

Novel bacteriocinogenic *Lactobacillus plantarum* strains and their differentiation by sequence analysis of 16S rDNA, 16S-23S and 23S-5S intergenic spacer regions and randomly amplified polymorphic DNA

ABSTRACT

Six strains of bacteriocinogenic *Lactobacillus plantarum* (TL1, RG11, RS5, UL4, RG14 and RI11) isolated from Malaysian foods were investigated for their structural bacteriocin genes. A new combination of plantaricin EF and plantaricin W bacteriocin structural genes was successfully amplified from all studied strains, suggesting that they were novel bacteriocin-producing *L. plantarum* strains. A four-base pair variable region was detected in the short 16S-23S intergenic spacer regions of the studied strains by a comparative analysis with 17 *L. plantarum* strains deposited in the GenBank, implying they were new genotypes. The studied *L. plantarum* strains were subsequently differentiated into four groups on the basis of the detected four-base pair variable region of the short 16S-23S intergenic spacer region. Further analysis of the DNA sequence of 23S-5S intergenic spacer region revealed only one type of 23S-5S intergenic spacer region present in the studied strains, indicating it was highly conserved among the studied *L. plantarum* strains. Three randomly amplified polymorphic DNA experiments using three different combinations of arbitrary primers successfully differentiated the studied *L. plantarum* strains from each other, confirming they were different strains. In conclusion, the studied *L. plantarum* strains were shown to be novel bacteriocin producers and high level of strain discrimination could be achieved with a combination of randomly amplified polymorphic DNA analysis and the analysis of the variable region of short 16S-23S intergenic spacer region present in *L. plantarum* strains.

Keyword: Bacteriocin gene; Differentiation; *Lactobacillus plantarum*; Ribosomal intergenic spacer region.