

Development of Genome-Probing Microarrays for Monitoring Lactic Acid Bacteria during Kimchi Fermentation

Yong-Ha PARK

Department of Applied Microbiology, Yeungnam University, Republic of Korea

Kimchi, a kind of pickled vegetable, was first created as a representative food in Korea around the 7th century. At the moment, more than 1.5×10^6 tons of Kimchi is consumed per year in South Korea, a phenomenon that is now rapidly growing and spreading to other Asian countries. Despite its great impact on Asian health, the microbiology of Kimchi has only been explored by non-quantitative PCR-based pattern analyses. In order to find correlations between Kimchi types and their bacterial compositions, genome probing microarrays (GPM) comprising 150 distinct lactic acid bacterial (LAB) genomes deposited on a glass slide have been developed to meet the pressing need for a more sensitive, quantitative and high-throughput analysis tool. Compared to current oligonucleotide microarrays, GPM offers a specificity approaching that of the species-specific level with a sensitivity of 0.25 ng of genomic DNA (100 times higher sensitivity). In an assessment of the applicability of GPM in monitoring the community dynamics of lactic acid bacteria, about 100 species were quantitatively analyzed and shown to be actively involved in Kimchi fermentation. Several species from the genera *Lactobacillus*, *Leuconostoc* and *Weissella* were also found to be the most dominant microflora in Kimchi fermented at 4°C. GPM profiles of Kimchi samples evolved significantly after 7-9 days of fermentation, showing that some *Streptococcus* and *Lactobacillus* species disappear after a decrease in pH. Recently, we were able to design Kimchi with special features, such as anti-Corona virus or anti-*Helicobacter* activity, by using probiotic *Lactobacilli* as starter cultures. In order to monitor whether starter LAB can proliferate in the fermented Kimchi or not, we are fabricating starter strain-specific microarrays by using genes amplified after subtractive suppression hybridization as microarray probes.