

A Post-Genome Study of *Thermus caldophilus* GK24: Toward Biosynthetic Machinery Engineering for Carbohydrates

Doo-Il Kim, Jung-Don Bae, Bo-Hyun Park, Chul-Hong Kim, Han-Soo Kang, Jung-Eun Park, Kwang-Ho Kim, Jong-Su Kim, Soo-Jin Jo, Dae-Sil Lee

Korea Research Institute of Bioscience and Biotechnology (KRIBB)

In studying the collective enzyme engineering of carbohydrates using thermostable enzymes, *Thermus caldophilus* GK24 genome was analyzed through Shot-gun method with a large number of clones containing about 5 kbp long genome insertsm and along with the cosmid clone analysis. The resulting genome sequences were subject to the home-made DNA/protein database-analysis system at Linux platform (OSCA) to assemble contigs and ORF identifications, particularly carbohydrate-related enzyme database, showed reliable performance to find a number of genes corresponding to the carbohydrate biosynthesis.

Microbial Genomics and Metabolic Engineering

Sang Yup Lee

Dept. Chemical and Biomolecular Eng., KAIST, Daejeon, Korea

Metabolic engineering can be defined as purposeful modification of metabolic pathways by using recombinant DNA and related techniques to achieve goals such as overproduction of metabolites, production of new metabolites, degradation of xenobiotics and broadening substrate utilization range. Recent completion of sequencing the entire genomes of numerous microorganisms and other organisms is setting up a new paradigm of biotechnological research. Namely, cells and their metabolism can now potentially be studied in a large scale. Furthermore, transcriptome and proteome analysis allow us to better understand cellular physiological states at large scale. In this lecture, the impact of genomics combined with transcriptome and proteome analysis on metabolic engineering will be discussed.