

# ISOLATION AND CHARACTERISATION OF PATHOGENESIS-RELATED GENE 1 (*PR-1*) FROM *MUSA* SPP. AGAINST *MELOIDOGYNE INCOGNITA* INFESTATION

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The root-knot nematodes (*Meloidogyne* spp.) are a major threat to many crops including *Musa* spp. which can cause extensive economic loss. In a compatible host-nematode interaction, the secretion of avirulent effector molecules will suppress plant's defence system. A background proteomics study conducted on a compatible banana-*M. incognita* interaction revealed that Pathogenesis-related-gene-1 (*PR-1*) protein was present at a significantly low abundance level ( $p < 0.05$ ) in nematode-inoculated root samples when compared to control samples suggesting the crucial role of this gene in banana defense mechanism against nematode infestation. Data mining in Banana Genome Hub was carried out to search for other sequences that share similarity with *PR-1* peptide detected in the proteomics study. Thirty-five protein sequences revealed to have similar peptide sequence and the confirmed *PR-1* protein from Banana Genome Hub shared 99% similarity with the detected peptide. Therefore, a pair of primers was then designed to amplify this gene from Berangan and Grand naine cultivars. We had successfully isolated 56 genomic sequences and 15 transcripts of *PR-1* gene. Our analysis revealed that compared to *PR-1* sequences available in the database, our clones contain an intronic region between two exons. Nucleotide diversity analysis revealed high sequence diversity value ( $\pi$ ) of 0.17760 at the 3' end of the coding region of *PR-1 like* gene and the genes clustered into four groups in a Neighbour Joining tree. However, our Southern blot analysis suggested the presence of two to three copies of *PR-1* in the genome of these two banana varieties.

**Keywords:** banana, *Meloidogyne* spp., *Pathogenesis-related-gene-1 (PR-1)*, intronic region, sequence diversity