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## Shotgun metagenomic analysis of microbial communities in the surface waters of the Eastern South China Sea

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### ABSTRACT

**Aims:** The South China Sea (SCS) harbours a rich biodiversity. However, few studies have been published on its diverse communities, particularly its microbial counterparts. As key players behind many of the vital processes carried out in the ocean, microbes are the focus of this study, placing particular emphasis on community composition, structure, and function.

**Methodology and results:** By employing next generation shotgun sequencing technologies (Illumina HiSeq2000), we assessed the taxonomic structure and functional diversity of the prokaryotic communities in surface waters collected from 3 representative sites in the Eastern SCS: Sarawak (Kuching), Sabah (Kota Kinabalu), and Philippines (Manila). Comparisons were undertaken to similar studies from coastal and open ocean environments. All 3 locations were dominated by members of the *Proteobacteria* (*Alpha*- and *Gamma*-) and *Cyanobacteria* (*Synechococcus* sp. and *Prochlorococcus* sp.). The highest proportion of *Gammaproteobacteria* was found in Sarawak, representing an approximate 20% of total sequences. Archaeal assemblages were made up largely of *Euryarchaeota* and unclassified sequences, while *Crenarchaeota* and *Thaumarchaeota* were present in much smaller proportions, except in the Philippines where *Thaumarchaeota* made up almost 40% of the entire taxa.

**Conclusion, significance and impact of study:** The majority of the microbial communities adhered to a core set of functional genes across the different locations. However, differences existed particularly in Sarawak waters which are hypothesized to be due to local environmental parameters such as riverine influence. The results obtained from this study provide the first comparison of prokaryotic communities in the surface waters of the eastern SCS and will serve as a good platform for prospective studies in the field of environmental science.

**Keywords:** Metagenomics, microbial communities, South China Sea

### INTRODUCTION

Microbes make up a vast proportion of the marine community, far exceeding their multi-cellular counterparts in terms of abundance, biomass and activity (Pomeroy and Darwin, 2007). As key players in the marine ecosystem, microbes mediate a large percentage of the vital biogeochemical processes carried out in the ocean —

all of which bear great impact on the marine community as a whole (Das *et al.*, 2006; Dang *et al.*, 2008). Processes such as nutrient cycling, toxin neutralization and degradation, and other biogeochemical cycles carried out by these microbes mediate the flow of energy and matter within the different trophic levels that exist, which on a

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