



Comparison of DNA Extraction Methods for Optimal Recovery of Metagenomic DNA from Human and Environmental Samples

Mohita Gaur¹ · Aarushi Vasudeva¹ · Anoop Singh¹ · Vishal Sharma¹ ·
Himani Khurana¹ · Ram Krishan Negi¹ · Jung-Kul Lee² · Vipin Chandra Kalia² ·
Richa Misra³ · Yogendra Singh¹

Received: 31 August 2019 / Accepted: 4 October 2019
© Association of Microbiologists of India 2019

Abstract Metagenomics is the study of gene pool of an entire community in a particular niche. This provides valuable information about the functionality of host-microbe interaction in a biological ecosystem. Efficient metagenomic DNA extraction is a critical pre-requisite for a successful sequencing run in a metagenomic study. Although isolation of human stool metagenomic DNA is fairly standardized, the same protocol does not work as efficiently in fecal DNA from other organisms. In this study, we report a comparison of manual and commercial DNA extraction methods for diverse samples such as human stool, fish gut and soil. Fishes are known to have variable microbial diversity based on their food habits, so the study included two different varieties of fishes. A modified protocol for effective isolation of metagenomic DNA from human milk samples is also reported, highlighting critical precautions. Recent studies have emphasized the importance of studying functionality of human milk metagenome to understand its influence on infants' health. While manual method works well with most samples and therefore can be a method of choice for testing new samples, broad-range commercial kit offers advantage of high purity and quality. DNA extraction of different samples would go a long way in unraveling the unexplored

association between microbes and host in a biological system.

Keywords Metagenomic DNA · Stool · Fecal · Milk · Fish gut · Soil

Introduction

It is an undeniable fact that the microorganisms have played a crucial role in the sustenance of life on earth, since its formation. The diversity and abundance of these microscopic entities vary as per their surrounding environment [1–3]. So, the information about flourishing microbes in a particular environment is the key to understand the characteristics and the functional attributes of a particular habitat, and are often used as bioindicators [4–9]. This knowledge has greatly advanced with use of the next-generation DNA sequencing (NGS) technology. As the genome characterization of an organism offers insight into its unique characteristics (genomics); similarly, metagenomic characterization reflects the community ecosystem and offers clues about its functional composition [10, 11]. The prerequisite for a successful NGS run remains isolation of high-quality metagenomic DNA from the desired samples. Extensive work on the NGS over the past few years has led to introduction of variety of protocols to extract DNA from samples; nonetheless, most of these protocols are limited to soil DNA and human fecal DNA extraction. Protocols for efficient DNA extraction from samples such as fish gut, sputum, milk still remain a major challenge [12–14]. Several commercial DNA extraction kits are available in the market (Qiagen, MP Biomedicals, MoBio DNA), but these kits are mostly limited to the commonly studied samples such as soil and stool. Additionally, the

✉ Richa Misra
richamisra@svc.ac.in

✉ Yogendra Singh
ysinghdu@gmail.com

¹ Department of Zoology, University of Delhi, Delhi, India

² Department of Chemical Engineering, Konkuk University, Seoul 05029, Republic of Korea

³ Department of Zoology, Sri Venkateswara College, University of Delhi, Delhi, India