Genome Sequence of *Pseudoalteromonas flavipulchra* JG1, a Marine Antagonistic Bacterium with Abundant Antimicrobial Metabolites

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The marine bacterium *Pseudoalteromonas flavipulchra* JG1 can synthesize various antibacterial metabolites, including protein and small molecules. The draft genome of JG1 is about 5.36 Mb and harbors approximate 4,913 genes, which will provide further insight into the synthesis of antimicrobial agents and antagonistic mechanisms of *P. flavipulchra* against pathogens.

The genus *Pseudoalteromonas* is ubiquitous in the marine environment and can synthesize a range of extracellular compounds (4, 8) with antimicrobial activity (3, 5), especially the pigmented species (1, 6). The marine antagonistic bacterium *Pseudoalteromonas flavipulchra* JG1, with a golden yellow color, was isolated from water used to rear healthy turbot (*Scophthalmus maximus*) in Qingdao, China (7). JG1 was confirmed to show excellent antibacterial activities against many fish pathogens and could synthesize a range of antibacterial compounds, including the protein PfaP and five small molecules (12). Due to these properties, JG1 and/or its products could be used as potential probiotics or antibiotics in aquaculture. Here we report a draft genome sequence for *P. flavipulchra* JG1 to gain insight into the genetic features involved in the biosynthesis of various antimicrobial metabolites.

The genome of *P. flavipulchra* JG1 was sequenced using the Illumina HiSeq2000 with a 500-bp paired-end library, which achieved about 111.9-fold coverage. The reads were assembled using SOAPdenovo assembler software, and putative coding sequences (CDSs) were identified with Glimmer 3.0 (2). Annotation was performed using the KEGG, COG, Swiss-Prot, TrEMBL, Gene Ontology, and NCBI nonredundant (NR) databases.

The draft genome of *P. flavipulchra* JG1 (about 5.36 Mb) contains 122 contigs, ranging from 128 bp to 264,447 bp (the *N50* and *N90* contig sizes are 107,608 bp and 34,132 bp, respectively), which can be assembled into 61 scaffolds ranging from 500 bp to 879,239 bp (*N50* and *N90* scaffold sizes are 338,061 bp and 74,731 bp, respectively). The G+C content is 43.23%, and approximately 87.71% of nucleotides were predicted to be in protein-coding regions. A total of 4,913 protein-encoding genes, 104 tRNA-encoding genes, and 4 rRNA operons were predicted to be in the draft genome of JG1. Among the predicted genes, 2,928 (59.6%) are assigned to COG categories and 3,187 (64.9%), 4,301 (87.5%), 3,050 (62.1%), and 4,284 (87.2%) genes are found within the KEGG, NR, Swiss-Prot, and TrEMBL databases, respectively. Phylogenetic analysis between *P. flavipulchra* JG1, *Pseudoalteromonas tunicata* D2 (11), *Pseudoalteromonas haloplanktis* TAC125 (9), *Pseudoalteromonas atlantica* T6c, and two *Pseudoalteromonas* strains, TW-7 and SM9913 (10), indicated that JG1 was most closely related to *P. tunicata* D2, which was considered a model to study the mechanisms of antimicrobial production (1). A comprehensive comparison between the genomes is under way and will allow further analysis and application of antimicrobial compounds.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank un-

der accession number [AJMP00000000](#). The version described in this paper is the first version, AJMP01000000.

ACKNOWLEDGMENTS

This work was supported by grants from the National Natural Science Foundation of China (no. 40876067), the International Science and Technology Cooperation Programme of China (no. 2012DFG31990), and the National High Technology Research Development Program of China (863 Programs, no. 2007AA09Z434).

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Received 10 April 2012 Accepted 23 April 2012

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doi:10.1128/JB.00598-12