16S-Based Metagenomics Analysis of Microbial Communities Associated with Toxic and Non-Toxic Dinoflagellate Cultures

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Abstract. Interactions between bacteria and marine dinoflagellates play a vital role in harmful algae bloom formation and toxin production by dinoflagellates. However, the precise association of bacteria with dinoflagellates is still not well understood. Hence, this study aims to identify the bacterial community associated with some toxic and non-toxic dinoflagellate cultures using the 16S-based metagenomics approach toward a better understanding of the bacteria-dinoflagellate relationship. Total DNA from the dinoflagellate cultures was extracted and used as templates for PCR amplification of the V3 region of 16S rDNA. The PCR products were sequenced on an Illumina Miseq platform. Generated sequence reads were then assembled and classified to elucidate the associated bacterial communities. Analysis revealed that cultures of both toxic and non-toxic dinoflagellate species were mainly dominated by *Proteobacteria* (69.3%), followed by *Bacteroidetes,* (19.85%) Phyla of *Fusobacteria* (2.62%), *Actinobacteria* (4.65%), and *Firmicutes* (2.62%) were also found to be minority communities. The results suggest that many different bacterial species are associated with dinoflagellates, some of which are common to each of the dinoflagellate cultures examined, whereas others appear to be unique to a particular dinoflagellate. This association may indicate the possible role of the bacterial communities in dinoflagellates physiology and toxigenesis. The present study showed that the 16S-metagenomic sequencing approach was able to better assess the diversity of these associated bacteria.

INTRODUCTION

Dinoflagellates are a very large and diverse group of eukaryotic organisms that play a major role in aquatic food webs of both, freshwater and marine habitats. Some dinoflagellates species can produce toxins known as paralytic shellfish toxins (PST) which causes paralysis and writhing in people who consume the contaminated shellfish [1], thereby, causing damage to the fisheries industry and public health. Almost all PSP outbreaks have been caused by 10 toxic *Alexandrium* species including *A. tamiyavanichii,* and *A. minutum* [2].

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