and likely was associated with nuclear functions of this effector (83). An additional intriguing finding was that HgGland18 shared significant similarity to an effector of *Plasmodium* spp., the malaria parasites. Although this similarity is most likely due to convergent evolution rather than homology, a malaria effector domain could phenocopy the defense suppression when incorporated into an HgGland18 effector mutant. Another example of an effector's mode of action in altering plant defenses is provided by *Heterodera* effector 4E02 (57). This effector protein was shown to specifically bind to *Arabidopsis* vacuolar papain protease RD21A, a well-established enzyme in regulating plant defenses. Interestingly, 4E02 did not inhibit protease activity but rather resulted in a translocation of RD21A from the plant vacuole to the cytoplasm and nucleus, effectively removing this protease from its site of defense regulation and into novel compartments. It appears likely that this nematode manipulation served the dual function of inactivating defenses and repurposing of a plant enzyme by exposing it to novel substrates in its new site of accumulation, thereby resulting in cell wall compositional changes. One more intriguing example of modulating a plant defense signal transduction pathway is provided by the study of the *Heterodera* 28B03 effector. This novel protein was shown to specifically bind and inhibit

an *Arabidopsis* stress-response kinase resulting in the disruption of a kinase cascade leading to the phosphorylation of a plant syntaxin protein (T. Baum, unpublished data) that had been shown to condition the release of antimicrobial pathogenesis-related proteins into the apoplastic space (58).

Effectors apparently involved in ubiquitin-related processes have been identified in PPNs and have been shown to suppress plant defenses. In earlier discoveries, effectors representing ubiquitin-extension proteins have been identified in *Globodera* (14). After secretion into the plant, the extension peptide is cleaved and can interfere with plant defenses. In addition, a recently discovered potato CN effector with ubiquitin ligase function has been shown to be a potent inhibitor of plant defenses (63). Similarly, plant annexin-like effectors from several nematodes have been shown to interfere with plant defenses or cause plant cell death (2, 68).

There are at least two examples of nematode effectors directly binding to, and presumably inactivating, pathogenesis-related plant proteins. The *Heterodera* effector 30C02 was shown to bind to pathogenesis-related protein β-1,3-endoglucanase, likely interfering with its function (39). In support, knocking out the β-1,3-endoglucanase gene or expressing a 30C02 coding sequence in planta resulted in increased plant susceptibility. Furthermore, RNAi-based knockdown of 30C02 expression in infecting nematodes reduced their infectivity (39). Similarly, the MO237 effector of *M. graminicola* was shown to bind to host pathogenesis-related proteins. Furthermore, this effector was capable of suppressing plant defense mechanisms like specific gene expressions, callose deposition, and reactive oxygen bursts (11).

Reactive oxygen responses are powerful defense components of plants. Studies of nematode effectors have shown that nematodes deploy proteins to specifically counteract these potent plant responses. *Heterodera* effector 10A06 was shown to target host plant spermidine synthase, thereby increasing spermidine contents and downstream polyamine enzymatic activities, which in turn elevated the cellular antioxidant machinery in host plants (43). Similarly, reactive oxygen scavenging systems were activated by the RKN MjTTL5 effector (67). Another *Meloidogyne* effector, Mg01965, was shown to suppress the reactive oxygen burst triggered by flg22 when accumulating in the apoplast (128). The reactive oxygen burst was also inhibited by *Heterodera* effector GLAND5, which additionally altered defense gene expression and callose deposition in *Arabidopsis* (122).

In addition to functionally characterizing known nematode effector molecules in detail using a range of experimental approaches, defense-suppressing effectors can be recognized by their ability to interfere with expected defense mechanisms in other pathosystems. In a recent high-throughput assessment of *Heterodera* effectors, 10 of 51 tested effectors were able to suppress defense mechanisms triggered by bacterial pathogens and also altered plant defense gene expressions (89). Similarly, two *Meloidogyne* effectors, MilSE5 and MilSE6, were able to suppress cell death triggered by a bacterial pathogen (97). In other approaches, known nematode effectors were assessed for their abilities to block effects of plant defense-triggering compounds. In such an approach, the *Heterodera* 16B09 effector was found to suppress flg22-induced gene expression changes (49). Similarly, the *Meloidogyne* effector MSP18 suppressed cell death induced by an elicitin (36). Furthermore, defense-suppressing nematode effectors have been identified for their ability to interfere with documented inducers of cell death (11, 82, 123). The *Heterodera* Ha18764 effector was shown to be a powerful suppresser of cell death in several systems and was able to suppress reactive oxygen responses, defense gene expression, and callose deposition (123). The *Meloidogyne* Mg16820 effector was shown to suppress cell death and was documented to be secreted to the apoplast as well as the host cell cytoplasm during different times of parasitism (79). Yet another *Meloidogyne* effector, MgGPP, could suppress plant cell death and was shown to undergo substantial posttranslational modification as well as transport first into the plant ER and then the nucleus, underscoring the molecular complexities of nematode parasitism (12).

Although the abovementioned effectors are produced in the esophageal glands and secreted through the stylet, other effector proteins can be released from other nematode tissues/organs. In a recent and intriguing example, MIF-like effectors of *Meloidogyne* were found to be secreted from the nematode hypodermis. These effectors suppress cell death triggered by several stimuli and interact with plant annexin. These latter interactions are likely instrumental in inhibiting plant defenses (124). MIF-2, in particular, had additional defense-suppressing activities such as reactive oxygen protection and cell death suppression (125).

4.2. Current Status of and Perspectives on Defense-Suppressing Effectors

A diverse collection of nematode effectors has been shown to function in the suppression of plant defenses. Although the modes of action for many of these effectors have been determined, additional effectors have so far been shown to only suppress defenses without revealing the underlying mechanisms of this action. The extent and diversity of mechanisms that nematodes utilize to block host defenses reflect their importance to successful parasitism. PPNs invest much of their genome in efforts to suppress host defense. Some of these genes, such as VAPs, are widespread among parasitic nematodes throughout the phylum. However, many effectors are novel genes found only in limited groups of PPNs and attack many aspects of plant defense/PTI. As discussed above, for some cases, this can result in increased susceptibility to other pathogens. This defense suppression may be a factor in the induced susceptibility of nematode-infected plants to other pathogens. Continued investigation of these nematode defense suppressors should provide better understanding of the plant's PTI response.

5. CONCLUSIONS AND VISIONS FOR THE FUTURE

Clearly, nematode–plant interactions are very complex cross-kingdom signal exchanges and reactions. The fact that nematodes are animals and are governed by nerve centers and deliberate actions adds significant complexity to these pathosystems. PPNs are highly evolved to recognize and attack suitable hosts and have evolved a plethora of novel strategies to block host defenses. We are only beginning to understand how plants recognize these attacking pathogens, what defenses are launched, and which aspects of the plant's defenses are most effective for nematode control. Early stages of interaction between nematodes and their hosts, before the extended, biotrophic interaction where the losses occur is established, are prime targets for nematode control. Although it is apparent that complete comprehension of these events is daunting, recent insights into the early stages of nematode–plant recognition and mutual responses have already suggested several promising avenues for intervention with the goal to develop novel management tools against these devastating pathogens. The evidence for functional similarity of genes for chemosensory perception and signal transmission suggests that *C. elegans* is a useful system for identifying new targets for PPN management, even though the lifestyles and food sources of these parasites are very different. Information is accumulating on the identity of nematode molecules involved in perception by the host as well as the nematode effectors that block host responses. Advances in genome resources, proteomics, natural product chemistry, biotechnology, and molecular manipulation of hosts promise to facilitate our understanding and lead to translation of this basic understanding into much needed environmentally safe management strategies.

DISCLOSURE STATEMENT

The authors are not aware of any affiliations, memberships, funding, or financial holdings that might be perceived as affecting the objectivity of this review.

LITERATURE CITED

1. Abad P, Gouzy J, Aury JM, Castagnone-Sereno P, Danchin EGJ, et al. 2008. Genome sequence of the metazoan plant-parasitic nematode *Meloidogyne incognita*. *Nat. Biotechnol.* 26:909–15
2. Ali MA, Azeem F, Li H, Bohlmann H. 2017. Smart parasitic nematodes use multifaceted strategies to parasitize plants. *Front. Plant Sci.* 8:1699
3. Ali S, Magne M, Chen S, Obradovic N, Jamshaid L, et al. 2015. Analysis of *Globodera rostochiensis* effectors reveals conserved functions of SPRYSEC proteins in suppressing and eliciting plant immune responses. *Front. Plant Sci.* 6:623
4. Bargmann CI. 2006. Chemosensation in *C. elegans*. *WormBook*. **https://doi.org/10.1895/wormbook.1.123.1**
5. Beeman AQ, Njus ZL, Pandey S, Tylka GL. 2016. Chip technologies for screening chemical and biological agents against plant-parasitic nematodes. *Phytopathology* 106:1563–71
6. Bell CA, Mobayed W, Lilley CJ, Urwin PE. 2021. Monosaccharide constituents of potato root exudate influence hatching of the white potato cyst nematode. *PhytoFrontiers* 1:258–66
7. Bird DM, Jones JT, Opperman CH, Kikuchi T, Danchin EGJ. 2015. Signatures of adaptation to plant parasitism in nematode genomes. *Parasitology* 142:S71–S84
8. Bird DM, Williamson VM, Opperman CH. 2015. Exploiting solved genomes of plant-parasitic nematodes to understand parasitism. *Adv. Bot. Res.* 73:241–58
9. Boutrot F, Zipfel C. 2017. Function, discovery, and exploitation of plant pattern recognition receptors for broad-spectrum disease resistance. *Annu. Rev. Phytopathol.* 55:257–86
10. Cepulyte R, Danquah WB, Bruening G, Williamson VM. 2018. Potent attractant for root-knot nematodes in exudates from seedling root tips of two host species. *Sci. Rep.* 8:10847
11. Chen J, Hu L, Sun L, Lin B, Huang K, et al. 2018. A novel *Meloidogyne graminicola* effector, MgMO237, interacts with multiple host defence-related proteins to manipulate plant basal immunity and promote parasitism. *Mol. Plant Pathol.* 19:1942–55
12. Chen J, Lin B, Huang Q, Hu L, Zhuo K, Liao J. 2017. A novel *Meloidogyne graminicola* effector, MgGPP, is secreted into host cells and undergoes glycosylation in concert with proteolysis to suppress plant defenses and promote parasitism. *PLOS Pathog.* 13:e1006301
13. Choe A, von Reuss SH, Kogan D, Gasser RB, Platzer EG, et al. 2012. Ascaroside signaling is widely conserved among nematodes. *Curr. Biol.* 22:772–80
14. Chronis D, Chen SY, Lu SW, Hewezi T, Carpenter SCD, et al. 2013. A ubiquitin carboxyl extension protein secreted from a plant-parasitic nematode *Globodera rostochiensis* is cleaved in planta to promote plant parasitism. *Plant J.* 74:185–96
15. Cotton JA, Lilley CJ, Jones LM, Kikuchi T, Reid AJ, et al. 2014. The genome and life-stage specific transcriptomes of *Globodera pallida* elucidate key aspects of plant parasitism by a cyst nematode. *Genome Biol.* 15:R43
16. Couto D, Zipfel C. 2016. Regulation of pattern recognition receptor signalling in plants. *Nat. Rev. Immunol.* 16:537–52
17. Crisford A, Calahorro F, Ludlow E, Marvin JMC, Hibbard JK, et al. 2020. Identification and characterisation of serotonin signalling in the potato cyst nematode *Globodera pallida* reveals new targets for crop protection. *PLOS Pathog.* 16:e1008884
18. Curtis RHC. 2008. Plant-nematode interactions: environmental signals detected by the nematode's chemosensory organs control changes in the surface cuticle and behavior. *Parasite* 15:310–16
19. Curtis RHC, Robinson AF, Perry RN. 2009. Hatch and host location. In *Root-Knot Nematodes*, pp. 139–62. Wallingford, UK: CABI
20. Da Rocha M, Bournaud C, Dazeniere J, Thorpe P, Bailly-Bechet M, et al. 2021. Genome expression dynamics reveals parasitism regulatory landscape of the root-knot nematode *Meloidogyne incognita* and a promoter motif associated with effector genes. *Genes* 12:771
21. Dalzell JJ, Kerr R, Corbett MD, Fleming CC, Maule AG. 2011. Novel bioassays to examine the host-finding ability of plant-parasitic nematodes. *Nematology* 13:211–20
22. de Boer JM, McDermott JP, Davis EL, Hussey RS, Popeijus H, et al. 2002. Cloning of a putative pectate lyase gene expressed in the subventral esophageal glands of *Heterodera glycines*. *J. Nematol.* 34:9–11

23. de Boer JM, Smant G, Goverse A, Davis EL, Overmars HA, et al. 1996. Secretory granule proteins from the subventral esophageal glands of the potato cyst nematode identified by monoclonal antibodies to a protein fraction from second-stage juveniles. *Mol. Plant-Microbe Interact.* 9:39–46
24. de Boer JM, Yan YT, Wang XH, Smant G, Hussey RS, et al. 1999. Developmental expression of secretory beta-1,4-endoglucanases in the subventral esophageal glands of *Heterodera glycines*. *Mol. Plant-Microbe Interact.* 12:663–69
25. De Kesel J, Gomez-Rodriguez R, Bonneure E, Mangelinckx S, Kyndt T. 2020. The use of PTI-marker genes to identify novel compounds that establish induced resistance in rice. *Int. J. Mol. Sci.* 21:317
26. Decraemer W, Hunt DJ. 2006. Structure and classification. In *Plant Nematology*, ed. RN Perry, M Moens, pp. 3–32. Wallingford, UK: CABI
27. DeFalco TA, Zipfel C. 2021. Molecular mechanisms of early plant pattern-triggered immune signaling. *Mol. Cell* 81:3449–67
28. Dossey AT, Reale V, Chatwin H, Zachariah C, Debono M, et al. 2006. NMR analysis of *Caenorhabditis elegans* FLP-18 neuropeptides: implications for NPR-1 activation. *Biochemistry* 45:7586–97
29. Duceppe MO, Lafond-Lapalme J, Palomares-Rius JE, Sabeh M, Blok V, et al. 2017. Analysis of survival and hatching transcriptomes from potato cyst nematodes, *Globodera rostochiensis* and *G. pallida*. *Sci. Rep.* 7:3882
30. Dutta TK, Powers SJ, Gaur HS, Birkett M, Curtis RHC. 2012. Effect of small lipophilic molecules in tomato and rice root exudates on the behaviour of *Meloidogyne incognita* and *M. graminicola*. *Nematology* 14:309–20
31. Eisenback JD. 1985. Detailed morphology and anatomy of second-stage juveniles, males, and females of the genus *Meloidogyne* (root-knot nematodes). In *An Advanced Treatise on* Meloidogyne, Vol. 1: *Biology and Control*, ed. JN Sasser, CC Carter, pp. 47–78. Raleigh: N. C. State Univ. Graphics
32. Futai K. 2013. Pine wood nematode, *Bursaphelenchus xylophilus*. *Annu. Rev. Phytopathol.* 51:61–83
33. Gao XQ, Starr J, Gobel C, Engelberth J, Feussner I, et al. 2008. Maize 9-lipoxygenase ZmLOX3 controls development, root-specific expression of defense genes, and resistance to root-knot nematodes. *Mol. Plant-Microbe Interact.* 21:98–109
34. Gardner M, Verma A, Mitchum MG. 2015. Emerging roles of cyst nematode effectors in exploiting plant cellular processes. *Adv. Bot. Res.* 73:259–91
35. Goverse A, Smant G. 2014. The activation and suppression of plant innate immunity by parasitic nematodes. *Annu. Rev. Phytopathol.* 52:243–65
36. Grossi-de-Sa M, Petitot AS, Xavier DA, Sá MEL, Mezzalira I, et al. 2019. Rice susceptibility to root-knot nematodes is enhanced by the *Meloidogyne incognita* MSP18 effector gene. *Planta* 250:1215–27
37. Gust AA, Pruitt R, Nurnberger T. 2017. Sensing danger: key to activating plant immunity. *Trends Plant Sci.* 22:779–91
38. Hada A, Kumari C, Phani V, Singh D, Chinnusamy V, Rao U. 2020. Host-induced silencing of FMRFamide-like peptide genes, *flp*-1 and *flp*-12, in rice impairs reproductive fitness of the root-knot nematode *Meloidogyne graminicola*. *Front. Plant Sci.* 11:894
39. Hamamouch N, Li CY, Hewezi T, Baum TJ, Mitchum MG, et al. 2012. The interaction of the novel 30C02 cyst nematode effector protein with a plant beta-1,3-endoglucanase may suppress host defence to promote parasitism. *J. Exp. Bot.* 63:3683–95
40. Han Z, Boas S, Schroeder NE. 2017. Serotonin regulates the feeding and reproductive behaviors of *Pratylenchus penetrans*. *Phytopathology* 107:872–77
41. Harris G, Wu TH, Linfield G, Choi MK, Liu H, Zhang Y. 2019. Molecular and cellular modulators for multisensory integration in *C. elegans*. *PLOS Genet.* 15:e1007706
42. Hewezi T, Baum TJ. 2013. Manipulation of plant cells by cyst and root-knot nematode effectors. *Mol. Plant-Microbe Interact.* 26:9–16
43. Hewezi T, Howe PJ, Maier TR, Hussey RS, Mitchum MG, et al. 2010. *Arabidopsis* spermidine synthase is targeted by an effector protein of the cyst nematode *Heterodera schachtii*. *Plant Physiol.* 152:968–84
44. Hilger D, Masureel M, Kobilka BK. 2018. Structure and dynamics of GPCR signaling complexes. *Nat. Struct. Mol. Biol.* 25:4–12

45. Hillary KK, Lucy KM, John JB, Torto B. 2018. Elicitation of differential responses in the root knot nematode *Meloidogyne incognita* to tomato root exudate cytokinin, flavonoids, and alkaloids. *J. Agric. Food Chem.* 66(43):11291–300
46. Hobert O. 2013. The neuronal genome of *Caenorhabditis elegans*. *WormBook*. **https://doi.org/10.1895/wormbook.1.161.1**
47. Holden-Dye L, Walker RJ. 2011. Neurobiology of plant parasitic nematodes. *Invert. Neurosci.* 11:9–19
48. Holterman M, Karegar A, Mooijman P, van Megen H, van den Elsen S, et al. 2017. Disparate gain and loss of parasitic abilities among nematode lineages. *PLOS ONE* 12:e0185445
49. Hu Y, You J, Li C, Pan F, Wang C. 2019. The *Heterodera glycines* effector Hg16B09 is required for nematode parasitism and suppresses plant defense response. *Plant Sci.* 289:110271
50. Hu YF, You J, Li CJ, Williamson VM, Wang CL. 2017. Ethylene response pathway modulates attractiveness of plant roots to soybean cyst nematode *Heterodera glycines*. *Sci. Rep.* 7:41282
51. Hua C, Li CJ, Jiang Y, Huang MH, Williamson VM, Wang CL. 2020. Response of soybean cyst nematode (*Heterodera glycines*) and root-knot nematodes (*Meloidogyne* spp.) to gradients of pH and inorganic salts. *Plant Soil* 455:305–18
52. Hubbard JE, Flores-Lara Y, Schmitt M, McClure MA, Stock SP, Hawes MC. 2005. Increased penetration of host roots by nematodes after recovery from quiescence induced by root cap exudate. *Nematology* 7:321–31
53. Jaubert S, Laffaire JB, Abad P, Rosso MN. 2002. A polygalacturonase of animal origin isolated from the root-knot nematode *Meloidogyne incognita*. *FEBS Lett.* 522:109–12
54. Johnson SN, Nielsen UN. 2012. Foraging in the dark: chemically mediated host plant location by belowground insect herbivores. *J. Chem. Ecol.* 38:604–14
55. Jones JDG, Vance RE, Dangl JL. 2016. Intracellular innate immune surveillance devices in plants and animals. *Science* 354(6316):aaf6395
56. Jones JT, Haegeman A, Danchin EGJ, Gaur HS, Helder J, et al. 2013. Top 10 plant-parasitic nematodes in molecular plant pathology. *Mol. Plant Pathol.* 14:946–61
57. Pogorelko G, Wang J, Juvale PS, Mitchum MG, Baum TJ. 2020. Screening soybean cyst nematode effectors for their ability to suppress plant immunity. *Mol. Plant Pathol.* 21:1240–47
58. Kalde M, Nuhse TS, Findlay K, Peck SC. 2007. The syntaxin SYP132 contributes to plant resistance against bacteria and secretion of pathogenesis-related protein 1. *PNAS* 104:11850–55
59. Kammerhofer N, Radakovic Z, Regis JMA, Dobrev P, Vankova R, et al. 2015. Role of stress-related hormones in plant defence during early infection of the cyst nematode *Heterodera schachtii* in *Arabidopsis*. *New Phytol.* 207:778–89
60. Kihika R, Murungi LK, Coyne D, Ng'ang'a M, Hassanali A, et al. 2017. Parasitic nematode *Meloidogyne incognita* interactions with different *Capsicum annum* cultivars reveal the chemical constituents modulating root herbivory. *Sci. Rep.* 7:2903
61. Kimber MJ, McKinney S, McMaster S, Day TA, Fleming CC, Maule AG. 2007. flp gene disruption in a parasitic nematode reveals motor dysfunction and unusual neuronal sensitivity to RNA interference. *FASEB J.* 21:1233–43
62. Klessig DF, Manohar M, Baby S, Koch A, Danquah WB, et al. 2019. Nematode ascaroside enhances resistance in a broad spectrum of plant-pathogen systems. *J. Phytopathol.* 167:265–72
63. Kud J, Wang W, Gross R, Fan Y, Huang L, et al. 2019. The potato cyst nematode effector RHA1B is a ubiquitin ligase and uses two distinct mechanisms to suppress plant immune signaling. *PLOS Pathog.* 15:e1007720
64. Kumari C, Dutta TK, Chaudhary S, Banakar P, Papolu PK, Rao U. 2017. Molecular characterization of FMRFamide-like peptides in *Meloidogyne graminicola* and analysis of their knockdown effect on nematode infectivity. *Gene* 619:50–60
65. Lee MW, Huffaker A, Crippen D, Robbins RT, Goggin FL. 2018. Plant elicitor peptides promote plant defences against nematodes in soybean. *Mol. Plant Pathol.* 19:858–69
66. Li C, Kim K. 2008. Neuropeptides. *WormBook*. **https://doi.org/10.1895/wormbook.1.142.1**
67. Lin BR, Zhuo K, Chen SY, Hu LL, Sun LH, et al. 2016. A novel nematode effector suppresses plant immunity by activating host reactive oxygen species-scavenging system. *New Phytol.* 209:1159–73

68. Liu SM, Kandoth PK, Warren SD, Yeckel G, Heinz R, et al. 2012. A soybean cyst nematode resistance gene points to a new mechanism of plant resistance to pathogens. *Nature* 492:256–60
69. Lolle S, Stevens D, Coaker G. 2020. Plant NLR-triggered immunity: from receptor activation to downstream signaling. *Curr. Opin. Immunol.* 62:99–105
70. Lozano-Torres JL, Wilbers RHP, Warmerdam S, Finkers-Tomczak A, Diaz-Granados A, et al. 2014. Apoplastic venom allergen-like proteins of cyst nematodes modulate the activation of basal plant innate immunity by cell surface receptors. *PLOS Pathog*. 10:e1004569
71. Manohar M, Tenjo-Castano F, Chen S, Zhang YK, Kumari A, et al. 2020. Plant metabolism of nematode pheromones mediates plant-nematode interactions. *Nat. Commun.* 11:208
72. Manosalva P, Manohar M, von Reuss SH, Chen SY, Koch A, et al. 2015. Conserved nematode signalling molecules elicit plant defenses and pathogen resistance. *Nat. Commun.* 6:7795
73. Mantelin S, Thorpe P, Jones JT. 2015. Suppression of plant defences by plant-parasitic nematodes. *Adv. Bot. Res.* 73:325–37
74. Masler EP. 2007. Responses of *Heterodera glycines* and *Meloidogyne incognita* to exogenously applied neuromodulators. *J. Helminthol.* 81:421–27
75. Massalha H, Korenblum E, Tholl D, Aharoni A. 2017. Small molecules below-ground: the role of specialized metabolites in the rhizosphere. *Plant J.* 90:788–807
76. Mei Y, Wright KM, Haegeman A, Bauters L, Diaz-Granados A, et al. 2018. The *Globodera pallida* SPRYSEC effector GpSPRY-414-2 that suppresses plant defenses targets a regulatory component of the dynamic microtubule network. *Front. Plant Sci.* 9:1019
77. Mendy B, Wang'ombe MW, Radakovic ZS, Holbein J, Ilyas M, et al. 2017. *Arabidopsis* leucine-rich repeat receptor-like kinase NILR1 is required for induction of innate immunity to parasitic nematodes. *PLOS Pathog.* 13:e1006284
78. Murungi LK, Kirwa H, Coyne D, Teal PEA, Beck JJ, Torto B. 2018. Identification of key root volatiles signaling preference of tomato over spinach by the root-knot nematode *Meloidogyne incognita*. *J. Agric. Food Chem.* 66:7328–36
79. Naalden D, Haegeman A, de Almeida-Engler J, Birhane Eshetu F, Bauters L, Gheysen G. 2018. The *Meloidogyne graminicola* effector Mg16820 is secreted in the apoplast and cytoplasm to suppress plant host defense responses. *Mol. Plant Pathol.* 19:2416–30
80. Nakhamchik A, Zhao ZY, Provart NJ, Shiu SH, Keatley SK, et al. 2004. A comprehensive expression analysis of the *Arabidopsis* proline-rich extensin-like receptor kinase gene family using bioinformatic and experimental approaches. *Plant Cell Physiol.* 45:1875–81
81. Nicol JM, Turner SJ, Coyne DL, den Nijs L, Hockland S, Maafi T. 2011. Current nematode threats to world agriculture. In *Genomics and Molecular Genetics of Plant-Nematode Interactions*, ed. J Jones, G Gheysen, C Fenoll, pp. 21–43. Dordrecht, Neth.: Springer
82. Niu JH, Liu P, Liu Q, Chen CL, Guo QX, et al. 2016. Msp40 effector of root-knot nematode manipulates plant immunity to facilitate parasitism. *Sci. Rep.* 6:19443
83. Noon JB, Qi MS, Sill DN, Muppirala U, Eves-van den Akker S, et al. 2016. A *Plasmodium*-like virulence effector of the soybean cyst nematode suppresses plant innate immunity. *New Phytol.* 212:444–60
84. Ochola J, Coyne D, Cortada L, Haukeland S, Ng'ang'a M, et al. 2021. Cyst nematode biocommunication with plants: implications for novel management approaches. *Pest Manag. Sci.* 77:1150–59
85. Oota M, Tsai AY-L, Aoki D, Favery B, Ishikawa H, Sawa S. 2020. Identification of naturally occurring polyamines as nematode *Meloidogyne incognita* attractants. *Mol. Plant* 13(4):658–65
86. Opperman CH, Bird DM, Williamson VM, Rokhsar DS, Burke M, et al. 2008. Sequence and genetic map of *Meloidogyne hapla*: a compact nematode genome for plant parasitism. *PNAS* 105:14802–7
87. Peng HC, Kaloshian I. 2014. The tomato leucine-rich repeat receptor-like kinases SlSERK3A and SlSERK3B have overlapping functions in bacterial and nematode innate immunity. *PLOS ONE* 9:0093302
88. Perry RN. 2005. An evaluation of types of attractants enabling plant-parasitic nematodes to locate host root. *Russ. J. Nematol.* 13:83–88
89. Pogorelko G, Wang J, Juvale PS, Mitchum MG, Baum TJ. 2020. Screening soybean cyst nematode effectors for their ability to suppress plant immunity. *Mol. Plant Pathol.* 21:1240–47

90. Postma WJ, Slootweg EJ, Rehman S, Finkers-Tomczak A, Tytgat TO, et al. 2012. The effector SPRYSEC-19 of *Globodera rostochiensis* suppresses CC-NB-LRR-mediated disease resistance in plants. *Plant Physiol.* 160:944–54
91. Ragsdale EJ, Ngo PT, Crum J, Ellisman MH, Baldwin JG. 2009. Comparative, three-dimensional anterior sensory reconstruction of *Aphelenchus avenae* (Nematoda: Tylenchomorpha). *J. Comp. Neurol.* 517:616–32
92. Ranf S. 2017. Sensing of molecular patterns through cell surface immune receptors. *Curr. Opin. Plant Biol.* 38:68–77
93. Rengarajan S, Hallem EA. 2016. Olfactory circuits and behaviors of nematodes. *Curr. Opin. Neurobiol.* 41:136–48
94. Reynolds AM, Dutta TK, Curtis RH, Powers SJ, Gaur HS, Kerry BR. 2011. Chemotaxis can take plant-parasitic nematodes to the source of a chemo-attractant via the shortest possible routes. *J. R. Soc. Interface* 8:568–77
95. Rosso MN, Favery B, Piotte C, Arthaud L, de Boer JM, et al. 1999. Isolation of a cDNA encoding a beta-1,4-endoglucanase in the root-knot nematode *Meloidogyne incognita* and expression analysis during plant parasitism. *Mol. Plant-Microbe Interact.* 12:585–91
96. Shah SJ, Anjam MS, Mendy B, Anwer MA, Habash SS, et al. 2017. Damage-associated responses of the host contribute to defence against cyst nematodes but not root-knot nematodes. *J. Exp. Bot.* 68:5949–60
97. Shi Q, Mao Z, Zhang X, Zhang X, Wang Y, et al. 2018. A *Meloidogyne incognita* effector MiISE5 suppresses programmed cell death to promote parasitism in host plant. *Sci. Rep.* 8:7256
98. Shivakumara TN, Dutta TK, Chaudhary S, von Reuss SH, Williamson VM, Rao U. 2019. Homologs of *Caenorhabditis elegans* chemosensory genes have roles in behavior and chemotaxis in the root-knot nematode *Meloidogyne incognita*. *Mol. Plant-Microbe Interact.* 32:876–87
99. Siddique S, Grundler FMW. 2018. Parasitic nematodes manipulate plant development to establish feeding sites. *Curr. Opin. Microbiol.* 46:102–8
100. Sikder MM, Vestergard M. 2019. Impacts of root metabolites on soil nematodes. *Front. Plant Sci.* 10:1792
101. Smant G, Jones J. 2011. Suppression of plant defences by nematodes. In *Genomics and Molecular Genetics of Plant-Nematode Interactions*, ed. J Jones, G Gheysen, C Fenoll, pp. 273–86. Dordrecht, Neth.: Springer
102. Smant G, Stokkermans JPWG, Yan YT, de Boer JM, Baum TJ, et al. 1998. Endogenous cellulases in animals: isolation of beta-1,4-endoglucanase genes from two species of plant-parasitic cyst nematodes. *PNAS* 95:4906–11
103. Sun Y, Li L, Macho AP, Han Z, Hu Z, et al. 2013. Structural basis for flg22-induced activation of the *Arabidopsis* FLS2-BAK1 immune complex. *Science* 342:624–28
104. Teillet A, Dybal K, Kerry BR, Miller AJ, Curtis RH, Hedden P. 2013. Transcriptional changes of the root-knot nematode *Meloidogyne incognita* in response to *Arabidopsis thaliana* root signals. *PLOS ONE* 8:e61259
105. Teixeira MA, Wei LH, Kaloshian I. 2016. Root-knot nematodes induce pattern-triggered immunity in *Arabidopsis thaliana* roots. *New Phytol.* 211:276–87
106. Topalovic O, Bredenbruch S, Schleker ASS, Heuer H. 2020. Microbes attaching to endoparasitic phytonematodes in soil trigger plant defense upon root penetration by the nematode. *Front. Plant Sci.* 11:138
107. Torres JLL. 2019. *Proline-rich extensin-like receptor kinases mediate damage-triggered immune responses to nematode infections*. Paper presented at IS-MPMI XVIII Congress, Glasgow, UK, Jul. 18
108. Tsai AYL, Higaki T, Nguyen CN, Perfus-Barbeoch L, Favery B, Sawa S. 2019. Regulation of root-knot nematode behavior by seed-coat mucilage-derived attractants. *Mol. Plant* 12:99–112
109. Tsai AYL, Iwamoto Y, Tsumuraya Y, Oota M, Konishi T, et al. 2021. Root-knot nematode chemotaxis is positively regulated by L-galactose sidechains of mucilage carbohydrate rhamnogalacturonan-I. *Sci. Adv.* 7(27):eabh4182
110. Umemoto N, Kakitani M, Iwamatsu A, Yoshikawa M, Yamaoka N, Ishida I. 1997. The structure and function of a soybean beta-glucan-elicitor-binding protein. *PNAS* 94:1029–34
111. Vanholme B, Van Thuyne W, Vanhouteghem K, De Meutter J, Cannoot B, Gheysen G. 2007. Molecular characterization and functional importance of pectate lyase secreted by the cyst nematode *Heterodera schachtii*. *Mol. Plant Pathol.* 8:267–78

112. Veronico P, Melillo MT, Saponaro C, Leonetti P, Picardi E, Jones JT. 2011. A polygalacturonase-inhibiting protein with a role in pea defence against the cyst nematode *Heterodera goettingiana*. *Mol. Plant Pathol.* 12:275–87
113. Vidal B, Aghayeva U, Sun H, Wang C, Glenwinkel L, et al. 2018. An atlas of *Caenorhabditis elegans* chemoreceptor expression. *PLOS Biol.* 16:e2004218
114. Wang CL, Lower S, Williamson VM. 2009. Application of Pluronic gel to the study of root-knot nematode behaviour. *Nematology* 11:453–64
115. Warnock ND, Wilson L, Canet-Perez JV, Fleming T, Fleming CC, et al. 2016. Exogenous RNA interference exposes contrasting roles for sugar exudation in host-finding by plant pathogens. *Int. J. Parasitol.* 46:473–77
116. Warnock ND, Wilson L, Patten C, Fleming CC, Maule AG, Dalzell JJ. 2017. Nematode neuropeptides as transgenic nematicides. *PLOS Pathog.* 13:e1006237
117. Wilbers RHP, Schneiter R, Holterman MHM, Drurey C, Smant G, et al. 2018. Secreted venom allergen-like proteins of helminths: conserved modulators of host responses in animals and plants. *PLOS Pathog.* 14:e1007300
118. Williamson VM, Kumar A. 2006. Nematode resistance in plants: the battle underground. *Trends Genet.* 22:396–403
119. Wyss U, Grundler FMW. 1992. Feeding behavior of sedentary plant parasitic nematodes. *Neth. J. Plant Pathol.* 98:165–73
120. Wyss U, Zunke U. 1986. Observations on the behaviour of second stage juveniles of *Heterodera schachtii* inside host roots. *Rev. Nematol.* 9:153–65
121. Yan Y, Davis EL. 2002. Characterisation of guanylyl cyclase genes in the soybean cyst nematode, *Heterodera glycines*. *Int. J. Parasitol.* 32:65–72
122. Yang SS, Pan L, Chen Y, Yang D, Liu Q, Jian H. 2019. *Heterodera avenae* GLAND5 effector interacts with pyruvate dehydrogenase subunit of plant to promote nematode parasitism. *Front. Microbiol.* 10:1241
123. Zhang X, Peng H, Zhu S, Xing J, Li X, et al. 2020. Nematode-encoded RALF peptide mimics facilitate parasitism of plants through the FERONIA receptor kinase. *Mol. Plant* 13:1434–54
124. Zhao J, Li L, Liu Q, Liu P, Li S, et al. 2019. A MIF-like effector suppresses plant immunity and facilitates nematode parasitism by interacting with plant annexins. *J. Exp. Bot.* 70:5943–58
125. Zhao J, Mao Z, Sun Q, Liu Q, Jian H, Xie B. 2020. MiMIF-2 effector of *Meloidogyne incognita* exhibited enzyme activities and potential roles in plant salicylic acid synthesis. *Int. J. Mol. Sci.* 21(10):3507
126. Zheng Q, Putker V, Goverse A. 2021. Molecular and cellular mechanisms involved in host-specific resistance to cyst nematodes in crops. *Front. Plant Sci.* 12:641582
127. Zhou D, Godinez-Vidal D, He J, Teixeira M, Guo J, et al. 2021. A G-lectin receptor kinase is a negative regulator of *Arabidopsis* immunity against root-knot nematode *Meloidogyne incognita*. bioRxiv 459316. **https://doi.org/10.1101/2021.09.07.459316**
128. Zhuo K, Naalden D, Nowak S, Xuan Huy N, Bauters L, Gheysen G. 2019. A *Meloidogyne graminicola* C-type lectin, Mg01965, is secreted into the host apoplast to suppress plant defence and promote parasitism. *Mol. Plant Pathol.* 20:346–55
129. Zipfel C. 2014. Plant pattern-recognition receptors. *Trends Immunol.* 35:345–51

Annual Review of Phytopathology

Volume 60, 2022

Contents

Point-of-Care DNA Amplification for Disease Diagnosis and Management
José R. Botella 1

Going Viral: Virus-Based Biological Control Agents for Plant Protection
Jeroen Wagemans, Dominique Holtappels, Eeva Vainio, Mojgan Rabiey, Cristina Marzachì, Salvador Herrero, Mohammadhossein Ravanbakhsh, Christoph C. Tebbe, Mylène Ogliastro, María A. Ayllón, and Massimo Turina 21

Rooting Out the Mechanisms of Root-Knot Nematode–Plant Interactions
William B. Rutter, Jessica Franco, and Cynthia Gleason 43

The Phloem as an Arena for Plant Pathogens
Jennifer D. Lewis, Michael Knoblauch, and Robert Turgeon 77

Peptide Effectors in Phytonematode Parasitism and Beyond
Melissa G. Mitchum and Xunliang Liu 97

Yellow Dwarf Viruses of Cereals: Taxonomy and Molecular Mechanisms
W. Allen Miller and Zachary Lozier 121

Recognition and Response in Plant–Nematode Interactions
Shahid Siddique, Alison Coomer, Thomas Baum, and Valerie Moroz Williamson 143

Pathogen Adaptation to the Xylem Environment
Leonardo De La Fuente, Marcus V. Merfa, Paul A. Cobine, and Jeffrey J. Coleman 163

Exploring the Emergence and Evolution of Plant Pathogenic Microbes Using Historical and Paleontological Sources
Carolyn M. Malmstrom, Michael D. Martin, and Lionel Gagnevin 187

Diversity, Evolution, and Function of *Pseudomonas syringae* Effectoromes
Cedoljub Bundalovic-Torma, Fabien Lonjon, Darrell Desveaux, and David S. Guttman 211

Molecular Interactions Between *Leptosphaeria maculans* and *Brassica* Species
M. Hossein Borhan, Angela P. Van de Wouw, and Nicholas J. Larkan 237

Future of Bacterial Disease Management in Crop Production
Anuj Sharma, Peter Abrahamian, Renato Carvalho, Manoj Choudhary, Mathews L. Paret, Gary E. Vallad, and Jeffrey B. Jones 259

Ecology of Yellow Dwarf Viruses in Crops and Grasslands: Interactions in the Context of Climate Change
Jasmine S. Peters, Beatriz A. Aguirre, Anna DiPaola, and Alison G. Power 283

Mycovirus Diversity and Evolution Revealed/Inferred from Recent Studies
Hideki Kondo, Leticia Botella, and Nobuhiro Suzuki 307

Facilitating Reforestation Through the Plant Microbiome: Perspectives from the Phyllosphere
Posy E. Busby, George Newcombe, Abigail S. Neat, and Colin Averill 337

Climate Change Effects on Pathogen Emergence: Artificial Intelligence to Translate Big Data for Mitigation
K.A. Garrett, D.P. Bebber, B.A. Etherton, K.M. Gold, A.I. Plex Sulá, and M.G. Selvaraj 357

Exploring Soybean Resistance to Soybean Cyst Nematode
Andrew F. Bent 379

Errata

An online log of corrections to *Annual Review of Phytopathology* articles may be found at http://www.annualreviews.org/errata/phyto