

Root Knot Nematode (Meloidogyne spp.): Insights of Host Parasite Interactions

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Root Knot Nematode (*Meloidogyne spp.*): Insights of Host Parasite Interactions

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ABSTRACT

Plant-parasitic root-knot nematodes are minute worms that cause serious harm to crops and incite major agrarian misfortunes around the world. These parasitic worms enter the roots of host and then induce the formation of specialized feeding structures, which supply the necessary resources for the development of nematodes. These life forms cause sensational changes in the physiology and morphology of the plant. This paper sums up the latest advancements in plant-nematode cooperation and the different methodologies used to enhance host opposition in contrast to root-knot nematode (RKN). The current progress in genome sequencing innovations are explained including focus on genome altering which are adding to the critical advancement in understanding the plant-nematode cooperation systems. In like manner, molecular approaches to manage improvement in plant resistance in contradiction to nematodes which are considered.

Key words: Parasitism, Plant-nematode interaction, Effectors, Transcriptomics, Nematode control

The world's ever increasing population rate in past several years is a huge challenge in regard to eradicate all forms of hunger and providing enough food supply [1]. Plant nematodes are responsible for significant agricultural loss. These organisms have emerged as nature's best of all plant parasites. Root-knot nematodes (RKN) are considered among the most devastating plant parasites all throughout the planet. The harm by nematodes is studied to a loss of around hundred billion dollars yearly in common plant produce [2], notwithstanding the entirety of present utilized approaches for nematode control. In India, nematodes have been estimated to cause around 21.3% of crop loss which amounts to Rs. 102,039 million annually [3]. Moreover, the increase in worldwide temperature because of environmental changes seem to have influenced nematode populaces either by speeding up their life cycle as the soil temperature increments, or by changing host plant physiology which depends upon the infection and interaction [4].

Nematodes can also be determined as Roundworms (phylum Nematoda). These are cosmopolitan in nature, found in almost every ecological niche in practically all territories throughout the planet [5]. Most nematodes are free-living and support themselves by devouring micro-organisms or other minute living beings while other species are parasites of plants or animals. The three most important nematodes are Cyst

nematodes (CN), root-knot nematodes (RKN) and Lesion nematodes (LN) that can contaminate, feed and duplicate on a huge variety of plant species [6]. The most common species of Cyst nematodes, root-knot nematodes and Lesion nematodes are *Heterodera* and *Globodera*, *Meloidogyne sp.* and *Pratylenchus sp.* respectively. An egg, four juvenile stages and an adult stage are six stages of nematode life cycle. In their life cycle, they go through 4 moults from juvenile to adult phase. The, root-knot nematodes juvenile moves intercellularly, infiltrating the root, relocating to the plant cortex throughout the root tip. The juveniles, at that point, enter the foundation of the vascular chamber and relocate up the root [7]. They build up a perpetual feeding site in the separation zone of the root by instigating nuclear division without cytokinesis in those cells. This interaction leads to formation of huge multinucleate giant cells (GC). The plant cells in the region of feeding site swell and divide, leading to galls or 'root knot' formation. The nematodes enter the cytoplasm of the plant-determined giant cells through their stylets and change into pear-molded, egg laying females after three moults. Syncytia and giant cells fill up as metabolic sinks, and channelize plant assets to the parasitic nematode. An online chase offers a hint of the growing interest worldwide in view about the association among, root-knot nematodes and their host plants. This paper further reviews current technique used to analyze the sub-molecular reason of the association, and genomics advancements. Finally, it summarizes the couple of approaches to manage the complete data about molecular go between of the plant-, root-knot nematodes correspondence alongside genome planning headways towards developing nematode resistance. At last, it

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will sum up the few ways to deal with carry out the information about sub-molecular mediators of the plant-, root-knot nematodes interaction.

Plant- Root knot nematode (RKN) interaction

The external protective layer of plant cell wall offers mechanical help to the plant cell across the intracellular pressure. Flexible cell wall structures are expected to react to different advancement conditions, abiotic and biotic improvement [8]. Plant cell wall structure and its synthesized substances act as a boundary to numerous vermin including nematodes. RKN has a stylet which is utilized as an instrument for compelling itself through the plant cell wall. Regardless of this, host cell walls are processed by the protein emitted by RKN. This works with fruitful infiltration into the root and relocation inside the plant cell and become stationary. Effector proteins are discharged in the plant cells from the dorsal organ of RKN to begin the advancement of feeding site in the plant root. RKN takes supplements from this exceptional feeding site. Thus, these effector proteins boost the host to benefit RKN and protect the latter against the plant guard [9]. The secretions that are produced by the nematodes play a vital role in different aspects of plant nematode interaction and pathogenesis [10].

Nematode sets up a direct relationship with the host during disease. Giant cell (GC) comprises of numerous nuclei, which results from repeated nuclear division without cell division. At first, a subsequent nucleus is viewed as an indication of interference of cell advancement by RKN. The condition appears to be that cell will partition into two, but results in a cell with two nuclei due to the disturbance in formation of the cell plate. Division of nuclei continues until GC contains around hundreds of nuclei. The size of GC might be up to multiple times greater than standard root vascular cells. RKN continually extricates cytoplasm from the contaminated cell, changing over it as a metabolic sink for the host. Division of cell close by RKN and GC lead to an expansion resulting into the development of bunches in the base of the host. Protection reaction is initiated in the host during pathogenesis by the parasitic nematode. As reported earlier, injury responsive jasmonate and ethylene pathways are endless supply of nematode in rice. A solid diminishing of chemical pathway identified with safeguard fundamentally ethylene and salicylate has been set apart in GC, creating nerves and encompassing tissues [11].

The genome of root knot nematode

Genetic sequences of various organisms and their important stages represent valuable information which can further be used in both *in-vivo* and *in-silico* tools to unlock the details of these genetic sequences. With large quantities of the data and the right tool to analyze, comparative genomic studies have elucidated several mechanisms by which organisms (parasites) have adapted parasitic mode of life. Acquisition, deletion, diversion and conservation of genetic components are some of the probable mechanisms which have helped adapting parasitic mode of life. A few genomes of horticulturally significant species of RKN have been sequenced utilizing short-read sequencers [12]. The genomes of asexual *Meloidogyne* species are polyploid and comprise of copied locales with high nucleotide dissimilarity (8%) [13]. In addition, the genome of sexual *Meloidogyne hapla* contain less transposable components (TEs) than the asexual *Meloidogyne sp.* genome. These highlights may present genomic versatility and utilitarian disparity between quality

duplicates without sex and meiosis. These genomic highlights make it actually hard to produce coterminous organizations utilizing short peruses. The detailed genome sequences of the asexual *Meloidogyne* species, like *Meloidogyne incognita*, *Meloidogyne arenaria* and *Meloidogyne javanica*, are profoundly contrasted with the *M. hapla* genome sequences [14].

The RKNs haploid genome proportion was outlined to associate with eighty-six Mb in size [15]. Regardless, genome sequencing of three root-knot nematodes species was made in 2017 using Illumina and 454 levels of progress and uncovered an amassed collecting of 236, 258, and 184 Mb for *M. javanica*, *M. arenaria* and *M. incognita*, unreservedly [15]. These outcomes recommend polyploidy of other three *Meloidogyne* species, since their genomes are 3–5 times greater than the *M. hapla* genome. Utilizing further developed computational investigation instruments, these examinations assessed the genomes of the previously mentioned contemplated *Meloidogyne spp.* to hold at any rate 43,718, 97,208, 14,700 and 103,001, protein coding qualiknots for *M. incognita*, *M. javanica*, *M. hapla* and *M. arenaria*, separately [13].

Likewise, the sequence genomes sizes were affirmed with flow cytometry. The all-out size of the amassed genome of model *Caenorhabditis elegans* nematode is involved hundred Mb [16]. The primary reference genome of *M. incognita* was distributed in 2008 [12] and consequently modified (promotion GCA_900182535.1). To dissect the type of our sequence reference genome, short peruses were planned onto both genome sequencing and planning rates were thought about. Planning rates were comparative, demonstrating that the designs of the two-genome sequencing were likewise comparative. This highlights that emerging genome sequencing innovations can convey extraordinary genomes of root-knot nematodes and will enable careful examination of the development of RKN later on.

Molecular analysis of plant- root knot nematode interaction Transcriptomics

Transcriptomics is the investigation of the transcriptome—the total arrangement of RNA records that are delivered by the genome, under explicit conditions or in a particular cell—utilizing high-throughput techniques, for example, microarray examination. Correlation of transcriptomes permits the distinguishing proof of qualities that are differentially communicated in unmistakable cell populaces, or in light of various medicines.

Present day transcriptomics utilizes high-throughput techniques to investigate the declaration of various records in various physiological or obsessive conditions and this is quickly extending our comprehension of the connections between the transcriptome and the aggregate across a wide scope of living elements. The transcriptomic changes in *Arabidopsis thaliana* at starting stages after illness with cyst nematodes and RKN and found that 1161 characteristics were up-coordinated in giant cells, of which 529 characteristics were similarly activated in the syncytia, showing that there is transcriptomic cover provoked by the two kinds of nematodes [17]. The qualities controlled in monster cell arrangement are influenced by phytohormones, particularly auxin and ethylene, like the homeobox protein HAT1 and ethylene-responsive record part such as ESE3. These findings underscored the role of high throughput transcriptome sequencing for research on root knot nematode.

Root-knot nematodes effectors

Root-knot nematodes discharge atoms called "effectors," to work with attack of the host root, surpass the plant protection reactions and reconstruct root cells to frame particular feeding sites. These effectors are delivered essentially in three oesophageal salivary organs and are then infused into plant cells through the needle like stylet. The movement of the oesophageal organs is formatively managed. The two subventral organs discharge effectors permitting second juvenile (J2) infiltration and movement in the root while proteins emitted during parasitism are created by subventral organs, especially by the dorsal organ [18]. A few effectors may likewise be delivered in other secretory organs, for example, chemosensory amphids, or straightforwardly discharged through the PPN fingernail skin. Sub-molecular discourse contemplates have zeroed in generally on discharged proteinaceous effectors [19-20] despite the fact that other emitted particles, like phytohormones, have been appeared to support these co-operations [21].

Researchers have recognized a few effectors discharged by , root-knot nematodes to work with parasitism by stifling their host's safety reaction. The *Meloidogyne* effector protein mimsp40 focuses on the plant microorganism related sub-molecular example (PAMP) set off resistance (PTI). Overexpression of mimsp40 in *Arabidopsis* plants brought about solid contamination and feeble defenseless plants by smothering PTI as well as ETI signals (effector-set off resistance). In such a way, expanded plant weakness to nematodes as the quantity of galls and eggs fundamentally expanded following a month and a half of vaccination [22]. Protein, Mc1194, was uncovered as an effector that works with the disease of *M. chitwoodi* by collaborating with the protease and granulin areas of RD21A in *Arabidopsis*, which is an individual from the papain-like cysteine proteases (PLCP) that are engaged with customized cell demise. The cysteine proteinase RD21A was assumed as a part in the protection reaction against the necrotrophic parasitic microorganism *Botrytis cinerea* in *Arabidopsis* [23]. These models show that RKN utilize a vast number of effectors to control host plant roots. Nonetheless, many effectors not yet published and still unknown.

Control strategies for root-knot nematode

Control refer to the exact plan to decrease the amount of parasitic nematodes while management has the purpose of reduce the losses in economy and believe the whole system of treatment and care of plant crop pests [24]. Diverse administration alternatives that are generally utilized for plant-parasitic nematodes are pertinent for *Meloidogyne spp.* on tomato as mentioned underneath.

Cultural control

The utilization of social control techniques to oversee root-knot nematodes is the most naturally reasonable and possibly best strategy for restricting root-knot nematode harm. Nonetheless, on the grounds that root-knot nematodes have enormous host ranges, social control techniques require cautious arranging. Vegetable fields plagued with *M. hapla* can possibly be planted to a nonhost harvest like corn, however, the producer's momentary economic return could be lessened. If the grower can identify an alternative nonhost crop with high financial return, crop rotation can be very successful. In contrast, *M. incognita* on cotton, as discussed earlier can usually be managed effectively with crop rotation [25].

Another social control methodology is the utilization of cover crops. Cover crops can be utilized outside the typical horticultural developing season, and some are hostile to nematodes. Cover crops, for example, Sudan grass and marigolds really produce synthetics that are harmful to nematodes. Cover crops have the additional advantages of balancing out dirt and improving soil quality. Similarly, as with crop rotation, nonetheless, particular gear might be needed to manage distinctive cover crops. Different strategies, including flooding and solarization of fields, have controlled nematodes, however just in warm environments and when a specific field can be eliminated from development for significant stretches during the treatment [26]. While social control techniques are amazingly important instruments, they require broad thought, arranging and financial speculation before fruitful execution can be accomplished.

Chemical control

Truly, chemical control has been the main methodology to lessen *Meloidogyne* populaces [27]. 78.3% of the ranch counselors in south-eastern Spain referenced compound soil fumigation as the most ordinarily utilized administration strategy for root-knot nematodes, trailed by non-fumigant nematicides (59.8%). A mix of nematicides with soil solarization and joining on safe rootstocks were viewed as the best techniques for root-knot nematode protection. Expanding natural and wellbeing concerns brought about the boycott of methyl bromide, and compound nematicides are being debilitated explicitly as a sole administration technique. Notwithstanding, new ages of less destructive nematicides are opening up because of rejuvenated interest by the yield insurance industry [28].

Biological control

Biopesticides can be characterized as the pesticides made of living beings or their components and they are utilized to guard plants against attacking microbes. The microorganisms utilized as biopesticides are ingested by the host life form (the plant microbe) and can cause tissue obliteration, and emit poisonous substances that influence the host living being. There are a few nematode-hostile biocontrol specialists that have distinctive nematophagous properties and are characterized into various classes appropriately. The method of activity of these biocontrol specialists contrasts from one another and they could be explicit to the nematode formative stage. For example, *Paecilomyce lilacinus* assaults eggs of *Meloidogyne spp.* in tomato plant [29]. Another biocontrol specialist concentrated to test its impact in the concealment of RKN contamination comprised of two unique strains of the organism *Verticillium lecanii*. Soil vaccination with the two strains separately smothered the RKN egg numbers. The two strains stifled RKN even in the wake of being autoclaved, which showed that the created substance that represses nematodes is heat-stable [30].

Integrated nematode management

The best ways to deal with nematode control depend on integrated pest management systems (IPM). IPM joins the board alternatives to keep up nematode densities underneath financial boundary levels. IPM methods can in any case be hard to carry out against a microorganism as forceful and strong as root-knot nematodes. Altogether, a mixture of the board strategies/devices, including social practices (rotation with nonhost harvests and cover crops that favor the development of nematode rivals), safe cultivars, and synthetic

soil medicines, if vital, for the most part give worthy control of root-knot nematodes. The level of this accomplishment, in any case, is dependent after having careful damage boundary densities and open and expeditiously good safe cultivars.

CONCLUSION

Root-knot nematodes are viewed as one of the genuine irritations that cause immense prudent misfortune to various rural plants and decrease the yield. Misfortunes range from minor impact to heavy yield loss. Root-knot nematodes are exceptionally hard to control first and foremost similar to a soil borne microorganism and furthermore having a more extensive host range. Numerous synthetic substances are tried and utilized generally to control the root-knot nematodes yet they are demonstrated to be harmful, costly and cause genuine impact to nature. The other option as organic control, botanicals and safe cultivars can be utilized for the administration of root-knot nematodes and decrease of the harm caused. Subsequently, understanding the molecular function of plant nematode associations and recognizing key qualities and proteins associated with the process of infection and the plant opposition reaction will help in growing new strategies to deliver plant lines more impervious to nematode contamination. The molecular level of the interaction between root-knot nematodes and plant by various methodologies was dealt in this paper. These methodologies describe effectors of root knot nematode to be potential targets for gene silencing by their expression profiles. Additionally, it may be proposed to utilize genes from biocontrol specialists, for example, *Paecilomyces javanicus* to activate and fortify the plant

immune reaction against infection with root-knot nematodes. It will similarly give a significant gadget to reproducing programs by successfully joining the opposition of root knot nematode into improved cultivars. In any case, these methodologies should be warily applied to stay away from rise of new hyper-harmful root knot nematode populaces and pleiotropic impacts on plant development and fruit quality that could reduce crop yields. This review is aimed to seek attention to the significant parts of genome technologies to study the basis of root-knot nematodes resistance and to comprehend the molecular angles behind the interaction with their host plant towards plant security against nematode resistance. These plant parasitic nematode cause agricultural losses every passing year. Presently, measures to control nematodes are inadequate and contain the usage of bromomethane or planting crops. The accessibility of chemical pesticides is falling and host resistance is inadequate. The population of nematode those are risky on safe plants keep on showing up. The nematode genes identification that is implicated in specific processes of nematode and their parasitism (RNAi), Nematode genome and microarrays projects that are freshly established techniques in PPN biology should assist to accelerate the procedure of gene discovery.

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