Whole genome sequence data of a marine bacterium, Marinobacter adhaerens PBVC038, associated with toxic harmful algal bloom

ABSTRACT

Marinobacter adhaerens (PBVC038) was isolated from a harmful algal bloom event caused by the toxic dinoflagellate Pyrodinium bahamense var. compressum (P. bahamense) in Sepanggar Bay, Sabah, Malaysia, in December 2012. Blooms of P. bahamense are frequently linked to paralytic shellfish poisoning, resulting in morbidity and mortality. Prior experimental evidence has implicated the role of symbiotic bacteria in bloom dynamics and the synthesis of biotoxins. The draft genome sequence data of a harmful algal bloom-associated bacterium, Marinobacter adhaerens PBVC038 is presented here. The genome is made up of 21 contigs with an estimated 4,246,508 bases in genome size and a GC content of 57.19%. The raw data files can be retrieved from the National Center for Biotechnology Information (NCBI) under the Bioproject number PRJNA320140. The assessment of bacterial communities associated with harmful algal bloom should be studied more extensively as more data is needed to ascertain the functions of these associated bacteria during a bloom event.