

A modified SDS-based DNA extraction method for high quality environmental DNA from seafloor environments

N. VENGADESH PERUMAL^{1,2}, XINXU ZHANG^{1,2},
YUKI MORONO³, FUMIO INAGAKI³, AND
FENGPING WANG^{1,2*}

¹ State Key Laboratory of Microbial Metabolism,
School of Life Sciences and Biotechnology,
Shanghai Jiao Tong University, Shanghai,
200240, People's Republic of China.
(*Correspondence: fengpingw@sjtu.edu.cn)

² State Key Laboratory of Ocean Engineering,
Shanghai Jiao Tong University, Shanghai,
200240, People's Republic of China.

³ Geomicrobiology Group, Kochi Institute for Core
Sample Research, Japan Agency for Marine-
Earth Science and Technology (JAMSTEC),
Monobe B200, Nankoku, Kochi 783-8502, Japan.

Recovering high quality genomic DNA from environmental samples is a crucial primary step to understand genetic, metabolic, and evolutionary characteristics of microbial communities through various molecular ecological approaches. However, it is often challenging because of the difficulty of effective cell lysis without fragmenting the genomic DNA. This work aims to improve the previous SDS-based DNA extraction methods for high-biomass seafloor samples, such as pelagic sediments and metal sulfide chimneys, to obtain high quality and high molecular weight genomic DNA for the subsequent molecular ecological analyses including metagenomics. We newly standardized the modified SDS-based DNA extraction method (M-SDS), of which results were then compared to those extracted by other DNA extraction methods (the hot-alkaline method and a commercial DNA extraction kit). Consequently, the M-SDS method resulted in higher DNA yield and cell lysis efficiency, lower DNA shearing, and higher diversity scores than other two methods compared, providing a comprehensive DNA assemblage of microbial community in the seafloor environment.