



Isolation and characterization of nucleotide-binding site and C-terminal leucine-rich repeat-resistance gene candidates in bananas

Y. Lu^{1,2}, W.H. Xu³, Y.X. Xie², X. Zhang², J.J. Pu², Y.X. Qi² and H.P. Li¹

¹College of Natural Resources and Environment,
South China Agriculture University, Wushan, China

²Environment and Plant Protection Institute,
Chinese Academy of Tropical Agriculture Sciences, Hainan, China

³Shangrao Normal University, Zhimin State in Shangrao, JiangXi, China

Corresponding author: H.P. Li
E-mail: ytluy2010@163.com

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ABSTRACT. Commercial banana varieties are highly susceptible to fungal pathogens, as well as bacterial pathogens, nematodes, viruses, and insect pests. The largest known family of plant resistance genes encodes proteins with nucleotide-binding site (NBS) and C-terminal leucine-rich repeat (LRR) domains. Conserved motifs in such genes in diverse plant species offer a means for the isolation of candidate genes in banana that may be involved in plant defense. Six degenerate PCR primers were designed to target NBS and additional domains were tested on commercial banana species *Musa acuminata* subsp *malaccensis* and the *Musa* AAB Group propagated *in vitro* and plants maintained in a greenhouse. Total DNA was isolated by a modified CTAB extraction technique. Four resistance gene analogs were amplified and deposited in GenBank and assigned numbers HQ199833-HQ199836. The predicted amino acid sequences compared to the amino acid sequences of known resistance genes (*MRGL1*, *MRGL2*, *MRGL3*, and *MRGL4*) revealed significant sequence similarity. The presence of consensus do-

mains, namely kinase-1a, kinase-2 and hydrophobic domain, provided evidence that the cloned sequences belong to the typical non-Toll/interleukin-1 receptor-like domain NBS-LRR gene family.

Key words: Resistance genes; NBS-LRR; Banana