DNA-BASED CHARACTERISATION OF PARASITIC NEMATODES IN BANANA

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Abstract

In this study, different species of plant parasitic nematodes were identified and classified based on molecular taxonomy. Internal transcribed spacer (ITS) region was used as a taxonomic molecular marker for identification and characterization of Aphelenchus spp., Rotylenchulus reniformis, Meloidogyne spp., Xiphinema spp., Helicotylenchus dihystera and Pratylenchus spp. All samples were collected from banana tree roots in University Malaya. Initial identification was performed based on morphological characteristics using a light microscope. Internal transcribed spacer (ITS) regions of ribosomal DNA encoding the structure of ribosome are frequently used for molecular identification for many organisms. Genomic DNA of the nematodes was extracted using different extraction methods and the results showed that there is relationship between DNA extraction methods and different type of nematode species. Polymerase chain reaction (PCR) method was used to amplify the ITS regions using universal primers from Fallas-Kaplan (Fallas et al., 1996; Kaplan et al., 2000). ITS region was successfully amplified because the sequences are highly conserved in the rDNA genes. In this study the primers were able to successfully amplify ITS regions in different species with different length (~700bp and ~1163bp). ITS sequence could classification different nematode species into different cluster. It was interesting because ITS heterogeneity in individuals and populations have been recognized in some nematode taxa and maybe occurs due to transposition phenomena. These changes together with other mutations such as endoduplication in the entire genome, entire chromosome or portions of chromosomes as well as chromosome rearrangements can affect both the cell size and the body size in many nematode species. Consequently, it was suggested that the ITS region is useful for identification and characterization of plant parasitic nematode species.
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### Table of contents

Abstract .................................................................................................................i

Acknowledgement .................................................................................................ii

Table of contents .................................................................................................iii

List of figures .........................................................................................................viii

List of tables ..........................................................................................................xi

List of symbols and abbreviations ........................................................................xii

Chapter 1: Introduction ..........................................................................................1

1.1. Introduction of Banana ..................................................................................1

1.2. What are nematodes? .....................................................................................2

1.3. Classification of plant nematodes ....................................................................3

1.4. Physical structures of a nematode ...................................................................3

1.5. Biology of plant parasitic root nematodes ....................................................5

1.6. Damage of nematode .....................................................................................6

1.7. Chemical and biological treatment against nematodes ..................................7

1.8. Different types of plant parasitic nematodes ................................................8

1.8.1. *Meloidogyne* spp ....................................................................................8
1.8.2. *Rotylenchulus reniformis* ......................................................... 10

1.8.3. *Pratylenchus* spp........................................................... 12

1.8.4. *Helicotylenchus* spp.................................................... 13

1.8.5. *Aphelenchus* spp.......................................................... 14

1.8.6. *Xiphinema* spp............................................................. 15

1.9. Secondary infection ............................................................ 16

1.10. Characteristic and identification of plant parasitic nematode .......... 17

1.11. Internal transcribed space (ITS) ........................................... 18

1.12. Polymerase chain reaction and gene cloning ............................. 18

1.13. Objective ........................................................................... 20

Chapter 2: Materials and methods ...................................................... 21

2.1. Sample collection ..................................................................... 21

2.2. Nematode extraction from soil and root ...................................... 21

2.2.1. Separation of roots from soil ............................................... 21

2.2.2. Nematode extraction from soil samples .................................. 23

2.2.3. Nematode extraction from the root samples ............................ 26

2.2.4. Morphological identification of nematode ............................... 27

2.3. DNA extraction ....................................................................... 27
2.3.1. Modified Madania et al., 2005 method .............................................27

2.3.2. Modified G-spin™ Genomic DNA Extraction kit ..............................28

2.3.3. Modified QIAamp DNA Mini kit .....................................................29

2.4. Qualitative and quantitative analysis ..................................................30

2.5. Polymerase chain reaction (PCR) .......................................................31

2.6. PCR product analysis .....................................................................32

2.6.1. Agarose gel electrophoresis ..........................................................32

2.6.2. Sample loading .............................................................................32

2.7. Purification of PCR product by gel extraction .................................33

2.8. Cloning .........................................................................................35

2.8.1. Luria Bertani (LB) agar plate .......................................................35

2.8.2. Luria Bertani (LB) broth medium .................................................35

2.8.3. Preparation of competent cells .....................................................36

2.8.4. DNA ligation ...............................................................................36

2.8.5. Transformation by heat shock method ..........................................37

2.8.6. Colonies screening .......................................................................37

2.8.7. Colony PCR ................................................................................38

2.8.8. Plasmid extraction .......................................................................39
2.8.9. Restriction enzyme digestion.....................................................40

2.9. Sequencing analysis.................................................................41

Chapter 3: Results

3.1. DNA extraction.................................................................42

3.2. Polymerase chain reaction (PCR).............................................43

3.3. Gel extraction and post gel extraction.....................................46

3.4. Cloning screening...............................................................49

3.4.1. Blue and white colony screening.......................................49

3.4.2. Colony screening by PCR................................................50

3.4.3. Optical density reading for plasmid extraction.....................52

3.4.4. Restriction enzyme digestion.............................................53

3.5. Samples send to sequencing................................................54

3.6. Sequence homology result...................................................55

3.6.1. Sequence homology result of clone C4m2a2 of Meloidogyne spp. using BLAST.................................................................55

3.6.2. Sequence homology result of clone C4m1d4 of Meloidogyne spp. using BLAST.................................................................57

3.7. Phylogenetic tree...............................................................59

3.7.1. Phylogenetic tree of samples with band (~700bp)................59
3.7.2. Phylogenetic trees of samples with band (~1163bp)..........................60

Chapter 4: Discussion..................................................................................61

4.1. Sequence analysis and Blast.................................................................61

4.2. ITS heterogeneity..................................................................................63

4.3. Phylogenetic analysis.............................................................................65

5: Conclusion and future work......................................................................68

6: References...............................................................................................69
List of figures

Figure 2.1: Untreated roots ................................................................. 22
Figure 2.2: Untreated soil .................................................................. 22
Figure 2.3: Sieve layered with damp tissues ....................................... 24
Figure 2.4: Oostenbrink funnel .......................................................... 24
Figure 2.5: Sieves with untreated soil .................................................. 25
Figure 2.6: Sieve containing ground banana roots .............................. 26

Figure 3.1: PCR product of *Meloidogyne* spp. (C4m1 and C4m2) run on 1% agarose gel using Fallas-Kaplan universal primer pair. DNA was extracted using modified Madania *et al.*, 2005 method with overnight incubation option ................................................. 43

Figure 3.2: 1% agarose gel electrophoresis of PCR product amplified from *Pratylenchus* spp. using Fallas-Kaplan universal primer pair. DNA was extracted using modified Madania *et al.*, 2005 method and incubated overnight ......................................................... 44

Figure 3.3: 1% agarose gel electrophoresis of PCR products amplified from *Aphelenchus* spp. (Aph3), *Helicotylenchus dihystera* (Hd6), *Xiphinema* spp. (Xip9 and Xip10) and *Rotylenchulus reniformis* (Rr27) using Fallas-Kaplan universal primer pair. DNA was extracted with modified QIAamp DNA Min kit (tissue protocol) ................................................................. 45

Figure 3.4: Agarose gel electrophoresis (1%) of amplified ITS1 and ITS2 region to follow gel extraction steps ........................................................................ 47
Figure 3.5: Agarose gel electrophoresis (1%) of PCR product post gel purification to check the presence of the purified DNA of *Rotylenchulus reniformis* (Rr27) and *Xiphinema* spp. (Xip10)……………………………………………………………………………………...48

Figure 3.6: Ampicillin-resistant white and blue bacterial colonies grown on Ampicillin/IPTG/X-Gal-supplemented LB agar plates……………………………………………………49

Figure 3.7: 1% agarose gel of PCR products clone screening using M13 primers. Samples showing band size of ~950bp were selected for plasmid extraction………………………………50

Figure 3.8: 1% agarose gel of PCR products for *Helicotylenchus dihystera* clone screening using M13 primers of (cloning of DNA fragment ~1163bp). The samples showing band size of ~1400bp were selected for plasmid extraction step……………………………………….51

Figure 3.9: Restriction enzyme digestion result of *Aphelenchus* spp………………………….53

Figure 3.10: The samples send to sequencing. The samples that have the correct inserts after restriction enzyme digestion were diluted and sequenced…………………………………54

Figure 3.11: Phylogenetic tree showing the relationship between *Xiphinema* spp. (Xip9 and Xip10), *Aphelenchus* spp. (Aph3), *Rotylenchulus reniformis* (Rr27), *Helicotylenchus dihystera* (Hd6), *Pratylenchus* spp. (Pra8), *Meloidogyne* spp. (C4m1 and C4m2) with band (~700bp) and out-group (*C. elegans*)……………………………………………………………………59

Figure 3.12: Phylogenetic tree showing the relationship between *Xiphinema* spp. (Xip9 and Xip10), *Aphelenchus* spp. (Aph3), *Helicotylenchus dihystera* (Hd6), *Rotylenchulus reniformis* (Rr27) with band (~1163bp) and out-group (*C. elegans*)…………………………………60
Figure 4.1: The position of 18S, ITS1, 5.8S, ITS2 and 28S regions; (B) the difference in length between the two ITS variants.
List of tables

Table 1.1: Categorization of plant parasitic nematodes ........................................5

Table 3.1: Optical density of plasmid extraction obtained from DNA cloning of fragment ~700bp ..........................................................52

Table 3.2: Optical density of plasmid extraction obtained from DNA cloning of fragment ~1163bp ..........................................................52

Table 4.1: Blast sequence analysis results of Xiphinema spp., Helicotylenchus dihystera, Aphelenchus spp. and Rotylenchulus reniformis indicating clone homology to Meloidogyne arenaria ..........................................................62