

Sequence analysis of 16S rRNA gene and 16S–23S rRNA gene intergenic spacer region for differentiation of probiotics Lactobacillus strains isolated from the gastrointestinal tract of chicken

ABSTRACT

Twelve probiotic Lactobacillus strains which were previously identified with classical biochemical tests were re-identified using molecular methods. Comparative sequence analyses of the 16S rRNA gene and 16S–23S rRNA gene intergenic spacer region (ISR) were applied. Results of the study showed that mis-identification at species level occurred at high rate when classical biochemical tests were used. Nine of the strains showed discrepancy in their identity. These nine strains which were previously identified through biochemical tests as *L. brevis* C1, *L. brevis* C10, *L. fermentum* C16, *L. brevis* C17, *L. crispatus* I12, *L. acidophilus* I16, *L. fermentum* I24, *L. fermentum* I25 and *L. acidophilus* I26 were re-identified as *L. reuteri* C1, *L. reuteri* C10, *L. reuteri* C16, *L. panis* C17, *L. brevis* I12, *L. gallinarum* I16, *L. salivarius* I24, *L. brevis* I25 and *L. gallinarum* I26, respectively, using 16S rRNA gene and 16S–23S rRNA gene ISR analysis. Lactobacillus strains I16 and I26 initially could not be classified into a single taxon by 16S rRNA gene sequencing but the identities of these two strains were eventually resolved by 16S–23S rRNA gene ISR sequence analysis as *L. gallinarum*. Sequence analysis of 16S rRNA gene in complementary with 16S–23S rRNA gene ISR could be potentially useful for rapid and reliable identification of bacteria.

Keyword: Lactobacillus spp.; 16S rRNA gene; 16S–23S rRNA gene intergenic spacer region (ISR); Phylogenetic analysis