Proc. KSAM International Symposium
June 20-22, 2001, Chonan, Korea

Functional Analysis of the Genome of the Model Bacterium, *Escherichia coli* K-12

Katsumi Isono

Department of Biology, Faculty of Science, Kobe University, Rokkodai, Kobe 657-8501,
Japan (E-mail: isono@biol.kobe-u.ac.jp)

Since the completion of nucleotide sequencing of its genome, we have been concerned with the functional analysis of some 2,000 ORFs that have been predicted to exist, and are functionally unknown, in the bacterium *Escherichia coli* K-12, strain W3110. If we accomplish this goal, then we shall become able to compare the functionally homologous genes in other organisms so that characteristics of *E. coli* will be made clear. Also, we shall be able to perform analysis of the evolution of *E. coli* and other organisms from an entirely different point of view. Bearing these in mind, we have organized a working project team in Japan and have started construction of clones containing each of the putative ORFs so as to make disruption and cloning of individual genes/ORFs easy. They will serve as valuable tools for systematic analysis of the effects of their absence as well as of their forced expression *in vivo*. In addition, we have started collection of various genetic and biochemical papers of *E. coli* published in the past and analyses of the data from informatics points of view. In accordance with these approaches, we have also started analysis of the roles and functional differences, if any, of individual cells in *E. coli* colonies, hoping to elucidate the genes important for cell-to cell communi-cation and to make E. coli colonies as a model for multicellular organisms.