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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