

A metagenomic study of bacterial communities associated with the saxitoxin producing dinoflagellate, *Pyrodinium bahamense* var. *Compressum*

ABSTRACT

Aim: A number of reports have implicated the role of the symbiotic bacterial communities associated with toxic dinoflagellates in the biosynthesis of saxitoxin during harmful algal blooms (HABs). However, the exact mechanisms by which the bacteria facilitate toxin production remain inconclusive. The toxic dinoflagellate, *Pyrodinium bahamense* var. *compressum*, is the causative organism responsible for paralytic shellfish poisoning in the coastal waters of Sabah, and it is caused by the consumption of filter-feeding shellfish contaminated with the neurotoxin, saxitoxin. The present study aimed at characterizing the species diversity of symbiotic bacteria occurring within a monoalgal culture of *P. bahamense* var. *compressum*. Methodology and results: The total bacterial DNA was amplified using paired-end 16S community sequencing on the Illumina platform, targeting the V3–V4 region of the 16S ribosomal RNA gene. Bacteria were classified into 20 classes, 43 orders, 60 families, and 105 genera. A total of 10 phyla were present, where the major phylum was Proteobacteria (69.5%). The major genera were *Pseudoruegeria* (32%), *Roseibium* (16%), *Hyphomonas* (16%), *Phaeobacter* (7%), *Lutimaribacter* (5%) and *Methylophaga* (5%). This study showed that the previous method of assessing microbial diversity occurring in *P. bahamense* var. *compressum* has underestimated the actual species diversity. Conclusion, significance and impact of study: The high-throughput sequencing of the 16S metagenomes revealed hitherto unreported bacterial taxa associated with *P. bahamense* var. *compressum*. The findings of the present work will pave the way for further studies aimed at isolating and characterizing symbiotic bacteria that are likely to be associated with the biosynthesis of toxins.