

From Diversity to Genomics of Marine and Extreme Microorganisms

Sang-Jin Kim¹*, Sung Gyun Kang¹, Kae Kyung Kwon¹, Jung-Hyun Lee¹,
Sun-Shin Cha¹, and Jang-Cheon Cho²

¹ Marine Biotechnology Research Centre, KORDI, Ansan 426-744, Korea, s-jkim@kordi.re.kr*

² Dept of Oceanography, Inha Univ., Incheon

Since 2004 Marine & Extreme Genome Research Centre program (<http://www.megrc.re.kr>) was supported by the Ministry of Land, Transportation and Maritime Affairs under the name of the National Marine Biotechnology Program. Under this program we have been established the marine & extreme bioresources (<http://www.megrc.re.kr/mebic>) and genome data bank, and also carried out the whole genome study on several microbial strains.

To develop useful biocatalysts and to elucidate the novel functions from marine and extreme bio-resources, we are currently putting a lot of efforts to collect marine resources from a variety of marine environments such as cold seep, hydrothermal vent, deep sea, sediment, tidal flat area, marine organisms and so on. The collected samples were routinely pretreated or enriched with various reagents for the purpose of enhancing the survival of useful target microorganisms, and then the isolated bacteria were stored systemically based on the analysis of 16S rRNA sequences. The collected resources were distributed to collaborators and tested for various biocatalytic activities. In addition to developing useful biocatalysts by screening isolated bacterial resources in a conventional approach, the genomic approach has been also applied to determine whole genome sequence of a limited number of microorganisms collected from various extreme environments, showing extraordinary physiological characteristics. The collected genetic information is put on intensive bioinformatic analysis to develop useful biocatalyst *in silico*, and also to reveal the function and survival mode of microorganism in marine environments. In this review, the current research on biocatalysts, algicidal activity, bio-hydrogen production by hyperthermophilic archaea, and PAHs degrading and unculturable marine microorganism will be introduced with emphasis.