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**ORIGINAL ARTICLE**

# A NEW RECORD OF TWO NEMATODES, *MESORHABDITIS FRANSENI* FUCHS, 1933 (MESORHABDITIDAE) AND *PRATYLENCHUS GOODEYI* SHER AND ALLEN, 1953 (PRATYLENCHIDAE) WITH MOLECULAR DESCRIPTION FROM IRAQ

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## ABSTRACT

A rhabditid *Mesorhabditis franseni* Fuchs, 1933 (Family, Mesorhabditidae) and pratylenchid nematode *Pratylenchus goodeyi* Sher and Allen, 1953 (Family, Pratylenchidae). They were illustrated by molecular aspects. All specimens of both genera were cultured and reproduced for DNA extraction. *M. franseni* (IRQ.ZAh2 PP528819.1 isolate) was characterized. *P. goodeyi* (IRQ.ZAh5 PP535537 isolate) was also characterized. Selected specimens of these two species were molecularly characterized using the partial *ITS-rRNA* gene sequences. The *ITS-rRNA* sequence of IRQ.ZAh2 PP528819.1 isolate had a range of (98.62%-100%) sequence homology with *ITS-rRNA* sequence of *M. franseni* available in NCBI database. While, the *ITS-rRNA* sequence of IRQ.ZAh5 PP535537 isolate had (100%) sequence homology with *ITS-rRNA* sequence of *P. goodeyi* available in NCBI database. *M. franseni* (IRQ.ZAh2 PP528819.1 isolate) and *P. goodeyi* (IRQ.ZAh5 PP535537 isolate) are Iraq's first documented instance of these species.

Key words: Iraq, *ITS-rRNA* gene, *Mesorhabditis*, *Pratylenchus*, Soil.

## INTRODUCTION

Since nematodes are aquatic organisms, they need sufficient soil moisture to move through the soil (Koppenhöfer and Fuzy, 2007). The majority of the species are accountable for the causes of economic losses, but far less is known about the majority of the nematode community that contributes to soil health. Numerous advantageous nematodes function as

biological pesticides in controlled environments, while others manage the soil's nutrient cycle and natural ecology (Jabbar *et al*., 2024). A small percentage of nematodes feed on plants and algae (the first trophic level); others are grazers that consume fungi and bacteria (the second trophic level); yet others consume other nematodes (the higher trophic levels). Several trophic levels of the soil food chain are home to various nematodes. The surface soil horizon is where nematodes are most prevalent (Yadav *et al*., 2018). In soil food webs, microfauna predators such as nematodes and protozoa are essential for connecting primary consumers like bacteria and fungi to higher trophic levels. They contribute to soil nutrient cycling and mineralize elements contained in microbial tissue by preying on micro-organisms (Neidig *et al*., 2010; Kadhim, 2021, 2022).

The phylum Nematoda covers an extraordinarily diverse range of biological environments and natural histories, such as arid deserts and deep-sea sediments, as well as interstitial bacterivores and obligate parasites with several intermediate hosts (Eyualem-Abebe *et al*., 2006). Because of their diversity and abundance, nematodes in the crop rhizosphere provide a unique perspective on soil biological activity and are thought to be a reliable bioindicator for assessment the soil sustainability of a production system (Khan and Chandra, 2017). They are common because of their remarkable endurance to severe environments (Kitagami *et al*., 2016). It's important to note that none of the primary orders that make up this phylum's composition are found to span the entire ecological range; instead, they each cover a significant part of it. Although their presence in marine environments is minimal at best, confined to a small number of sublittoral species e.g. *Rhabditis marina* [= *Litoditis marina* (Bastian, 1865)], the Rhabditida appear to be the group that covers the greatest variety of habitats (Eyualem-Abebe *et al*., 2006). The genus *Mesorhabditis* Osche, 1952 is found all over the world, which considered as a subgenus of *Rhabditis* Dujardin, 1845 with 16 valid species (Ahmad *et al*., 2010), while Andrássy (1983) were listed 17 valid species and 3 species inquirendae. Although it is widely distributed, there is only one species *M. cranganorensis* Khera, 1968, that Andrássy (1982) has been known from India (Ahmad *et al*., 2010).

The most common nematodes found in temperate soil are those in the family Paratylenchidae. The genus *Paratylenchus* Micoletzky, 1922 is useful for studying how humans affect the soil because they may be used as indicators of changes in soil composition. The largest complaint raised during research on the tiny size of the genera' representatives is that they are absent from some of the researched sites, which may be partially explained by the losses incurred during soil sample extraction due to the small size fraction of nematodes and the rather challenging (Rosmaninho *et al*., 2022). The presence of adult males is necessary for diagnosis, and occasionally populations that exhibit widespread juvenile stage occurrences at the sites during extremely challenging and time-consuming operations may even be included (Čermák and Renčo, 2010). *Pratylenchus* Micoletzky, 1922 is an endoparasite, it is known as the "root-lession nematode." Because of its damage when it enters the roots and creates hollow channels while moving and feeding inside the root system (Piedrahita *et al*., 2012). Although the exact number of valid *Pratylenchus* species is still up

for debate, the experts believe that there are roughly 103 species (Nguyen *et al*., 2019). As stated by Bell and Watson (2001a), nematodes of the genus *Pratylenchus* Micoletzky, 1922 are the primary food rival of *P. nanus* Cobb, 1923 because they share a similar anatomical structure and a same food niche. Time, soil collection depth, and the presence of non-specific pathogenic microorganisms, such as fungi (predators) (e.g. *Arhrobotrys* Corda, 1839 and *Monacrosporium* Oudemans, 1885, or other factors that affected the presence of *Paratylenchus* Micoletzky, 1922 in the soil sample, considering the fact that mineral soil layers contain the highest concentration of plant parasitic nematodes (Magnusson, 1983). The spring and autumn sample dates have the largest abundances (Bell and Watson, 2001b; Háněl, 2002). Numerous writers have examined various facets of the taxonomy of *Pratylenchus* species since Sher and Allen's initial study of the genus in 1953, providing new viewpoints on identification (Loof, 1960; 1978; Café Filho and Huang, 1989; Frederick and Tarjan, 1989; Handoo and Golden, 1989; Palomares-Rius *et al*., 2010).

The scanning electron microscopy (SEM) characterization (Corbett and Clark, 1983; Hernández *et al*., 2000; Inserra *et al*., 2007), as well as intraspecific variation of the primary morphological diagnostic features (Taylor and Jenkins, 1957; Roman and Hirschmann, 1969; Tarte and Mai, 1976). Nematode systematics and the practical identification of plant-parasitic nematodes have benefited greatly from the development of novel methodologies based on biochemical, molecular, and phylogenetic investigations in recent decades (Faraj *et al*., 2019; Faraj and Al- Amery, 2020; Kamal *et al*., 2024).

The value of this method for identification and phylogenetic reconstruction within the genus *Pratylenchus* Micoletzky, 1922 was shown by more recent investigations using *ITS-rDNA* (Waeyenberge *et al*., 2009; Palomares-Rius *et al*., 2010), hence the current study aimed to identify and describe the two nematodes: rhabditid *M. franseni* Fuchs, 1933 and pratylenchid nematode *Pratylenchus goodeyi* Sher and Allen, 1953 for the first time in Iraq.

## MATERIALS AND METHODS

**Collecting of soil samples:** A total of 54 soil samples were collected from three crop fields located in the Al Rashidiya (33˚25ˈ13.4" N 44˚21ˈ45.3" E), Al Jadriya (33˚16ˈ35.7" N 44˚23ˈ26.3" E) and Abo- Ghareeb (33˚19ˈ15.5" N 44˚11ˈ57.1" E), as shown in Map (1). The samples were collected within two seasons (Spring from April to May 2023 and Summer during July 2023).

The soil sample for each sample was composed of 5-7 subsamples randomly collected around each plant in a square -shaped fashion using a hand spade at a depth of 15-20 cm (Adegbite *et al*., 2006). Sub-samples were placed and mixed into a plastic bag that tightly closed to prevent the content from drying out, labeled and keep the samples away from direct sunlight, then stored at 8-10 ˚C in a cooler container until they were sent to the laboratory to extraction and estimate the presence of the nematodes. Three samples were taken from different parts of each site. The weight of each soil sample was (1.5-2 kg). Three replicates were taken from each homogenized sub- sample for collecting nematodes (Coyne *et al*., 2007).

**Isolation of nematodes:** The Baermann funnel technique was used to extract nematodes from 250 grams of soil (Cairns, 1960). Ten ml water suspensions were collected from each replicate and specifically screened in 1 ml randomly chosen. Dissecting microscope was used to isolate the nematodes.

**Cultivation of nematodes:** For DNA extraction and reproduced the isolated nematodes, last larval stage of greater wax moth *Galleria mellonella* (Linnaeus, 1758) were killed by sterilized lancet laced into a Petri-dish (9cm in diameter) with two pieces of filter papers. The isolated nematodes were added to the Petri dish which was held at room temperature (22 ± 2 ºC) for 5-7 days. The reproduced nematodes were collected and transferred to Eppendorf tube (1.5 ml) and were kept in a fridge at 8-10 ºC. All specimens of both genera were cultured and reproduced for DNA extraction.

**Scanning electron microscopy:** Morphological features of adults were examined using scanning electron microscopy (SEM). For examination, the specimens (adults) were rinsed with distilled water three times. Then they were mounted on aluminum SEM stubs, coated with gold nano-particles. Then used plasma spattering coater (China) and studied using an inspect f 50 scanning electron microscope (FEI Company, Holland).

**DNA extraction, amplification and electrophoresis:** About 50 gram of cultured nematodes was used to extract the total genomic DNA. The DNA extraction was done using gSYNC ™ total DNA Extraction kit (Geneaid, Taiwan) in accordance with the manufacturer's instructions. A thermal cycler was used to amplify segments of *ITS* region. The primer set of TW81 (forward) (5`- GTT TCC GTA GGT GAA CCT GC-3`) and AB28 (reverse) (5`- ATA TGC TTA AGT TCA GCG GGT-3`) was used followed (Joyce *et al*., 1994). The PCR profile for all loci included 35 cycles of amplification in an Eppendorf thermocycler were following the program of 94 °C for 4 minutes of initial denaturation, 35 cycles of 94 °C for 1 minute, 55 °C for 1 minute, and 72 °C for 2 minutes, and a final extension for 10 minutes at 72 °C. Subsequently, the PCR product was electrophoresed on 1% agarose gels for 40 minutes using 10X TBE buffer 5%, and the gel was stained with green-viewer (SYBR). Ultimately, 3 µl of the PCR product and 2.5 µl of DNA ladder were added to each gel well. A 100-bp molecular DNA ladder (Bioneer, Korea) was used to determine the size of the amplified products, the final volume for amplicone is 25 µl (Al-Zaidawi *et al*., 2019).

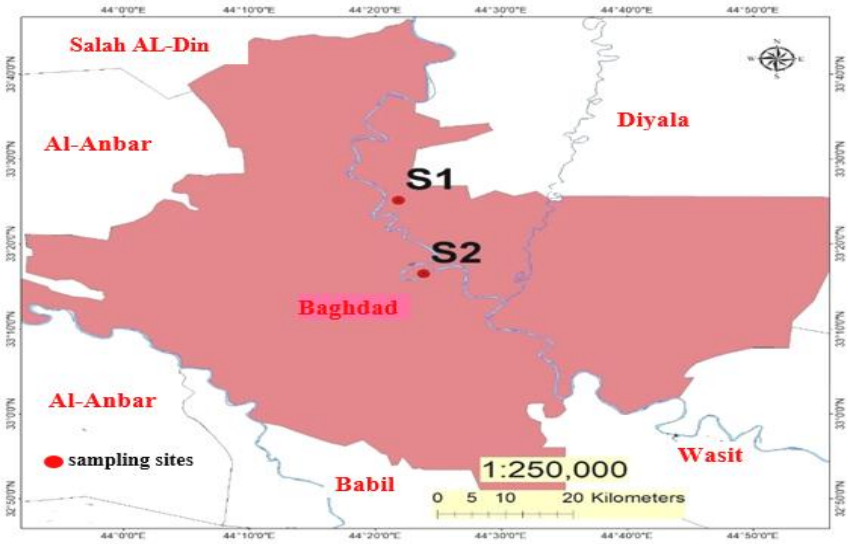
**DNA sequencing and analysis:** For sequencing, the PCR products were sent to Macrogen Co. in Korea. Next, chromatogram quality was assessed, and consensus sequences were generated using a DNA Baser Assembler (DNA Sequence Assembler v4 (2013), HeracleBioSoft, www.DnaBaser.com). The NCBI Blast tool (http://www.ncbi.nlm.nih.gov/) was utilized to perform homology searches for every sequence. The phylogenetic analyses and nucleotide distance was calculated by using MEGA.7 program (Al-Zaidawi *et al*., 2019).

For *M. franseni* Fuchs, 1933 the evolutionary history was inferred by used the Maximum Likelihood method based on the Kimura 2-parameter model (Kimura, 1980). The tree with the

highest log likelihood (-3777.42) was shown. The percentage of trees in which the associated taxa clustered together was shown next to the branches. Initial tree (s) for the heuristic search were obtained automatically by applied Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated by used the Maximum Composite Likelihood (MCL) approach, and then was selected the topology with superior log likelihood value. The tree was drawn to scale, with branch lengths measured in the number of substitutions per site. While, in *Pratylenchus goodeyi* Sher and Allen, 1953 the evolutionary history was inferred by used the Neighbor-Joining method (Saitou and Nei, 1987).

The optimal tree with the sum of branch length equal 1.53180421 was shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) was shown next to the branches (Felsenstein, 1985). The tree was drawn to scale, with branch lengths in the same units as those of the evolutionary distances was used to infer the phylogenetic tree. The evolutionary distances were computed using the Tamura 3-parameter method (Tamura, 1992) and were in the units of the number of base substitutions per site.

The analysis involved 23 nucleotide sequences for *Mesorhabditis franseni* and 15 nucleotide sequences for *Pratylenchus goodeyi* Sher and Allen, 1953 in addition local isolate, *Caenorhabditis elegans* Maupas, 1900 considered as outgroup. Among the codon positions were first, second, third, and noncoding. Every position that had lacking information or gaps was removed. There were a total of 600 positions for *Mesorhabditis franseni* and 632 for *P. goodeyi* Sher and Allen, 1953 in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar *et al*., 2016).




**Map (1):** Baghdad map shows the locality of sampling sites (S1) Al Rashidiya and (S2) Al Jadriya**.**

## RESULTS AND DISCUSSION

**Family**, Mesorhabditidae Andrassy, 1976

Genus, ***Mesorhabditis*** Osche, 1952

***Mesorhabditis franseni*** Fuchs, 1933

Among the nematode specimens that were collected from soil in Baghdad, Iraq. *M. franseni* was cultured and identified based on molecular technique. All the identified *M. franseni* in the present study had the most typical features of this species. Adult specimens had the following characteristic features: Head has six lips that distinctly separated, rounded and well developed, each ending in a setose papilla as shown in (Pl. 1- A1, A2). Amphids small, on the lateral lips. Cuticle conspicuously annulated. Stoma well-developed 2-3 times head diam. long. Cheilostom simple exceptionally cuticularized but small; Pharyngeal collar absent; Pharynx corpus (swollen bulb-like).

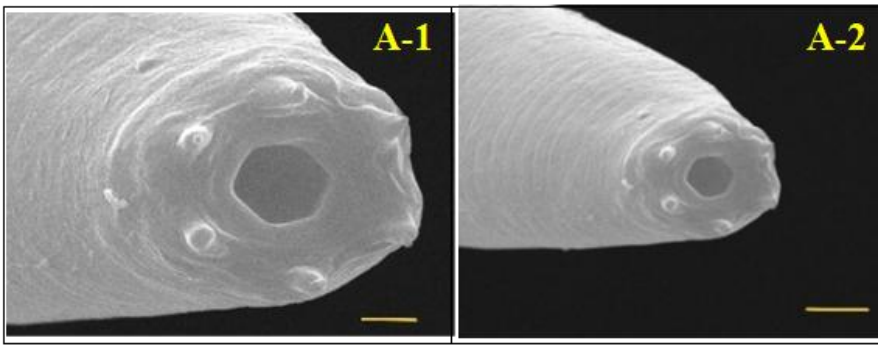



**Plate (1):** Scanning electron microscopy (SEM) photographs of *Mesorhabditis franseni* (female), Anterior cephalic with six lips that distinctly separated around the mouth, rounded and well developed, each ending in a setose papilla. [Scale bars: A1= 2 µm, A2= 5 µm].

**Analysis using *ITS* sequence for *Mesorhabditis franseni*:** The selected specimens of this species were subjected to molecular tactic using coding of DNA to verify the morphological identification of the isolated nematodes. The *ITS-rRNA* (1084 bp) amplicon from this selected individual represented single bands on agarose gels. Nucleotide sequence data reported from this isolate is available in the GenBank database. *ITS-rRNA* nucleotide sequence data is found under the accession numbers PP528819.1. Results in Diagram (1) showed that the sequence of the selected *M. franseni* isolate (Accession number PP528819.1) had 100% sequence homology with *ITS-rRNA* sequence of this species (Accession number MT710247) as well as it had 98.62% and 98.41% sequence homology with *ITS-rRNA* sequence of *M. franseni* (Accession number MT710246, and Accession number MT710245 respectively).

The mean inter-specific distance among *M. franseni* isolate IRQ.ZAh2 (Accession number PP528819.1) isolate and other isolates of *Mesorhabditis* were 0.232 % (range 0.00 – 1.095 %), which have been calculated using the Tamura 3-parameter model based on the *ITS* gene. Nucleotide distance between the isolates from Iraq and *M. franseni* JU3174 (Accession number MT710246.1) was 0% (Tab. 1). Results also showed that among *M. franseni* isolate IRQ.ZAh2 (Accession number PP528819.1) having a same node ancestor with the other previous recorded sequences of *M. crangsnorensis* Khera, 1968 under the accession number (MT710262) and *M. microbursaris* Steiner, 1926 under the accession number (MT710259).

The phylogenetic relationships within this group suggest diversification and hybrid incompatibility, indicating potential barriers between species. Additionally, there are indications that *Mesorhabditis* may have a single origin of pseudogamy. Overall, *M. franseni* is part of a complex evolutionary history within the genus of *Mesorhabditis* and its sister species, with implications for understanding diversification and hybrid incompatibility in auto-pseudogamous species (Launay *et al*., 2020; Sudhaus, 2023). Other study indicated that *M. franseni* and *M. cranganorensis* are sister species to *M. microbursaris*. The phylogenetic

relationships of *Mesorhabditis* species show that *M. franseni* and *M. cranganorensis* are closely related to *M. microbursaris*. The study included measurements from 11 strains of auto-pseudogamous *Mesorhabditis* species, corresponding to 6 species, which provided insights into the diversification and hybrid incompatibility within this group (Launay *et al.*, 2020). Additionally, a phylogenetic systematization and catalog of paraphyletic species included *M. cranganorensis* and *M. franseni*, further supporting their relationship to *M. microbursaris* (Sudhaus, 2023).

**Table (1):** Comparing several *Mesorhabditis* species and isolates pairwise based on the amount of nucleotide differences with *M. franseni* Fuchs, 1933 isolate IRQ.ZAh2 based on *ITS* sequences.

| No. | Species and isolates of nematodes | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | PP528819.1 *Mesorhabditis franseni* isolate IRQ.ZAh2 | | | | | | | | | | | | | | | |
| 2 | MT710245.1 *Mesorhabditis franseni* strain JU2870 | 0.008 | | | | | | | | | | | | | | |
| 3 | MT710246.1 *Mesorhabditis franseni* JU3174 | 0.000 | 0.008 | | | | | | | | | | | | | |
| 4 | KF999588.1 *Serpentirhabdias fuscovenosa* isolate 1 | 0.264 | 0.259 | 0.264 | | | | | | | | | | | | |
| 5 | EF990720.1 *Teratorhabditis stiannula* strain SB359 | 0.201 | 0.204 | 0.201 | 0.295 | | | | | | | | | | | |
| 6 | EF990721.1 *Teratorhabditis mariannae* strain SB170 | 0.185 | 0.183 | 0.185 | 0.286 | 0.106 | | | | | | | | | | |
| 7 | MT710275.1 *Mesorhabditis longespiculosa* strain DF5017 | 0.110 | 0.114 | 0.110 | 0.265 | 0.206 | 0.195 | | | | | | | | | |
| 8 | MT710270.1 *Mesorhabditis monhystera* strain JU2889 | 0.082 | 0.090 | 0.082 | 0.263 | 0.188 | 0.189 | 0.108 | | | | | | | | |
| 9 | MT710244.1 *Mesorhabditis paucipapillata* strain JU3003 | 0.025 | 0.027 | 0.025 | 0.266 | 0.208 | 0.189 | 0.126 | 0.095 | | | | | | | |
| 10 | MT710253.1 *Mesorhabditis littoralis* strain JU2848 | 0.010 | 0.008 | 0.010 | 0.259 | 0.199 | 0.178 | 0.110 | 0.084 | 0.019 | | | | | | |

| | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 11 | MT710233.1 *Mesorhabditis belari* strain JU3151 | 0.017 | 0.019 | 0.017 | 0.257 | 0.195 | 0.176 | 0.116 | 0.084 | 0.012 | 0.010 | | | | | |
| 12 | MT710242.1 *Mesorhabditis paucipapillata* JU3149 | 0.015 | 0.017 | 0.015 | 0.259 | 0.195 | 0.176 | 0.114 | 0.086 | 0.010 | 0.008 | 0.002 | | | | |
| 13 | MT710259.1 *Mesorhabditis microbursaris* PS1179 | 0.010 | 0.015 | 0.010 | 0.262 | 0.197 | 0.181 | 0.106 | 0.084 | 0.022 | 0.010 | 0.013 | 0.012 | | | |
| 14 | MT710262.1 *Mesorhabditis cranganorensis* JU3209 | 0.010 | 0.015 | 0.010 | 0.262 | 0.197 | 0.181 | 0.106 | 0.084 | 0.022 | 0.010 | 0.013 | 0.012 | 0.000 | | |
| 15 | MT710258.1 *Mesorhabditis vernalis* JU3428 | 0.008 | 0.010 | 0.008 | 0.262 | 0.199 | 0.178 | 0.108 | 0.082 | 0.017 | 0.002 | 0.008 | 0.007 | 0.008 | 0.008 | |
| 16 | KX572972.1 *Caenorhabditis elegans* | 1.095 | 1.106 | 1.095 | 1.152 | 1.260 | 1.176 | 1.130 | 1.128 | 1.108 | 1.115 | 1.097 | 1.106 | 1.088 | 1.088 | 1.106 |

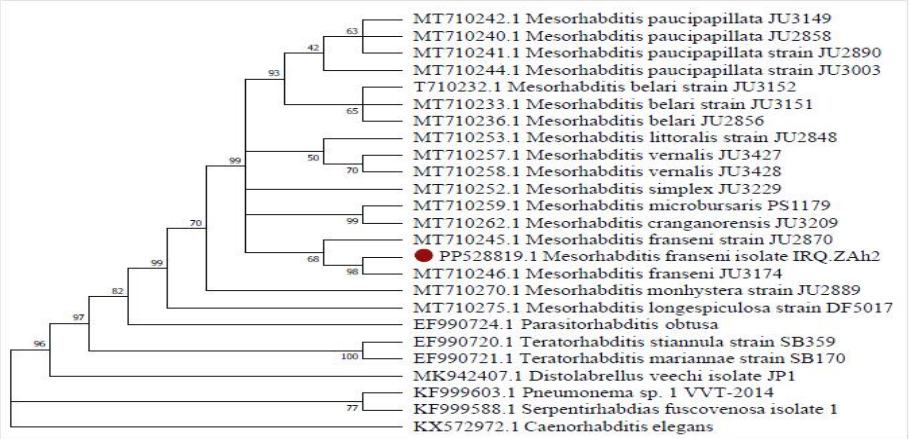



**Diagram (1):** Phylogenetic relationship of *Mesorhabditis franseni* isolate with 23 isolates of other species related to *Mesorhabditis* based on *ITS -rRNA* gene sequences as inferred from neighbour joining (NJ) analysis, *Caenorhabditis elegans* (KX572972) was used as outgroup, support values are presented near the nodes in the form: bootstrap in ML.

**Family, Pratylenchidae** Thorne, 1949

Genus, ***Pratylenchus*** Filipjev, 1936

***Pratylenchus goodeyi*** Sher and Allen, 1953

*Pratylenchus goodeyi* (Obligate migratory endoparasites of roots) is characterized by: Small nematodes (less than 1000 µm long) (Pl. 2-A), labial region with four annuli (Pl. 2 -B1,

B2) lateral fields with four inconspicuous lines, the two outer bands partially areolated, sub-rectangular in shape and tail conoid, ventrally concave.

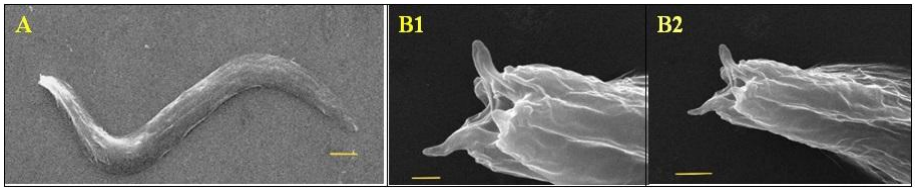



**Plate (2):** Scanning electron microscopy (SEM) photographs of *Pratylenchus goodeyi* adult; (A) Whole body, (B1 and B2) Anterior cephalic end to explain labial region with four annuli. [Scale bars: A= 50 µm, B1= 2µm, B2= 5 µm].

**Analysis using *ITS* sequence for *Pratylenchus goodeyi* Sher and Allen, 1953 isolate:** The specimens of *P. goodeyi* were subjected to molecular tactic using coding of DNA to verify the morphological identification of the isolated nematodes. The *ITS-rRNA* (778 bp) amplicon from this selected individual represented single bands on agarose gels. Nucleotide sequence data reported from this isolate is available in the GenBank database. *ITS-rRNA* nucleotide sequence data is found under the accession numbers PP535537. Results in Diagram (2) showed that the sequence of the selected *P. goodeyi* isolate (Accession number PP535537) had 100% sequence homology with *ITS-rRNA* sequence of *P. goodeyi* ZFJY HN (Accession number KM874803).

The mean inter-specific distance among *P. goodeyi* isolate IRQ.Zah5 (Accession number PP535537) isolate and other isolates of *Pratylenchus* 0.238 % (range 0.00 – 1.24 %), which have been calculated using the Tamura 3-parameter model based on the *ITS* gene. Nucleotide distance between the *P. goodeyi* isolates from Iraq and *P. goodeyi* ZFJY HN (Accession number KM874803) was 0% (Tab. 2). Results also showed that among *P. goodeyi* isolate (Accession number PP535537) having a same clade with the other previous recorded species of *Acrobeloides nanus* De Man, 1880 (Accession number MT476853 and LR594508). This result agreed with some previous results which indicated that *P. goodeyi* is in the same clade as *A. nanus* within the monophyletic Cephalobidae clade. The *ITS* sequence of *A. nanus* is sister to the *P. goodeyi* sequences, indicating a close relationship between the two species (Janssen *et al*., 2017; Hodda, 2022). This relationship is further supported by additional evidence of cryptic speciation within the genus *Pratylenchus*. The classification principles followed in the study also confirm the grouping of *P. goodeyi* with other nematode species (Janssen *et al*., 2017). Therefore, based on the available information, *P. goodeyi* and *A. nanus* are indeed in the same clade within the Cephalobidae group.

**Table (2):** Comparing several species and isolates of nematode pairwise based on the amount of nucleotide differences with *Pratylenchus goodeyi* Sher and Allen, 1953 isolate *IRQ.ZAh5* based on *ITS* sequences.

| No.. | Species and isolates of nematodes | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | PP535537 *Pratylenchus goodeyi* IRQ.ZAh5 | | | | | | | | | | | | | | | | |
| 2 | KM874803 *Pratylenchus goodeyi* ZFJY HN | 0.000 | | | | | | | | | | | | | | | |
| 3 | LC147070 *Pratylenchus sp.* Autumn75 | 0.005 | 0.005 | | | | | | | | | | | | | | |
| 4 | LC147069 *Pratylenchus* sp. Spring2 | 0.010 | 0.010 | 0.008 | | | | | | | | | | | | | |
| 5 | LR594508 *Acrobeloides nanus* | 0.024 | 0.024 | 0.023 | 0.031 | | | | | | | | | | | | |
| 6 | MT476853 *Acrobeloides nanus* LC13A | 0.023 | 0.023 | 0.021 | 0.029 | 0.002 | | | | | | | | | | | |
| 7 | LR594507 *Acrobeloides nanus* | 0.027 | 0.027 | 0.029 | 0.037 | 0.019 | 0.018 | | | | | | | | | | |
| 8 | KF856291 *Pratylenchus goodeyi* CICR Bhandara Mujbi58 | 0.117 | 0.117 | 0.123 | 0.128 | 0.119 | 0.117 | 0.122 | | | | | | | | | |
| 9 | MW327028 *Acrobeloides* sp. FHD002 | 0.121 | 0.121 | 0.124 | 0.128 | 0.132 | 0.130 | 0.128 | 0.168 | | | | | | | | |
| 10 | ON738667 *Zeldia punctata* HN3 | 0.130 | 0.130 | 0.136 | 0.138 | 0.130 | 0.128 | 0.122 | 0.123 | 0.156 | | | | | | | |
| 11 | EF371501 *Aphelenchoides arachidis* | 0.132 | 0.132 | 0.132 | 0.142 | 0.132 | 0.130 | 0.135 | 0.159 | 0.088 | 0.171 | | | | | | |

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 12 | KF700243 *Pratylenchus goodeyi* CICR Cot.Warud | 0.130 | 0.130 | 0.136 | 0.140 | 0.126 | 0.124 | 0.130 | 0.042 | 0.165 | 0.132 | 0.163 | | | | | |
| 13 | KF275665 *Pratylenchus goodeyi* CICR Cot. Warud Pg | 0.154 | 0.154 | 0.157 | 0.162 | 0.151 | 0.149 | 0.159 | 0.063 | 0.192 | 0.158 | 0.191 | 0.036 | | | | |
| 14 | DQ146428 *Zeldia* sp. JB118 | 0.133 | 0.133 | 0.137 | 0.137 | 0.134 | 0.132 | 0.132 | 0.119 | 0.145 | 0.093 | 0.159 | 0.119 | 0.152 | | | |
| 15 | DQ146427 *Zeldia punctata* voucher JB040 | 0.136 | 0.136 | 0.142 | 0.144 | 0.136 | 0.134 | 0.128 | 0.129 | 0.158 | 0.005 | 0.177 | 0.138 | 0.164 | 0.098 | | |
| 16 | DQ146426 *Zeldia punctata* voucher JB015 | 0.142 | 0.142 | 0.147 | 0.150 | 0.142 | 0.140 | 0.134 | 0.132 | 0.164 | 0.011 | 0.183 | 0.142 | 0.168 | 0.104 | 0.006 | |
| 17 | MW667579 *Caenorhabditis elegans* strain TG3 | 1.249 | 1.249 | 1.249 | 1.245 | 1.197 | 1.207 | 1.176 | 1.114 | 1.176 | 1.159 | 1.091 | 1.162 | 1.174 | 1.135 | 1.172 | 1.212 |

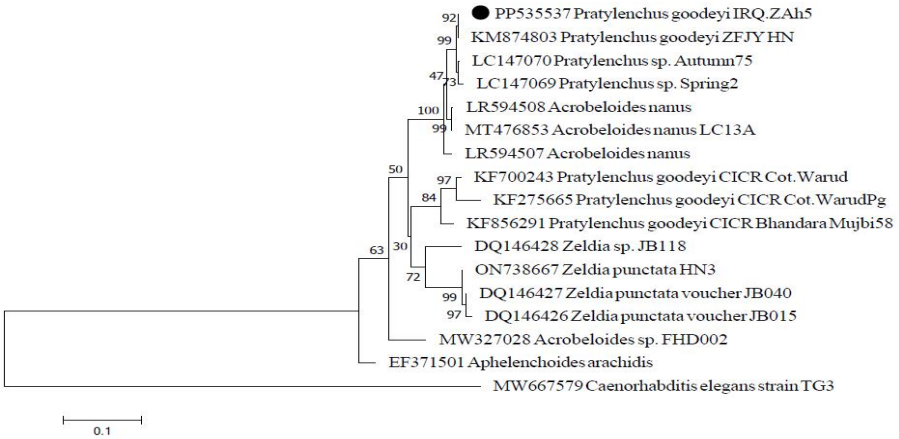



**Diagram (2):** Phylogenetic relationship of Pratylenchus goodeyi Sher and Allen, 1953 isolate with 15 isolates of other species related to Pratylenchus genus based on *ITS-rRNA* gene sequences as inferred from neighbour joining (NJ) analysis, Caenorhabditis elegans (MW667579) was used as outgroup, support values are presented near the nodes in the form: bootstrap in ML.

## CONCLUSIONS

This is the first presence of two nematode species that have been isolated from Baghdad city in Iraq; these are *M. franseni* and *P. goodeyi*. The *ITS-rRNA* sequence of *M. franseni* (IRQ.ZAh2 PP528819.1 isolate) had a range of (98%) sequence homology with *ITS-rRNA* sequence of *M. franseni* available in NCBI database. While, the *ITS-rRNA* sequence of *P. goodeyi* (IRQ.ZAh5 PP535537 isolate) had a range of (92%) sequence homology with *ITS-rRNA* sequence of *P. goodeyi* available in NCBI database.

## CONFLICTS OF INTEREST STATEMENT

"There are no disclosed conflicts of interest for the author"

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# تسجيل جديد للديدان الخيطية *Mesorhabditis franseni* Fuchs, 1933 (عائلة Mesorhabditidae) و *Pratylenchus goodeyi* Sher Allen, 1953 (عائلة Pratylenchidae) مع وصف جزيئي لها من العراق

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## الخلاصة

عزلت الدودتين الخيطيتين *Mesorhabditis franseni* Fuchs, 1933 (عائلة Mesorhabditidae)و *Pratylenchus goodeyi* Sher and Allen, 1953 (عائلة Pratylenchidae) من عينات التربة من منطقة الراشدية (33°25'13.4" شمالاً 44°21'45.3" شرقاً) و منطقة الجادرية ( 33°16'35.7"شمالاً 44° 23 ' 26.3" شرقاً) في بغداد- وسط العراق، تم تربية جميع النماذج المعزولة من كلا الجنسين و شُخصت جزيئياً. وُصفت كل من الدودتين *M. franseni*عزلة (IRQ.ZAh2 PP528819.1) و *P. goodeyi* عزلة (IRQ.ZAh5 PP535537 ). شُخصت العينات المختارة من هذين النوعين جزيئيًا باستخدام تسلسلات جين*ITS-rRNA* الجزيئية. كان لتسلسل *ITS-rRNA* لعزلة(IRQ.ZAh2 PP528819.1) نطاق من التماثل التسلسلي ( 98.62 %-100%) مع تسلسل *ITS- rRNA* لـ *M. franseni* المتوفر في قاعدة بيانات NCBI. بينما كان لتسلسل *ITS-rRNA* لعزلة (IRQ.ZAh5 PP535537) تماثل تسلسلي (100%) مع تسلسل *ITS-rRNA* لـ *P. goodeyi* المتوفر في قاعدة بياناتNCBI.عزلتي *M. franseni* عزلة (IRQ.ZAh2 PP528819.1) و *P. goodeyi* عزلة (IRQ.ZAh5 PP535537) هما أول مثال موثق لهذين النوعين في العراق.