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RANDOM AMPLIFIED POLYMORPHIC DNA

SUKUN KUNAWASEN: MOLECULAR TYPING OF LACTIC ACID  
BACTERIA ISOLATED DURING NHAM FERMENTATION. THESIS  
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Nham is one of the most favorite Thai traditional fermented meat products. Quality variation in Nham could affect acceptability and safety of the product. Such problem could be prevented by using the right of starter microorganisms for fermentation. The purpose of this study is to genetically identify the dominant groups of lactic acid bacteria important to the fermentation process of Nham. The polymerase chain reaction conditions and suitable oligonucleotide primers were screened for use in the molecular typing of lactic acid bacteria isolated from Nham fermentation. The method was able to differentiate closely related bacterial strains by their polymorphic differences. Based on these results, all the bacterial isolates were genetically grouped. The molecular typing method together with the phenotypic characteristics were used to identify selected strains of lactic acid bacteria from these genetic groups. In Nham I, 12 different genetic groups (A to L) were identified and only four were found to be dominant. Group A were identified as *Leuconostoc mesenteroides* subsp. *dextranicum* and were dominant throughout the fermentation with the proportion of population increased from 9 to 33%. Groups D and F were identified as *Lactobacillus* spp. and *Lactobacillus paracasei* respectively. They were also dominant throughout the fermentation. Group J identified as *Pediococcus pentosaceus*, was found at 36 h constituted 2% of the total population and increased to 22% at 84 h. The increase in the proportion of populations from groups D and F correlated well with the rapid decrease in pH from 6.2 to 4.6. Whereas the increase in the population of group J at the latter phase of fermentation from 36 to 84 h did cause a rapid decrease in pH from 4.9 to 4.6. However different bacterial profiles isolated from another production batch of Nham I and from 3 different commercial brands, II, III and VI, were observed. The bacterial strains found in another batch of Nham I were *Lactobacillus graminis*, *Lactobacillus sake* and *Enterococcus* spp. For other 3 commercial brands, *Lactobacillus graminis*, *L. sake*, *L. farciminis*, *L. curvatus*, *L. brevis*, *L. plantarum*, and *L. homohiochii* were found. The results could be used as the basic information for selecting lactic acid bacteria to be used as starter in Nham fermentation.