# BANANA NEMATODE INFESTATION IN PENINSULA MALAYSIA

**Syarifah Aisyafaznim Sayed Abdul Rahman**

Programme of Genetics and Molecular Biology, Institute of Biological Sciences, Faculty of Science, University of Malaya, Kuala Lumpur, Malaysia, 50603
Corresponding author: aisyafaznim@um.edu.my

Banana, the world's second largest fruit crop is under a serious nematode threat. At present, control measures adopted at macro level to manage its infection are ineffective while the only effective solution is the non-executable usage of toxic nematicides. The development of host natural resistance is gaining crop scientists' interest to mend the inefficiency of the conventional management system. In line with this notion, three inter-relating research aspects were addressed in this study namely (i) epidemiological information of nematode infestation in the Peninsula, (ii) the diagnostic utility of DNA-based nematode characterisation method and, (iii) plant-nematode interaction study at both biological and molecular level. A survey was first conducted to gauge and provide epidemiological information of nematode infestation in Peninsula Malaysia. From this survey, *Rotylenchulus reniformis* was found to be the most prominent species (31.23%, PV = 824.28) in the isolated soil samples while *Meloidogyne incognita* was predominant in the isolated root samples (42.99%, PV = 449.77). DNA-based species identification approach using ITS1-5.8S-ITS2 fragments of ribosomal DNA (rDNA) region was opted in order to assess molecular diversity of six nematode species frequently found in banana rhizosphere. Sequence analyses revealed that the size of the amplified product serves as a subfamily-level marker and intraindividual sequence heterogeneity was present in isolated ITS1-5.8S-ITS2 clones. The final work package of the study is to understand plant-nematode interaction in the quest of finding natural resistance sources in local banana cultivars. The host status of five banana cultivars towards *Meloidogyne incognita* infestation was first determined. A high-throughput proteomics approach was then employed to elucidate the proteins involved in a compatible banana cv. Grand naine - *M. incognita* interaction. A total of 114 Grand naine root proteins involved in this interaction were successfully profiled. Abundances of proteins in pathways associated with defence and giant cell maintenance in plants such as phenylpropanoid biosynthesis, glycolysis and citrate cycle were found to be significantly implicated ($p \leq 0.05$) by the infestation.

Keywords: banana, nematode, ribosomal DNA, *Meloidogyne incognita*, proteome