

Genomes of the Probiotic Bacteria *Bifidobacterium animalis* subsp. *lactis*, *Bifidobacterium bifidum*, and *Leuconostoc citreum*

Jihyun F. Kim¹, Haeyoung Jeong^{1*}, Dong Su Yu¹, Sang-Haeng Choi¹, Cheol-Goo Hur², Hong-Seog Park¹, Geun-Eog Ji³, Jung-Sook Lee⁴, and Tae Kwang Oh⁵

¹Industrial Biotechnology and Bioenergy Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), ²Bioinformatics Research Center, KRIBB, ³Department of Food and Nutrition, Research Institute of Human Ecology, Seoul National University, ⁴Biological Resource Center, KRIBB, ⁵21C Frontier Microbial Genomics and Applications Center

Human intestine harbors an enormous number of microorganisms that play a crucial role in maintaining human health by preventing pathogen colonization, degrading non-digestible compounds, producing vitamin K, facilitating absorption of ions, and enhancing gut mucosal immunity [1]. Among them, bifidobacteria and lactic acid bacteria have been drawing special interest for their health-promoting effect and are widely used as forms of enriched functional foods and drinks [2]. We determined the complete genome sequences of two species of bifidobacteria isolated from the fecal samples of healthy Koreans [3], and *Leuconostoc citreum* that dominates kimchi fermented at low temperature [4]. *Bifidobacterium animalis* subsp. *lactis* AD011 and *B. bifidum* BGN4 are reported to have high immunomodulatory activities [5, 6], and the latter especially exhibits a prominent adhesive capacity for intestinal epithelial cells [7]. Their genome sequences revealed compact circular chromosomes encoding limited biosynthetic functions (ca. 2 Mb) with no plasmid and low prophage content, which is in accordance with generic characteristics of bifidobacterial genomes [8]. We also found gene clusters possibly involved in polysaccharide biosynthesis and coincide with horizontally transferred genomic regions, and glycosyl hydrolases for the processing of food-borne oligosaccharides (bifidogenic factors). The genome of *L. citreum* KM20, on the other hand, encodes functions enriched in carbohydrate transport and metabolism, implying a lifestyle associated with plant-derived carbohydrates. Detailed genome analysis is underway to identify their probiotic effects and microbe-host interaction at the genome level, which will give us an insight into genome evolution and application potential of probiotic bacteria. [Supported by the 21C Frontier Microbial Genomics & Applications program, MEST, Korea]

References

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