Molecular Identification of *Meloidogyne javanica* occurring in Upper Egypt Based Polymerase Chain Reaction (PCR) Assays

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ABSTRACT

Molecular diagnosis represents one of the important trends in the confirmation of morphological identification to the root-knot nematodes which one of the most global pathogens. In this context, current study aimed to describe *Meloidogyne javanica* occurring in cucumber plants in Assiut governorate (Upper Egypt) using the random amplified polymorphic DNA-Polymerase Chain Reaction (RAPD-PCR) assay. Four mitochondrial and specific-specific sequences characterized amplified regions (SCAR) primers were used. The results showed that the SCAR primers, Fjav/Rjav and Far/Rar were efficiently amplified with 670 bp and 517 bp, respectively. On the contrary, the mitochondrial primers did not show any results. In conclusion, the present study recommended the SCAR primers as effective identified primers for the species of *Meloidogyne javanica*.

Keywords: Root-knot nematode, *Meloidogyne javanica*, RAPD-PCR, SCAR, Mitochondrial

INTRODUCTION

Identification of *Meloidogyne* species is increasingly important in designing the effective nematode management practices, such as crop rotation, plant resistance and agricultural quarantine purposes (Zijlistra, 2000; Zijlistra and Van Hoof, 2006). Molecular identification has confirmed the validity of a number of classical nematode species which were classified according to the molecular evidence (Holterman et al., 2006). Furthermore, incorporation of morphological and molecular analyses of nematodes provides a more effective means of identification (Thomas et al., 1997). The differentiation between Meloidogyne species can be very difficult using morphological and biological trait data because they are quite similar and can be regularly confused in inaccurate taxonomic comparisons (Coyne et al., 2009). The difficulty in identifying nematode species is due not only to the choice of the most accurate and adapted method, but also to several parameters that can affect the performance of the identification, such as the small size of the worms, the high number and diversity of nematodes in a sample, and/or the absence of specific morphological features (Chitwood, 2003). Microscopic examination, especially in groups such as nematodes with obvious structural differences, requires more significant technical and taxonomic expertise (De Ley et al., 2005). Traditionally, identification and description of *Meloidogyne* species was based mainly on perineal pattern morphology and supported by other morphological characteristics of female, juveniles (J2), and males (Karssen, 2002). The random amplified polymorphic DNA-

Polymerase Chain Reaction (RAPD-PCR) as a rapid technique was successfully used in identification of the root-knot nematode, *M. javanica* (Cenis, 1993)

Different methods based on DNA and PCR, such as RAPD, restriction fragment length polymorphism (RFLP), sequence characterized amplified regions (SCAR), Multiplex PCR, and amplified fragment length polymorphism (AFLP) have been developed and successfully used for identifying many of the nematode species (Tigano et al., 2010). A number of specific primers have been developed for the identification of *Meloidogyne* species based on species-specific DNA fragments (Dong et al., 2001). The species-specific sequence characterized amplified regions (SCAR- PCR) primers work at higher annealing temperatures than RAPD-PCR primers (Castagnone et al., 1999). Therefore, the aim of the current study is the identification of a root-knot nematode species collected from Upper Egypt based on RAPD-PCR techniques.

MATERIALS AND METHODS

Propagation of *Meloidogyne javanica* (Treub, 1885) Chitwood, 1949 in pure culture

A total of 50 naturally infested cucumber roots (cv. Hayel[®]) were collected from four localities in Assiut province (Abo-Teg, Assiut, Mangabad and Manfalot). A pure stock culture of the root-knot nematode *M. javanica* was prepared from infested roots. Individual egg masses with their mature females were removed from root tissues. Then, each egg mass was placed in a small glass capsule containing fresh water. The females from which egg masses were collected were preserved in glass capsules containing 4% formaldehyde solution. Each egg mass was identified to species level by perineal pattern according to Taylor and Netscher (1974). The nematodes were then transferred to 25-cm clay pots filled with-steam sterilized sandy loam soil planted with a seedling of cucumber cv. Hayel. Inoculated pots were placed in a greenhouse and watered as needed. After two months of inoculation, infected roots were then chopped and used as a source of inoculation for other series of clean cultivar Pritchard tomato seedlings. The previous procedure was repeated to obtain enough quantities of inoculation from stock cultures on the cucumber.

Identification of Meloidogyne species

Species of *Meloidogyne* were identified again on the basis of perineal pattern system of the mature females. Individuals of mature females of each root sample were singly transferred on slides, each one with a drop of hot lactophenol solution/slide. Then the posterior end of each mature female was cut off using a sharp razor blade and trimmed down to the area showing the pattern. Slides were gently covered with a clean cover slip and sealed with finger nail-polish (Taylor and Netscher, 1974). All preparations were examined using Carson digital microscope (model zPix MM-940). *Meloidogyne* species was identified according to morphological features described by Chitwood (1949) and Sasser (1954).

Molecular identification

Selection of primers

According to Powers and Harries (1993), mitochondrial encoded gene cytochrome oxidase subunit II had been used for identifying the five common *Meloidogyne* species whereas species-specific nuclear encoded have been used for the rapid identification of root-knot nematodes by SCAR-PCR (Munthali et al., 1992). In the present study, the populations found in 4 different localities were screened using four mitochondrial and nuclear encoded species specific primers as listed in Table (1).

Table 1: Nucleotide sequence of primer used for each mitochondrial and SCAR derived from the RAPD markers to identify the root-knot nematodes, *Meloidogyne javanica*.

Primers	Sequence	Reference sources
C2F3/Mel450R (mitochondrial)	5'-GGTACAATGTTCAGAAATTTGTGG-3' 5'-ATCCTAATAATAAAAAAATG-3'	Powers and Harris, 1993
Mjf/Mjr (SCAR)	5'-ACGCTAGAATTCGACCCTGG-3' 5'-GGTACCAGAAGCAGCCATGC-3'	and Meng et al., 2004
Far/Rar (SCAR)	5'-TCGGCGATAGAGGTAAATGAC-3' 5'-TCGGCGATAGACACTACAAACT-3'	Zijlistra et al., 2000
Fjav/Rjav (SCAR)	5'-TGCGCGATTGAACTGAGC-3' 5'-CAGGCCCTTCAGTGGAACTATAC-3'	

The extraction of DNA from females was obtained according to Miller et al., (1988) with some modifications as follows:

Tissue digestion and precipitation of proteins and cell debris

Six egg masses were crushed in liquid nitrogen until a fine white powder was formed, tissues digestion and precipitation of proteins and cell debris were carried out according to Sambrook et al. (1989).

Precipitation of nucleic acids

DNA precipitation occurred by adding 750 μ L of cold absolute ethanol to the supernatant and mixed vigorously for 30 seconds. The tubes were kept in freezer at -20°C for 15 minutes to allow better precipitation. Then the tubes were centrifuged at 14000 rpm for 5 minutes. The ethanol and the salts were carefully poured off to avoid disturbing the DNA pellet. The DNA pellet was rinsed by adding 400 μ L of 70% ethanol and centrifuging at 14000 rpm for 5 minutes to allow evaporating of excessive alcohol. The DNA pellet was suspended in 30 μ L of TE buffer (10mM Tris HCl and 1mM EDTA), and stored at 20C for PCR

Polymerase chain reaction

The polymerase chain reactions (PCR) were carried out using the extracted rootknot nematode DNA as the template. The master mix for 30 μ L PCR reactions was prepared according to Rychlik (1993) as follows: 17.8 μ L sterilized distilled water, 3.0 μ L buffer (10 ×), 3.0 μ L MgCl2 50mM), 3.0 μ L dNTPs 2mM, 1.0 μ L of forward and reverse primers, respectively, 0.2 Taq polymerase and 1.0 μ L of DNA template (μ l). All PCR reactions were carried out using Eppendorf mastercycler gradient thermocycler. First, the primers were optimized using a temperature gradient to select the most appropriate temperature. The optimized PCR programs for the different primer combinations were represented according to Rychlik (1993). The PCR products were purified using Kit-Ultra, and the purify was tested by electrophoresis on 1.5 % agarose gels (Paran and Michelmore, 1993). The gel was scanned and analyzed using Gel-pro 31 analyzer (version 3.1, 1998) to compare the sizes of bands against DNA hyper ladder I in Plat (1).

	SIZE (bp)	ng/BAND	
	10000 8000 6000 5000 4000 3000 2500 2000 1500	100 80 60 50 40 30 25 20 15	
IIII	1000 800 600 400 200	100 80 60 40 20	
	5µl Bioline HyperLadder I run on a 1% Bioline Agarose gel in TAE.		

Plat 1: DNA hyper ladder used for estimating band sizes of PCR product visualised on agarose gels.

RESULTS

All cucumber root samples showed (100%) infestation with root-knot nematodes under microscopic examination. For molecular identification, even selected primers were tested for the diagnosis and screening of the species specificity morphologically identified as *M. javanica*. In the present study, only SCAR primers Fjav/Rjav and Far/Rar were positive against DNA isolated from the females of the root-knot nematode *M. javanica*. All tested samples were PCR-positive to *M. javanica* using SCAR primers (Fig. 1). One sample was PCR-positive by using Fjav/Rjav primers (Fig. 2). PCR products were produced one specific band with molecular weight of 670 bp in both primers. The intensity of band was higher using SCAR primers than Fjav/Rjav. On the other side, the mitochondrial primer (C2F3/Mel450R) giving no product with any tested isolate of *M. javanica*, the agarose gel was clear from any bands.

DISCUSSION

The aim of the present study was assaying the polymerase chain reaction (PCR) with the five mitochondrial and species-specific sequences characterized amplified regions (SCAR) markers to identify the major root-knot nematode *M. javanica* species in Upper Egypt. Some of previous studies indicated that *M. javanica* represents the most prevalence of the root-knot nematodes species in vegetable crops, especially Cucurbitaceae family, in sampling area as a subtropical region, with annual temperatures between 20-40°C (Korayem et al., 2008 and Castagnone et al., 2013). Similar results were reported by Nono-Womdim et al. (2002) in a similar climate

(Tanzania) on some vegetable plants. Contrary to Eisenback et al. (1981) where *M. javanica* was the dominant species of *Meloidogyne*. This difference may be due to the difference in the nature of the climate (Jonasson et al.,1999 and Sikora et al.,2018). Through the development of taxonomy tools, real-time PCR assays were raised as a suitable device for identification of plant-parasitic nematodes in concurrently with morphological description especially the root-knot nematodes *M. javanica* (Berry et al., 2008 and Fargette et al., 2010). Recently, some nematologists prefer PCR technics for identification of nematodes for some reasons, the most important of them; PCR results are readily available through about three hours which saves time and efforts, compared to conventional methods; the technique can easily be prepared for analysis of many samples at a time; partially, in some scientific analysis, no high nematode taxonomical skills are needed, which save taxonomic expertise and time (Braun-Kiewnick and Kiewnick, 2018).



Figure 1: Agarose gel electrophoresis of PCR amplified from extracted DNA from females of *M. javanica* showing: (a) the specific distinct band at 670 bp using species-specific mitochondrial SCAR primer; (b) the positive specific band using Fjav/Rjav primer at 517 bp.

The PCR assay for six nematode isolates with the specific SCAR primer Fjav/Rjav clearly produced a specific DNA fragment at 670 bp , while using Mjf/Mjr primer the band for *M. javanica* was present in lower numbers in the population showing a weak band (517 bp), which was predictable for the *M. javanica* as reported by Berry et al. (2008). Similar findings were noted by Zijlstra et al. (2000) where the SCAR primers clearly produced the DNA fragment at 670 bp more than Mjf/Mjr . It might be due to favorable annealing and a better structure of the template DNA at the downstream located primer binding site (Dong et al., 2001; Randig et al., 2002; Meng et al., 2004). The primer C2F3/Mel450R (mitochondrial) did not give any products with any isolates of tested nematode, this agree with Tesarova et al. (2003) where C2F3/Mel450R primer developed from SEC protein gene sequences belonging to *M. incognita* was not used for *M. javanica* identification.

Finally, based on the current study the use of SCAR-PCR technique in nematology would be a highly valued technique for identification of the field nematode isolates that need further adaptive investigations.

REFERENCES

- Berry, S. D.; Fargette, M.;Spaull, V. W.; Morand, S., an Cadet, P. (2008). Detection and quantification of root-knot nematode (*Meloidogyne javanica*), lesion nematode (*Pratylenchus zeae*) and dagger nematode (*Xiphinema elongatum*) parasites of sugarcane using real-time PCR. Mol. Cell. Probes 22(3):168-176.
- Braun-Kiewnick, A. and Kiewnick, S. (2018). Real-time PCR, a great tool for fast identification, sensitive detection and quantification of important plant-parasitic nematodes. Eur. J. Plant Pathol. 152(2): 271-283.
- Castagnone-Sereno, P.; Danchin, E. G.; Perfus-Barbeoch, L.; and Abad, P. (2013). Diversity and evolution of root-knot nematodes, genus *Meloidogyne*: new insights from the genomic. Annu. Rev. Phytopathol. 51: 203-220.
- Castagnone-Sereno, P.; Leroy, F.; Bongiovanni, M.; Zijlstra, C. and Abad, P. (1999). Specific diagnosis of two root-knot nematodes, *Meloidogyne chitwoodi* and *M. fallax*, with satellite DNA probes. Phytopathol. J. 89(5):380-384.
- Cenis, J. L. (1993). Identification of four major *Meloidogyne* ssp. by random amplified polymorphic DNA (RAPD-PCR)." Phytopathology-New york and Baltimore Then St Paul 83: 76-76.
- Chitwood, B. G. (1949). Root-knot nematodes, part I. A revision of the genus *Meloidogyne*, 1887. Proc Helminthol Soc Wash. 16(2): 90-104.
- Chitwood, D. J. (2003). Research on plant parasitic nematode biology conducted by the United States Department of Agricultural Research Service. Pest Manag. Sci.59(6-7): 748-753.
- Coyne, D. L.; Fourie, H. H. and Moens, M. (2009). Current and Future Management Strategies in Resource-poor Farming. Root-knot nematodes, p. 444.
- De Ley, P.; De Ley, I. T.; Morris, K.; Abebe, E.; Mundo-Ocampo, M.; Yoder, M. and Baldwin, J. G. (2005). An integrated approach to fast and informative morphological vouchering of nematodes for applications in molecular barcoding. Philos. Trans. R. Soc. Lond., B. Biol. Sci 360(1462): 1945-1958.
- Dong, K.; Dean, R. A.; Fortnum, B. A.and Lewis, S. A. (2001). Development of PCR primers to identify species of root-knot nematodes: *Meloidogyne arenaria*, *M. hapla*, *M. incognita* and *M. javanica*. Nematropica 31(2): 271-280.
- Esbenshade, P. R., and Triantaphyllou, A. C. (1985). Use of enzyme phenotypes for identification of *Meloidogyne* species. J. Nematol., 17(1): 6.

- Fargette, M.: Berthier, K.: Richaud, M.: Lollier, V.; Franck, P.; Hernandez, A. and Frutos, R. (2010). Crosses prior to parthenogenesis explain the current genetic diversity of tropical plant-parasitic *Meloidogyne* species (Nematoda: Tylenchida). Infect. Genet. Evol. 10(6): 806-813.
- Holterman, M.; van der Wurff, A.; van den Elsen, S.; van Megen, H.,;Bongers, T.; Holovachov, O. and Helder, J. (2006). Phylum-wide analysis of SSU rDNA reveals deep phylogenetic relationships among nematodes and accelerated evolution toward crown clades. Mol. Biol. Evol. 23(9): 1792-1800.
- Jonasson, S.; Ruess, L.and Michelsen, A. (1999). Simulated climate change in subarctic soils: responses in nematode species composition and dominance structure. Nematology 1(5): 513-526.
- Karssen, G. (2002). The plant parasitic nematode genus *Meloidogyne* Goldi, 1892 (Tylenchida) in Europe. Brill Academic Publishers, Leiden, The Netherlands, pp.161.
- Korayem, A. M.; Noweer, E. M. A. and Mohamed, M. M. M. (2008). Threshold population of *Meloidogyne* species causing damage to some vegetable crops under certain conditions in Egypt. Egypt. J.Agronematol. 6:217-227.
- Meng, Q. P.; Long, H. and Xu, J. H. (2004). PCR assays for rapid and \mathbf{v} sensitive identification of three major root-knot nematodes, *Meloidogyne incognita*, *M. javanica* and *M. arenaria*. Act. Phytopathol. Sini. 34:204–210.
- Miller, S. A. and Martin, R. R. (1988). Molecular diagnosis of plant disease. Annu. Rev. Phytopathol. 26(1): 409-432.
- Munthali, M.; Ford-Lloyd, B. V. andNewbury, H. J. (1992). The random amplification of polymorphic DNA for fingerprinting plants. Genome Res. 1(4): 274-276.
- Nono-Womdim, R.; Swai, I. S.; Mrosso, L. K.; Chadha, M. L. and Opena, R. T. (2002). Identification of root-knot nematode species occurring on tomatoes in Tanzania and resistant lines for their control. Plant Disease 86(2): 127-130.
- Paran, I. and Michelmore, R. W. (1993). Development of reliable PCR-based markers linked to downy mildew resistance genes in lettuce. Theor. Appl. Genet. 85(8): 985-993.
- Powers, T. O. and Harris, T. S. (1993). A polymerase chain reaction method for identification of five major *Meloidogyne* species. J. Nematol. 25(1): 1-6.
- Randig, O.; Bongiovanni, M.; Carneiro, R. M. and Castagnone-Sereno, P. (2002). Genetic diversity of root-knot nematodes from Brazil and development of SCAR markers specific for the coffee-damaging species. Genome 45(5): 862-870.
- Rychlik, W. (1995). Selection of primers for polymerase chain reaction. Mol. Biotechnol. 3(2): 129-134.
- Sambrook J; Fritsch EF; Maniatis T. and Sambrook (1989). Molecular Cloning: A Laboratory Manual. 2nd edition. Cold Spring, NY, USA; Cold Spring Harbor Laboratory Press.
- Sasser, J. N. (1954). Identification and host-parasite relationships of certain root-knot nematodes (*Meloidogyne* spp.). Technical Bulletin. Maryland Agricultural Experiment Station (A-77).
- Sikora, R. A.; Coyne, D.; Hallmann, J. and Timper, P. (Eds.). (2018). Plant parasitic nematodes in subtropical and tropical agriculture.CABI, p. 20.
- Taylor, D. P. and Netscher, C. (1974). An improved technique for preparing perineal patterns of *Meloidogyne* spp. Nematologica 20(2): 268-269.

- Tesařová, B.; Zouhar, M. and Ryšánek, P. (2003). Development of PCR for specific determination of root-knot nematode *Meloidogyne incognita*. Plant Protect. Sci. 39(1):23.
- Thomas, W. K.; Vida, J. T.; Frisse, L. M.; Mundo, M., and Baldwin, J. G. (1997). DNA sequences from formalin-fixed nematodes: Integrating molecular and morphological approaches to taxonomy. J. Nematol. 29(3): 250.
- Tigano, M.; De Siqueira, K.; Castagnone-Sereno, P.; Mulet, K.; Queiroz, P.; Dos Santos, M. and Carneiro, R. (2010). Genetic diversity of the root-knot nematode *Meloidogyne enterolobii* and development of a SCAR marker for this guavadamaging species. Plant Pathol. 59(6): 1054-1061.
- Zijlstra, C. and Van Hoof, R. A. (2006). A multiplex real-time polymerase chain reaction (TaqMan) assay for the simultaneous detection of *Meloidogyne chitwoodi* and *M. fallax*. Phytopathol. 96(11):1255-1262.
- Zijlstra, C.; Donkers-Venne, D. T. and Fargette, M. (2000). Identification of *Meloidogyne incognita, M. javanica* and *M. arenaria* using sequence characterised amplified region (SCAR) based PCR assays. Nematol. 2(8): 847-853.

الملخص العربى

التعريف الجزيئى لنيماتودا تعقد الجذور Meloidogyne javanica فى صعيد مصر . باستخدام تقنية تفاعل البلمرة المتسلسل RAPD-PCR

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قسم الحيوان الزراعي والنيماتودا كلية الزراعة ، جامعة الاز هر أسيوط ، مصر

تم في هذه الدراسة عزل الحمض النووي الريبوزي منقوص الأكسجين (DNA) من الاناث البالغة لنيماتودا تعقد الجذور من النوع اعتمادا على تفاعل البلمرة المتسلسل PCR معتمدا على المناطق المتضاعفة من مصر), لتشخيص هذا النوع اعتمادا على تفاعل البلمرة المتسلسل PCR معتمدا على المناطق المتضاعفة من خلال الفحص المعتمد على التضاغف العشوائي متعدد الاشكال (RAPD-PCR) للـ DNA باستخدام اربعة انوع من البادئات مندرجة تحت المجموعتين (SCAR و Mitochondrial). اشارت النتائج الى ان استخدام تقنية RAPD-PCR هى طريقة فعالة لتعريف هذا النوع من نيماتودا التعقد , كما اشارت النتائج الى ان البادئات التى تنتمى الى مجموعة فعالة لتعريف هذا النوع من نيماتودا التعقد , كما اشارت النتائج الى ان البادئات التى تنتمى الى مجموعة معالة لتعريف هذا النوع من نيماتودا التعقد , كما اشارت النتائج الى ان البادئات الم تعتمي الى مجموعة علي النوع النوع ومن نيماتودا التعقد , كما اشارت النتائج الى ان البادئات التى تنتمى الى مجموعة الاناث البالغة حيث تم تضاعف الـ DNA بحجم م وقال و Fjav/Rjav and Far/Rar) هى الانسب لتعريف النوع على العكس من بادئات مجموعة المانوع من نيماتودا على حجم ازواج قاعدة على التوالي. الم تعلى يتائج محددة لهذا النوع من نيماتودا الذى اعلى حجم ازواج قاعدة الم الموالي.