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Mitogenome Sequencing of a Root-knot Nematode *Meloidogyne javanica* Infected Okra Plant in Iraq

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ABSTRACT

Background: *Meloidogyne javanica* is a plant-pathogenic nematode. In many parts of the world, it is a serious agricultural pest. PCR-based sequencing of nematode mtDNA remains challenging because genomes are frequently organized and sequence similarities among lineages are low.

Methods: Using next generation sequencing (NGS), the genome of nematode-infected okra was sequenced, including the mitochondrial genome. The Illumina platform produced high quality 246,065,254 reads. The whole genome sequencing (WGS) was performed on okra at a high sequencing depth, approximately 31X coverage. The assembled reads against mitochondrion reference genome were 75,174 reads that completely covered the sequence with 96.5% identity.

Result: *Meloidogyne javanica* mitochondrion isolate Kufa-Abbasiya consensus sequence of 17,654 nt length deposited in GenBank (accession number OR038715). Phylogeny revealed that the examined mitochondria genome was closely related to *M. javanica* and *M. incognita* isolated from USA. However, the alignment shows variation within repeat region.

Key words: *Meloidogyne javanica,* mtDNA, Okra plant, Next generation sequencing.

INTRODUCTION

Abelmoschus esculentus (L.) Moench, the okra plant, is a vegetable grown throughout Iraq. In comparison to countries like Jordan, Cyprus, Egypt and India, Iraq's production of okra varies seasonally but is still incredibly low per donum (1/4 hectare) also the good plant with good growth because increase the average of phosphorus rate (Alaa *et al.,* 2026; Sheerali *et al.,* 2025). For fiber, it has significant industrial or nutritional value. Its high vitamin, mineral, carbohydrate and fat content are some of its advantages. Because of its curative qualities, okra has been used in traditional medicine to treat boils and wounds. It may have anti-microbial, anti-diabetic, anti-cancer and anti-blood pressure properties (Agregán *et al.,* 2022). This low productivity is additional exacerbated by numerous agricultural pests and viral diseases predominant in the Iraqi environment (Al-Abedy *et al.,* 2019). The green pod fruits of okra are greatly sought after by many Iraqis when they are completely formed, tiny and soft because there are numerous uses for them. In the Najaf Governorate, the combined okra crop produced 253 tons in 2019, 1,161 tons in 2020 and 93,396 tons at the Iraqi level in 2021. (Iqbal *et al.,* 2011). Nematodes are the most frequent pathogen that naturally infects okra and drastically decreases productivity. They have been identified as a hazard to global food supply, depending on the worm species, crop and geographical region. Nematodes inject hormones into plant roots, reducing their ability to absorb water and minerals, as well as interfering with photosynthesis and mineral transfer (Sharma *et al.,* 2018). The roots of the okra plant are infected with many types of nematodes belonging to different genera, including *Meloidogyne* spp., which cause significant damage to the plant, which affects its growth and productivity (Ali and Wissam, 2023). *Meloidogyne javanica* is the most important nematode species because they infect more than 100 species of globally important vegetable crop, including the roots of okra, causing a sharp decline in growth (Ali and Wissam, 2023) When *Meloidogyne javanica* infests a variety of crops, including vegetables, it causes characteristic galls that significantly stunt growth (Miead and Aljuaifari, 2023). Besides nematodes, soil-borne fungal pathogens, such as *Fusarium culmorum* also cause severe damping-off and seed decay in okra plants, which can be alleviated by using biological control agents such as *Trichoderma* spp. (Mahmood and Al-Abedy, 2021). The mitochondrial of DNA, it is usually maternally transmitted in rot-knot nematodes (Hoolahan *et al.,* 2011; Gutie´rrez-Gutie´rrez *et al.,* 2011) and the polymorphism of

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this genome is therefore advantageous for tracking maternal lineages. The cox mitochondrial gene, for example, was used to investigate the genetic makeup of some pathogenic nematodes, such as dagger nematode (*Xiphinema* sp.) (Okimoto *et al.,* 1991). Despite the fact that the structure of the *M. javanica* mitochondrial DNA was characterized more than 20 years ago and that about 20% of the genome has been partially sequenced, they are not a reference for the mitochondrial genome currently accessible for root-knot nematodes (Okimoto *et al.,* 1991). In present times, the superfamily Hoplolaimoidea has three complete mitogenomes recorded in the databases collection (Jacob *et al.,* 2009; Gibson *et al.,* 2011), for the distantly related nematodes that include *Pratylenchus vulnus* (Pratylenchidae), *Heterodera glycines* (Heteroderidae) and *Radopholus similis*. As a result, little is known about this important nematode lineage's mitogenome differences. This also appears to demonstrate a determination to develop genetic tools based on variations in the mtDNA sequences for a variety of purposes, including phylogeography, population genetics and the identification of species or races. Furthermore, the development methods of PCR-according to sequence long mitochondrial DNA segments is hampered by the frequent mitogenome rearrangements observed in Hoplolaimoidea (Picard and Plantard, 2005) as well. Lastly, the genes found in the mitochondrial genomes of nematodes pose a problem, especially the frequently truncated transfer RNA genes that are hard to detect with the instruments available today. The sequencing of organellar genomes is undergoing a revolution thanks to recent advances in new sequencing technologies called next generation sequencing (NGS) (Hahn *et al.,* 2013). Although the mitochondrial genomes of several metazoan organisms have been produced using NGS, the method still usually depends on sequencing long-range polymerase chain reaction products. Although this approach has not been tested on nematodes, it offers the chance to rapidly associate the most common DNA regions in a genome with sequencing depth levels (Hahn *et al.,* 2013). In particular, 10 million short DNA segments can be produced using Illumina technology, such as HiSeq 2000 (Inc. Illumina, HiSeqTM. 2000) length of each read (100-base pair reads) that are utilized for this purpose. Here, a reference mitogenome for root-knot nematodes was created by routinely evaluating the Illumina technology on *Meloidogyne javanica*. The mitochondrial DNA genome's full sequence was published and compared to *Meloidogyne javanica*'s mitochondrial DNA gene map and other species in the Hoplolaimoidea superfamily. Finally, a brief discussion of the method's utility for producing extensive mitochondrial DNA resources in the *Meloidogyne javanica* nematode was given.

MATERIALS AND METHODS

Total nucleic acids (TNA)

After being submerged in RNALater solution in an Eppendorf tube, a small pieces of root tissues from infected plant was submitted to JS-Link Company (South Korea). Total nucleic acids (TNA) were extracted from 2 gr root-knots of examined sample as got from fresh DNA as done by Sonal *et al.* (2026) and using the CTAB-based protocol of Doyle and Doyle (1990), with minor modifications. This included grinding the material with liquid nitrogen, extracting it using CTAB buffer at 65°C, extracting it using a mixture of chloroform and isoamyl alcohol, precipitating it with isopropanol, washing it with ethanol, resuspending the TNA in sterile ultrapure water and storing it at -20°C. Agarose gel electrophoresis was used to evaluate the TNA's quality and a spectrophotometer (NanoDrop® ND-100 spectrophotometer, Thermo Scientific) was used to measure the concentrations. Plant material**,** On July 23, 2022, okra plants infected with nematodes were collected from the Kufa-Abbasiya district in Najaf, Iraq. The infected plant roots were cut into tiny pieces, about 0.5 cm in size and then submerged in a 5x volume of RNA in Eppendorf tubes. For the purpose of extracting DNA, the samples were designated as OD. Following that, the patterns were transferred to the DNA Link company in the Republic of Korea for sequencing.

DNA extraction

Approximately 2 g of root-knot were treated with cetyl-trimethylammonium bromide methods (Doyle and Doyle, 1990) with a little modification (preheating a CTAB buffer for fourth five minutes and spinning down speed up DNA for 5 minutes).

Illumina-next generation sequencing

The library of next generation sequencing concoction that had been attempted for company, through the using the Library of TruSeq DNA used kit of DNA sequencing. DNA was extracted from the samples that were sequenced at the JS-Link Company utilizing whole genome sequencing (PCR Free550), which was developed on the industrialist's step and Nova sequencing 6000 2×150 PE (Platform: NovaSeq6000; Application: WTS/mRNA). following the use of an Agilent 2100 Expert Bioanalyzer (Agilent) to assess DNA quality. In Geneious Prime® 2024.0.5, raw readings were trimmed using Trimmomatic-0.39 and BBduk v 37.22 (Minimum quality= 6). The minimum read length was 10 (Adapter/Quality Trimming Version 38.84; Brian Bushnell) and both ends were trimmed (Kearse *et al.,* 2012; www.geneious.com). The formula for calculating coverage for genome sequencing is (number of fastq reads × length of read)/genome size (1.19 Gb) (Khaffajah *et al.,* 2022).

Mapping to mitochondrion genome reference

Whole DNA reads (246,065,254 reads) were mapped to the sequence of *Meloidogyne javanica* mitochondrion (NC_026556) using Geneious map to reference v. 2024. The Geneious DNA mapper was used to perform the mapping with parameters set to "Medium-Low Sensitivity". The consensus sequence was extracted and then aligned with reference sequence to obtain the exact length of the

genome and then deposited in the NCBI-GenBank. Open reading frame finder and BlastN search were also applied. To ensure functionality, all protein-coding nucleotide sequences (CDS) were checked in their amino acids using MEGA 11 to x premature and truncated stop codons (Tamura *et al.,* 2021). The total number of reads used, the number of assembled reads, pairwise identity and coverage were provided in the report that presented the results.

Phylogenetic analysis

The mitochondrion genomes of *Caenorhabditis elegans* (NC_001328), *Meloidogyne incognita* (NC_024097), *M. arenaria* (NC_026554), *Meloidogyne enterolobii* (NC_026555), *M. javanica* (NC_026556), *M. graminicola* (NC_056772) and the examined nematode mitochondria genome were selected as input for phylogenetic analysis. The sequences were first aligned using Clustwal alignments in Geneious prime. The best substitution model Hasegawa-Kishino-Yano (HKY) was applied to build maximum likelihood tree and 1,000 bootstraps were used to infer the tree. The phylogenetic tree has been reconstructed by using the General Time Reversible (GTR). Bayesian phylogeny inference applied with Bayesian inference of phylogeny (MrBayes 3.2.6) (Mukhtar *et al.,* 2014).

RESULTS AND DISCUSSION

Genome assembly

The NGS Illumina platform produced high quality reads with about 246,065,254 reads. The WGS was performed on okra at a high sequencing depth, approximately 31X coverage. The assembled reads against mitochondrion reference genome were 75,174 reads that completely covered the sequence with 96.5% identity. The consensus sequence with 17,654 nt length representing the whole sequence of *Meloidogyne javanica* mitochondrion isolate Kufa-Abbasiya was extracted and deposited in Genbank under accession number OR038715. The genome has 12 genes and two ribosomal RNA, 22 transcribed RNA and one repeat region (Fig 1, Table 1).

Phylogeny revealed that the examined mitochondria genome was closely related to *M. javanica* (NC_026556) isolated from USA (Fig 2). However, the mitochondrion sequence has one long repeat region and it is longer than those in isolates of *M. javanica* (NC_026556) and *M. incognita* (NC_024097) and also lack control region (1025 nt). The length of the repeat region reached 2560 nt, while in *M. javanica* and *M. incognita*, the repeat region has divided to three regions 894, 76 and 564 nt with control region (1030 nt) in the middle (Fig 3). Our isolate and *M. javanica* (NC_026556) had a pairwise identity of 96.5%. The identity between *M. javanica* and *M. incognita* in mitochondria genomes probably reflect their highly resemblance in morphology.

A major problem for agriculture is the presence of plant-parasitic nematodes (PPNs). PPNs infect mostly angiosperms (monocots and dicots), although some of them can infect gymnosperms (Poinar, 1991). It is highly variable what type of PPNs feed (ectoparasites, endoparasites and semiendoparasites), how they reproduce (amphimixis, parthenogenesis and hermaphroditism), which plant organ they infect (roots, tubers, bulbs, stems and leaves) and what conditions they prefer. A recent survey indicated that root-knot nematodes (*Meloidogyne* spp.), burrowing nematode (*Radopholus similis*), cyst nematodes (*Heterodera* and *Globodera*), stem and bulb nematode (*Ditylenchus dipsaci*), reniform nematode (*Rotylenchulus reniformis*), dagger nematode (*Xiphinema index*), root-lesion nematodes (*Pratylenchus* spp.), false root-knot nematode (*Nacobbus aberrans*), pine wilt nematode (*Bursaphelenchus xylophilus*) and rice tip nematode (*Aphelenchoides besseyi*) are regarded as the

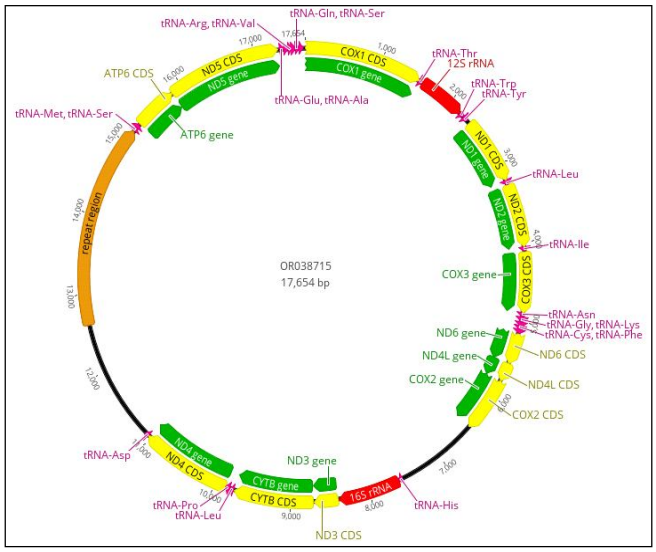

Fig 1: Genome organization of *Meloidogyne javanica* mitochondrion drawn by Geneious prime.

most important plant-parasitic nematodes worldwide (Jones *et al.,* 2013). Studies of PPNs' genetic structure have been conducted using mitochondrial DNA (Sultana *et al.,* 2013; Habib *et al.,* 2016). Based on the 18S region of the nuclear ribosomal RNA gene array, (Kiewnick *et al.,* 2014) found little variation within *Meloidogyne*, but more variation when mitochondrial DNA was analyzed. Molecular analysis of genetic variation across diverse environments is essential for characterizing varied plant-associated pathogens (Abdullah *et al.,* 2019). To distinguish

Table 1: Genes, rRNA, tRNA and repeat annotated regions with their IDs and lengths in the genome of *Meloidogyne javanica* mitochondrion isolate Kufa-Abbasiya.

Region	ID	Length nt	Region	ID	Length nt
Genes	ATP6	552	Genes	ND6	396
	ND5	1471		ND4L	237
	COX1	1522		COX2	693
	ND1	850		ND3	312
	ND2	802		CYTB	1015
	COX3	762		ND4	1173
rRNA	12S	610			
	16S	805			
Repeat		2560			

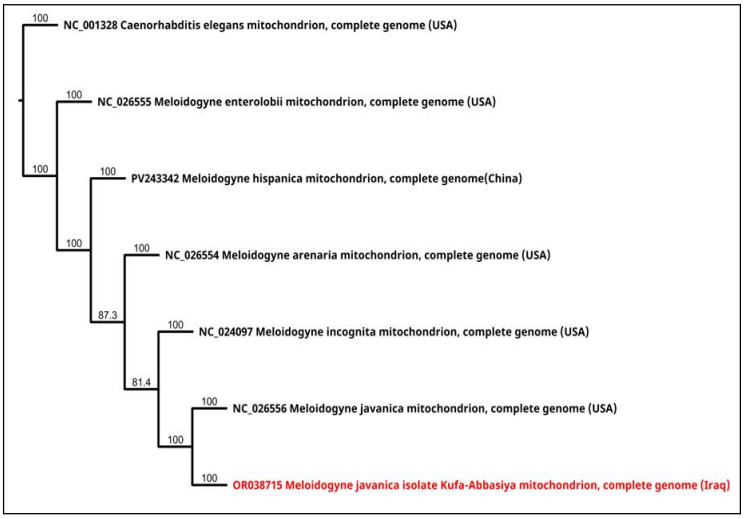

Fig 2: A Neighbour joining method tree based on the complete mitochondria genome sequences of *Meloidogyne* species. The number next to each nod indicates bootstrap support values.

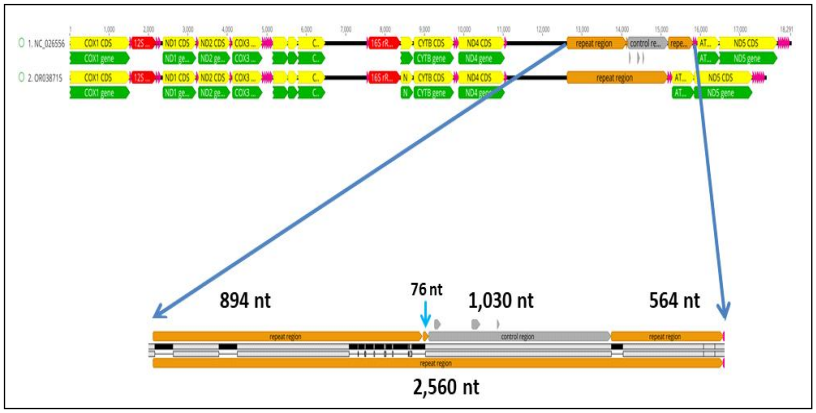

Fig 3: Repeat region differences were shown in pairwise alignment between mitochondria genomes of *M. javanica* isolate Kufa-Abbasiya (OR038715) and *M. javanica* (NC_026556) isolated from USA.

Meloidogyne species, (Armstrong *et al.,* 2000) developed two nuclear (18S and 28S) and mitochondrial DNA markers (cox1 and cox2). Similar molecular diagnostics and genetic diversity analyses have been effectively used to identify fungal pathogens, for example *Sclerotinia sclerotiorum* isolates causing white mold in solanaceous crops such as eggplants (Al-Shujairi *et al.,* 2022). There are 11 mt genomes of PPNs published, *i.e.*, *M. chitwoodi*, *M. incognita, M. graminicola, Heterodera glycines, Globodera pallida, G. rostochiensis, Pratylenchus vulnus, R. similis, B. xylophilus, Bursaphelenchus mucronatus* and *Xiphinema americanum* (Armstrong *et al.,* 2000; Sun *et al.,* 2014; Humphreys-Pereira *et al.,* 2014; He *et al.,* 2005; Powers, 2004). Using new sequencing technologies will likely accelerate and improve the sequencing of more nematode genomes, for example (Zasada and Moore, 2014), which describes the use of Illumina NGS to sequence the genomes of single individuals of *X. americanum* from 12 populations. Phylogenetic analysis of the 12 mt protein-coding genes (PCGs) has been performed on nematodes within the phylum Nematoda. In Iraq, our study is considered the first ever to determine the mitochondrial genome of PPN like *M. javanica.* Except the repeat region, the whole sequence was highly matched mitochondrion of USA isolate.

CONCLUSION

The results showed that the assembled reads against mitochondrion reference genome were 75,174 reads that completely covered the sequence with 96.5% identity. The mitochondrion sequence has one long repeat region and it is longer than in related isolates and also lack control region. Phylogeny revealed that the examined mitochondria genome was closely related to *M. javanica* that was a pathogen in this study with *M. javanica* (NC_026556) isolated from USA.

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Disclaimers

The authors did not disclose any potential conflicts of interest.

Informed consent

Informed consent is not required for this research study, as it was carried out on basil plants and does not include any human participants.

Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

REFERENCES

Ali, S.A. and Wissam, A.R.A. (2023). The possibility of manufacturing a biocidal of *Bacillus* spp. and their growth. *Kufa Journal for Agriculture Sciences.* **15(2):** 33-42. https://doi.org/10.36077/kjas/2023/v15i2.10356.

Alaa, H.F., Ibrahim, A., Hadres, A.I.K., Albajary, Q.S., Sheikh, Z.A. and Abdulkareim. (2026). Interactions of phosphatic fertilizers and organic matter under different incubation periods for enhancement of phosphorous availability in soil. *Indian Journal of Agricultural Research.* doi: 10.18805/IJARe.AF-1018.

Agregán, R., Pateiro, M., Bohrer, B.M., Shariati, M.A., Nawaz, A., Gohari, G. and Lorenzo, J.M. (2022). Biological activity and development of functional foods fortified with okra (*Abelmoschus esculentus*). *Critical Reviews in Food Science and Nutrition*. **63(23):** 6018-6033. https://doi.org/10.1080/10408398.2022.2026874.

Armstrong, M.R., Blok, V.C. and Phillips, M.S. (2000). A multipartite mitochondrial genome in the potato cyst nematode *Globodera pallida*. *Genetics*. **154(1):** 181-92. https://doi.org/10.1093/genetics/154.1.181.

Abdullah, A.A., Dewan, M.M. and AL-Abedy, A.N. (2019). Genetic variation of some isolates of *Cladosporium sphaerospermum* isolated from different environments. *In IOP Conference Series: Earth and Environmental Science*. *IOP Publishing*. **388(1):** 012016.

Al-Abedy, A.N., Karem, M.H. and Al-Asade, K.A. (2019). Characterization of three new strains of *Tomato yellow leaf curl virus* in Iraq. *Arab Journal of Plant Protection*. **37(3):** 223-231.

Al-Shujairi, K.A., Albehadlli, H.K., Kamaluddin, Z.N., Al-Abedy, A.N. and Al-Taey, D.K. (2022). Genetic variation among some *Sclerotinia sclerotiorum* isolates causing white mold disease in eggplants (*Solanum melongena*). *International Journal of Agricultural and Statistical Sciences*. **18(1):** 399-407.

Doyle, J.J. and Doyle, J.L. (1990). Isolation of plant DNA from fresh tissue. *Focus*. **12(1):** 13-15.

Gibson, T., Farrugia, D., Barrett, J., Chitwood, D.J., Rowe, J., Subbotin, S. and Dowton, M. (2011). The mitochondrial genome of the soybean cyst nematode, *Heterodera glycines*. *Genome*. **54(7):** 565-574. https://doi.org/10.1139/g11-024.

Gutie´rrez-Gutie´rrez, C., Castillo, P., Cantalapiedra-Navarrete, C., Landa, B.B., Derycke, S. and Palomares-Rius, J.E. (2011). Genetic structure of *Xiphinema pachtaicum* and *X. index* populations based on mitochondrial DNA variation. *Phytopathology.* **101(10):** 1168-1175. https://doi.org/10.1094/PHYTO-07-10-0194.

Hahn, C., Bachmann, L. and Chevreux, B. (2013). Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads-A baiting and iterative mapping approach. *Nucleic Acids Res*earch. **41(3):** e129. https://doi.org/10.1093/nar/gkt371.

Habib, S.H., Kausar, H. and Saud, H.M. (2016). Plant growth-promoting rhizobacteria enhance salinity stress tolerance in okra through ROS-scavenging enzymes. *BioMed Research International*. **2016:** 6284547. https://doi.org/10.1155/2016/6284547.

He, Y., Jones, J., Armstrong, M., Lamberti, F. and Moens M. (2005). The mitochondrial genome of *Xiphinema americanum* sensu stricto (*Nematoda: Enoplea*): Considerable economization in the length and structural features of encoded genes. *Journal of Molecular Evolution.* **61(6):** 819-833. doi: 10.1007/s00239-005-0102-7.

Hoolahan, A.H., Blok, V.C., Gibson, T. and Dowton, M. (2011). Paternal leakage of mitochondrial DNA in experimental crosses of populations of the potato cyst nematode *Globodera pallida. Genetica.* **139(11-12):** 1509-1519.

Humphreys-Pereira, D.A., Flores-Chaves, L., Gómez, M., Salazar, L., Gómez-Alpízar, L. and Elling, A.A. (2014). *Meloidogyne lopezi* n. sp. 2014. (Nematoda: Meloidogynidae), a new root-knot nematode associated with coffee (*Coffea arabica* L.) in Costa Rica, its diagnosis and phylogenetic relationship with other coffee-parasitizing *Meloidogyne* species. *Nematology.* **16(6):** 643-661. https://doi.org/10.1163/15685411-00002794.

Iqbal, K., Jin, S.G., Pfeifer, G.P. and Szabó, P.E. (2011). Reprogramming of the paternal genome upon fertilization involves genome-wide oxidation of 5-methylcytosine. *Proceedings of the National Academy of Sciences*. **108(9):** 3642-3647. https://doi.org/10.1073/pnas.1014033108.

Jacob, J.E.M., Vanholme, B., Van Leeuwen, T. and Gheysen, G. (2009). A unique genetic code change in the mitochondrial genome of the parasitic nematode *Radopholus similis. BMC Research Notes.* **2:** 192. https://doi.org/10.1186/1756-0500-2-192.

Jones, J.T., Haegeman, A., Danchin, E.G.J., Gaur, H.S., Helder, J., Jones, M.G.K., Kikuchi, T., Manzanilla-Lopez, R., Palomares-Ruis, J.E., Wesemael, W.M.L. and Perry, R.N. (2013). Top 10 plant-parasitic nematodes in molecular plant pathology. *Molecular Plant Pathology*. **14(9):** 946-961. https://doi.org/10.1111/mpp.12057.

Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., *et al.* (2012). Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. **28(12):** 1647-1649.

Kiewnick, S., Holterman, M., van den Elsen, S., Frey, J.E. and Helder, J. (2014). Comparison of two short DNA barcoding loci (COI and COII) and two longer ribosomal DNA genes (SSU and LSU rRNA) for specimen identification among quarantine root-knot nematodes (*Meloidogyne* spp.) and their close relatives. *European Journal of Plant Pathology*. **140:** 97-110. https://doi.org/10.1007/s10658-014-0446-1.

Khaffajah, B., Alisawi, O. and Al Fadhl, F. (2022). Genome sequencing of eggplant reveals eggplant mild leaf mottle virus existence with associated two endogenous viruses in diseased eggplant in Iraq. *Archives of Phytopathology and Plant Protection*. **55(16):** 1930-1943. https://doi.org/10.1080/03235408.2022.2123601.

Mahmood, A.M. and Al-Abedy, A.N. (2021). Effect of some species of *Trichoderma* spp. and the chemical fungicide Topsin M in control of the disease of seed rot and seedling damping-off of okra caused by *Fusarium culmorum*. *International Journal of Agricultural and Statistical Sciences*. **17(1):** 1701-1710.

Miead, F.S. and Aljuaifari, W.A.R. (2023). Field evaluation of *Bacillus* spp. in controlling root-knot nematodes on okra plants (*Abelmoschus esculentus*). Accepted publish at Kufa Journal for Agriculture sciences.

Mukhtar, T., Hussain, M.A., Kayani, M.Z. and Aslam, M.N. (2014). Evaluation of resistance to root-knot nematode (*Meloidogyne incognita*) in okra cultivars. *Crop Protection*. **56:** 25-30. https://doi.org/10.1016/j.cropro.2013.10.019.

Okimoto, R., Chamberlin, H.M., Macfarlane, J.L. and Wolstenholme, D.R. (1991). Repeated sequence sets in mitochondrial DNA molecules of root-knot nematodes (*Meloidogyne*): Nucleotide sequences, genome location and potential for host-race identification. *Nucleic Acids Research*. **19(7):** 1619-1626. https://doi.org/10.1093/nar/19.7.1619.

Picard, D. and Plantard, O. (2005). What constitutes a population for the plant parasitic nematode *Globodera pallida* in its native area (Peru)? *International Journal for Parasitology*. **36(1):** 115-122. https://doi.org/10.1016/j.ijpara.2005. 08.015.

Poinar, G.O. (1991). Nematoda and nematomorpha. In: Ecology and Classification of North American Freshwater Invertebrates. [J.H. Thorp and A.P. Covich (Eds.)]. Academic Press. 2nd ed., pp. 255-295. https://doi.org/10.1016/B978-012690647-9/50010-7.

Powers, T. (2004). Nematode molecular diagnostics: From bands to barcodes. *Annual Review of Phytopathology.* **42:** 367-383. https://doi.org/10.1146/annurev.phyto. 42.040803.140348.

Sharma, N., Khajuria, Y., Sharma, J., Tripathi, D.K., Chauhan, D.K., Singh, V.K., Kumar, V. and Singh, V.K. (2018). Microscopic, elemental and molecular spectroscopic investigations of root- knot nematode infested okra plant roots. *Vacuum*. **158:** 126-135. https://doi.org/10.1016/j.vacuum.2018.09.039.

Sheerali, S.M.R., Aljuaifari, W.A.R. and Alyasiri, H.I . (2025). Effect of biological factors in physiological and growth indicators of okra plant [*Abelmoschus esculentus* (L.) Moench] and percentage of (NPK) elements with root-knot nematode (*Meloidogyne javanica*). *Agricultural Science Digest*. **45(6):** 1011. doi. 10.18805/ag.DF-735.

Sonal, M., Pandey, P. and Ramjibhai, G.P. (2026). Molecular characterization and transmission behaviour study of *Okra Enation Leaf Curl Virus* Infecting okra. *Agricultural Science Digest*. doi: 10.18805/ag.D-6466.

Sultana, T., Kim, J., Lee, S.H., Han, H., Kim, S., Min, G.S., Nadler, S.A. and Park, J.K. (2013). Comparative analysis of complete mitochondrial genome sequences confirms independent origins of plant-parasitic nematodes. *BMC Evolutionary Biology.* **13:** 12. https://doi.org/10.1186/1471-2148-13-12.

Sun, L., Zhuo, K., Lin, B., Wang, H. and Liao, J. (2014). The complete mitochondrial genome of *Meloidogyne graminicola* (Tylenchina): A unique gene arrangement and its phylogenetic implications. *PloS One*. **9(6):** e98558. https://doi.org/10.1371/journal.pone.0098558.

Tamura, K., Stecher, G. and Kumar, S. (2021). MEGA11: Molecular evolutionary genetics analysis version 11. *Molecular Biology and Evolution*. **38(7):** 3022-3027. https://doi.org/10.1093/molbev/msab120.

Zasada, I.A. and Moore, P.P. (2014). Host status of *Rubus* species and hybrids for the root lesion nematode, *Pratylenchus penetrans*. *HortScience*. **49(9):** 1128-1131. https://doi.org/10.21273/HORTSCI.49.9.1128.