

## Genome Analysis of *Escherichia coli* B

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*Escherichia coli*, a common inhabitant of the mammalian intestines, undoubtedly has been one of the best studied organisms and plays important roles in biological sciences, medicine, and industry. Derivatives of *E. coli* B have been serving not only as a research model for the study of phage sensitivity, restriction systems, and bacterial evolution in the laboratories, but a workhorse for protein expression in the biotechnological industry. The genome information of *E. coli* B REL606 was determined through an international collaboration that involved scientists in Korea, France, and the United States. Though the genome sequence of *E. coli* B REL606 was highly similar to that of *E. coli* K-12 MG1655, which incidentally is comparable to the difference between humans and chimpanzees, a number of genomic islands unique to either B or K-12 were identified. Many of the genes present in dozens of genomic regions specific to K-12 were those of prophages or IS elements; others included those involved in utilization of nutrients or production of surface molecules. A similar trend was obvious for B-specific islands; they were prophages, IS elements, fimbrial genes, genes for nutrient utilization, and gene clusters involved in exopolysaccharide biosynthesis. Interestingly, the genes for flagellar biogenesis were missing in B, while a second set of genes for type II protein secretion and genomic regions similar to those of *E. coli* O157:H7 or CFT073 were present. More strains of *E. coli* B including evolved descendants of REL606 and BL21 are being analyzed. Finally, in an effort to establish a comprehensive inventory of the -omics resources of *E. coli* B, a research platform for sequence analysis (genomics; genome informatics), gene expression analysis (transcriptomics), and phenotype analysis (phenomics) as well as an integrated database and a web portal is being developed. [This work was supported by the 21C Frontier Microbial Genomics and Applications Center Program, Ministry of Science and Technology, Republic of Korea]

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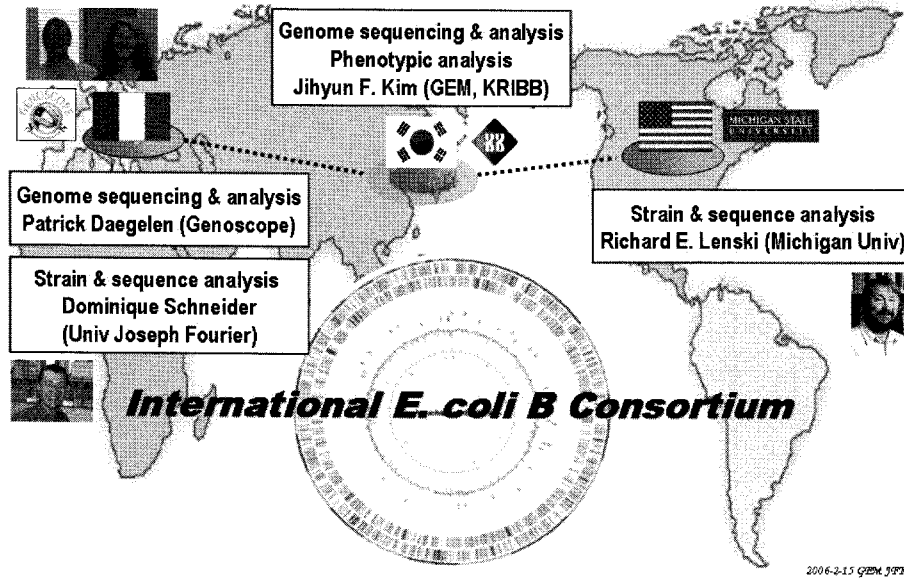


Fig. 1. Members of the International *E. coli* B Consortium

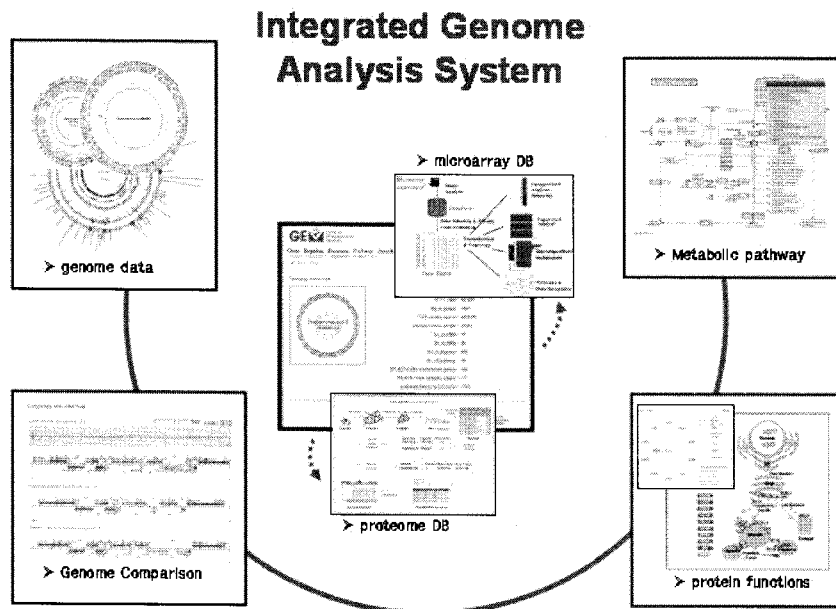


Fig. 2. Overview of a system for the integrated analysis of -omics information