

Functional Metagenomics Feeds Green Biotechnology Needs

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Because of global climate change, “green” technology such as bioremediation and environmental energy production has become strong research areas these days. Microbes are doing key roles in biodegradation of toxic pollutants and environmental energy production. In addition, microbes used in green technologies are working together as communities rather than individuals. Unfortunately, our current understanding about microbial ecology in bioremediation and environmental energy production is still very limited. This is mainly due to limitation of technology of analyzing microbial ecological behaviors. To provide more comprehensive information on microbial ecology, functional metagenomics is promising. In this work, titanium-base pyrosequencing - new generation sequencing - was used to efficiently provide information on novel populations and genes from tetrachloroethene and biphenyl degradation by marine-sediment (tidal mud) bacteria, energy-efficient “anammox” wastewater treatment microbial communities, and MFC (microbial fuel cell) microbial communities. Pyrosequencing was effectively integrated with a wide range of functional analysis methods such as stable isotope probing (SIP), gene-specific amplification, and whole metagenome sequencing. The quality of DNA significantly influenced the yield of good quality sequences while the different history and environmental conditions did not have significant effects on the yield of good sequences. 2-D Hierarchy cluster analysis was found to be useful in handling the huge amount of sequencing data for providing ecological profiling information on the whole system of microbial communities of interest. Candidate populations of interest could be informatively screened by hierarchy cluster analysis, and then further parsed using various databases including RDP-II, Greengenes, and GenBank. In this manner, novel populations were efficiently identified. When multiple displacement amplification (MDA) was used to amplify the SIP-isolated metagenomes, more diverse functional populations and genes could be detected compared to SIP only, although MDA provided a bias in metagenomic composition. Quantitative PCR analysis showed that the pyrosequencing metagenomic profiling provides semi-quantitative information on microbial community and functional gene composition. These findings suggest that functional metagenomic tools using pyrosequencing have power to provide ecological information which is needed for green biotechnology development.

This work was supported by KOSEF World Class University via a grant R33-2008-000-10076-0