

# INFECTION CONTROL AND CLINICAL MICROBIOLOGY

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## Pan-genome analysis and phylogenetical grouping of food-borne pathogens, *Bacillus cereus* isolated from South Korea

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Pan genome analysis is useful technique to compare whole genome sequences. It offers core proteins and strain specific proteins to users. Recently, it used to compare complete genomes of *Bacillus cereus* strains isolated from food samples causing food-borne outbreaks in South Korea. With the support of Ministry of Drug and Food Safety, South Korea, the Food-borne Pathogen Omics Research Center (FORC) was established for omics research and database construction of food-borne outbreak-associated pathogens detected in South Korea to perform this study. From the FORC database, nine strains of *B. cereus* were obtained and used for comparative analysis with all *B. cereus* genomes of Genbank. Interestingly, their average nucleotide identity (ANI) tree analysis showed that food-segregated *B. cereus* strains are located in the same branches as clinical isolates B4264 and ATCC 14579 (Group 2), but other *B. cereus* 8% branch of ANI value (Group 1). This result was revealed by pan-genome analysis using two Group 1 strains and four of Group 2. There are specific gene clusters in Group 1 (BCE-2148 to BCE-2159 of *B. Cereus* ATCC 10987) and specific peptide synthetase of Group 2 (FORC 24 \_ 2275 to FOR 24 - 2276 of *B. cereus* FORC - 024), and each specific gene would be a biomarker for detecting subgroup.

### Biography

Ju-Hoon Lee has completed his PhD from University of Minnesota, USA and Postdoctoral studies from Cargill Genomics Institute, University of Minnesota, USA. He has been Professor of Kyung Hee University in Korea since 2012. He has published more than 50 papers in reputed journals and has been serving as an Editorial Board Member of *Journal of Microbiology and Biotechnology* and *Food Science and Biotechnology*.

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