Two *Pseudoalteromonas* strains, SCSIO 04301 and SCSIO 11900, were isolated from the South China Sea, and both strains form biofilms. Here we present the draft genome sequences of these two strains, which will aid the study of marine microbes that are adapted to marine sediments or are associated with eukaryotic hosts.

*Pseudoalteromonas* (Gammaproteobacteria, *Alteromonadales*, *Alteromonadaceae*), a genus of Gammaproteobacteria, was differentiated from the *Alteromonas* genus in 1995 according to the difference in small-subunit rRNA gene sequences (1). *Pseudoalteromonas* is widespread in marine environments and has become an organism of interest to the fields of ecological and pharmaceutical sciences due to its influence on biofilms and its ability to synthesize bioactive molecules (2). So far, draft genome sequences of over 40 *Pseudoalteromonas* strains have been released to public databases, and three strains have complete genome sequences.

Here we present the genome sequences of two *Pseudoalteromonas* strains, *Pseudoalteromonas* lipolytica SCSIO 04301 and *Pseudoalteromonas* sp. strain SCSIO 11900. SCSIO 04301 was isolated from sediment at 63 m deep in the South China Sea (18°0′N, 109°42′E), and SCSIO 11900 was isolated from the surface mucus layer of the coral at 4 m deep in the South China Sea (18°13′N, 109°28′E). The 16S rRNA sequences of SCSIO 04301 share 100% similarity with *Pseudoalteromonas* sp. strain SCSIO 11900, and the circularizations of the small chromosomes were confirmed again by PCR and subsequent DNA sequencing. A comprehensive study combined with comparative genome analysis and phenotypic analysis is under way to explore the relationships between genetic variation and phenotypic variation of *Pseudoalteromonas* strains in different ecological niches.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers JDVB00000000 for SCSIO 04301 and JEMJ00000000 for SCSIO 11900.

**ACKNOWLEDGMENTS**

This work was supported by the National Basic Research Program of China (grant 2013CB955701) and by the National Science Foundation of China (grant 31290233).

**REFERENCES**


