

Genome-scale clustering analyses of the genomic contents for the elucidation of evolutionary relationships

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Abstract

As the number of complete genomes increases, the necessity of efficient methods for the analysis of genomic information becomes urgent. In this study, we proposed a novel method to identify the whole genome relationship using the information obtained from the orthology database.¹⁾ The metabolic capabilities of an organism were defined by the number of genes in each functional category. The archaeal, bacterial and eukaryotic genomes were compared simultaneously by using the two-step clustering procedures. We found that the clustering results showed different aspects compared with the RNA-based analysis, but they highly satisfied various phenotypic evidences among the organisms. Therefore, this approach is expected to be used to predict the phenotypic characteristics of the genomes and the relationships with other organisms by analyzing the metabolic functional capabilities. [This work was supported by the Korean Systems Biology Research Grant Program (M10309020000-03B5002-00000) from the MOST. Further supports by the BK21 program, LG Chemicals Chair Professorship, and IBM SUR program are appreciated.]

Reference

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