Rapid profiling of tropical marine cyanobacterial communities

ABSTRACT

Cyanobacteria are important organisms in the marine ecosystem as they play vital roles in nutrient cycling and oxygen production. In this study, tropical marine cyanobacterial communities from various sites in Southeast Asia and their associated ecological parameters were examined. 16S rRNA sequences of 1502 bp were obtained for barcode amplicon sequencing using the Nanopore MinION[™] sequencing platform. Planktonic and benthic cyanobacteria were observed with total of 40 genera and 46 species of cyanobacteria identified from sites in Sabah and Singapore. Species richness analyses showed that the cyanobacterial community from the West Johor Strait was approximately two times greater than that of the East Johor Strait and the Singapore Strait. This is due to the variability in ecological parameters measured between sites such as rainfall, salinity and temperature. This is the first study that has employed this technology for phytoplankton samples with species resolution, providing insight to the diversity of cyanobacteria present in tropical marine ecosystems. Furthermore, the portability of this sequencer enables the real-time monitoring of coastal environments for the specific detection and identification of harmful algal bloom species.