

Microbial Genomics to Omics-Based Systems and Synthetic Microbiology

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Since the first decoding of the complete sequence of a genome, sequencing has become an effective means of understanding life systems and increasing the utility of a particular organism or a consortium. There is no doubt that sequence information is not only the final goal of a particular genome or metagenome project, but it also serves as a starting point of so-called ‘-omics’ research and now is becoming the cornerstone of systems biology and synthetic biology [1,2].

There have been tens of microbial genome projects in Korea during the last decade [3]. Those run by my program include those of a proteorhodopsin-containing marine microbe *Donghaeana dokdonensis*, an algalicidal marine bacterium *Hahella chejuensis* [4,5], a dominant lactic acid bacterium of kimchi *Leuconostoc citreum* [6], a plant growth-promoting rhizobacterium *Paenibacillus polymyxa* [7, unpublished], a secondary metabolite producer *Streptomyces clavuligerus*, intestinal probiotic strains of *Bifidobacterium* spp. [8; unpublished], and a model industrial strain of *Escherichia coli* B and its derivatives that have underwent a long-term evolution experiment or a selection for better production of membrane proteins.

Strains of *E. coli* B, especially BL21, have been widely used as a workhorse for overproducing recombinant proteins and other biomolecules [9]. Almost all laboratory strains of *E. coli* are derivatives of K-12 or B strains. Recently, we determined partly as an international consortium activity the genome sequences of two *E. coli* strains of the B lineage, REL606 and BL21(DE3). We further integrated and compared the transcriptome, proteome and phenome data of B and K-12, and also applied a computational modeling approach, thus providing a framework to elucidate the phenotypic characteristics of organisms and offering a high-resolution system-wide view of the biological systems.

Finally, Genome Encyclopedia of Microbes (GEM; www.gem.re.kr) is an integrated database system and a web portal that was established to promote systems and synthetic microbiology by providing information on the microbial genomes we deciphered [3], as well as specialized databases such as one for pathogenicity islands [10,11] and one for microbial esterases and lipases [12,13], mirror sites of Comprehensive Microbial Resource [14] and Comparative Fungal Genomics Platform [15], and integrated analysis pipeline of multi-omics data.

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