Analyses of Structural Organization of Unidentified Open Reading Frames from Metagenome

Seung-Hye Park, Won-Ho Kim, Geun-Joong Kim[1] and Byung-Ki Hur
Department of Biological engineering, Inha University, Incheon, 402-751
[1]Department of Biological Sciences, College of Natural Sciences, Chonnam National University, Gwangju, 500-757

The exploitation of metagenome, the access to the natural extant of enormous potential resources, is the way for elucidating the functions of organism in environmental communities, for genomic analyses of uncultured microorganism, and also for the recovery of entirely novel natural products from microbial communities. The major breakthrough in metagenomics is opened by the construction of libraries with total DNAs directly isolated from environmental samples and screening of these libraries by activity and sequence-based approaches. Screening with activity-based approach is presumed as a plausible route for finding new catabolic genes under designed conditions without any prior sequence information. The main limitation of these approaches, however, is the very low positive hits in a single round of screening because transcription, translation and appropriate folding are not always possible in *E. coli*, a typical surrogate host. Thus, to obtain information about these obstacles, we studied the genetic organization of individual URF's (uncharacterized open reading frame from metagenome sequenced and deposited in GenBank), especially on the expression factors such as codon usage, promoter region and ribosome binding site(rbs), based on DNA sequence analyses using bioinformatics tools. Information derived from these comparative metagenomic analyses can provide some specific features or environmental blueprint available to screen a novel biocatalysts efficiently.

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References

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