

The role of culture collections and DNA banks in the Genomic Encyclopaedia of *Bacteria* and *Archaea*

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A recent symposium on reconciling microbial systematics and genomics resulted in the recommendation to coordinate an international effort to sequence the genomes of all 9000 type strains of the *Bacteria* and *Archaea*. Following this recommendation the Joint Genome Institute (USA) and the German Collection of Microorganisms and Cell Cultures entered a collaboration to generate a Genomic Encyclopaedia for *Bacteria* and *Archaea* (GEBA), with the aim to systematically fill the gaps in the genomic tree of life by sequencing along the branches of the tree. Although the wide variety of microbial sequencing projects undertaken throughout the world has already created a diverse collection of microbial genomes, strong biases in what has been sequenced thus far are evident. The here described project represents the first systematic attempt to use the tree of life itself as a guide to sequencing target selection. This phylogenomic approach will be of great value for: (I) improved identification of protein families; (II) improved phylogenetic anchoring of metagenomic data; (III) improved gene discovery; (IV) a better understanding of the processes underlying the evolutionary diversification and history of microbes; and (V) improved correlations of phenotype and genotype in microbes. To test the feasibility of the GEBA approach we have meanwhile started about 250 genome sequencing projects, with almost 150 of them already finished, all to be published in Standards in Genomics Sciences, an Open Access Journal that hosts the GEBA in a dedicated monthly section to make it available to the scientific community.

This presentation will especially feature the contribution of culture collections to (I) the selection of strains to be sequenced in GEBA, (II) extraction, analysis and storage of genomically sequenced DNAs in DNA banks, and (III) the usage of the genome sequences for an improved microbial taxonomy.