## Cellular Fatty Acid Composition and Genotypic Analysis of *Bifidobacterium longum*MK-G7

Jung, Hoo-Kil, Eung-Ryool Kim, Geun-Eog Ji<sup>1</sup>,
Jong-Hyun Park<sup>2</sup>, Sung-Kwan Cha<sup>3</sup>, and Suk-Lak Juhn
R&D, Central Research Institute, Maeil Dairy Industry Co., Ltd., Seoul, Korea

<sup>1</sup>Department of Food Science and Nutrition, Seoul National University, Seoul, Korea

<sup>2</sup>Department of Food and Bioengineering, Kyungwon University, Sungnam, Korea

<sup>3</sup>Korea Food Research Institute, Sungnam, Korea

It was considered that cellular fatty acid composition of Bifidobacteria depended upon the species and was regarded as very useful tools for the identification of Bifidobacteria. Cellular fatty acid of Bifidobacterium longum MK-G7 was shown to be composed of C160 FAME, C181 c18 DMA, C181 c18 9 FAME, C140 FAME, C190 CYC 9.10 DMA, Feature 7(C172 FAME), and Feature 10(C181 C11/19/16 FAME). Therefore, cellular fatty acid composition of Bifidobacterium longum MK-G7 is quite similar to that of Bifidobacterium longum, compared with Bifidobacterium adolescentis, Bifidobacterium breve, and Bifidobacterium suis. Especially Bifidobacterium longum contained cis-9,10-methylene octadecanoic acid(19:0 cyclo 9,10) so-called lactobacillic acid. As taxonomic and phylogenetic experimental results based on 16S rDNA sequencing analysis, Bifidobacterium longum MK-G7 showed 99.9 % homology similarity and showed the highest relatedness with Bifidobacterium longum ATCC 15707 Purified DNA of Bifidobacterium longum MK-G7 was harvested in the level of 1.8-fold purity at  $A_{260}/A_{280}$  and 30  $\mu g$  from 3 ml medium. Even though Bifidobacterium longum MK-G7 and Bifidobacterium longum ATCC 15707 showed 153 bp PCR products, Bifidobacterium lactis Y-4 did not make any band at all. It was same situation both in genomic DNA and in cell Therefore, it was shown that Bifidobacterium longum MK-G7 had 16S rRNA gene and should be classified taxonomically as Bifidobacterium longum. 8 Bifidobacteria strains were used in the test and their band pattern was confirmed by PFGE analysis. Bifidobacterium infantis Y-2, Bifidobacterium longum Y-3, Bifidobacterium longum Y-6, and Bifidobacterium adolescentis ATCC similar band patterns. However, Bifidobacterium longum MK-G7 and Bifidobacterium longum ATCC 15707 showed quite different band patterns. Consequently, it was confirmed that MK-G7 strain was identified as Bifidobacterium longum and Bifidobacterium longum MK-G7 did not belong to any commercial and type strains of Bifidobacterium longum.