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

Abstract

Twelve probioticLactobacillus 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 asL. brevis C1,L. brevis C10,L. fermentum C16,L. brevis C17,L. crispatus I12,L. acidophilus I16,L. fermentum I24,L. fermentum I25 andL. acidophilus I26 were re-identified asL. reuteri C1,L. reuteri C10,L. reuteri C16,L. panis C17,L. brevis I12,L. gallinarum I16,L. salivarius I24,L. brevis I25 andL. 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 asL. 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.