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GENOME ANNOUNCEMENT

Genome Sequences of Type Strains of Seven Species of the Marine Bacterium *Pseudoalteromonas*

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There are over 30 species in the marine bacterial genus *Pseudoalteromonas*. However, our knowledge about this genus is still limited. We sequenced the genomes of type strains of seven species in the genus, facilitating the study of the physiology, adaptation, and evolution of this genus.

The genus *Pseudoalteromonas* (*Gammaproteobacteria*, *Alteromonadales*, *Alteromonadaceae*) was proposed by Gauthier et al. (5) and is attracting much attention, because a number of *Pseudoalteromonas* species can produce a variety of compounds with antimicrobial, antifouling, algicidal, and various pharmaceutically relevant activities (3). There are over 30 species in the genus, all of which are found in the oceans. One interesting feature of the genus is that it can be divided into two clades: pigmented and nonpigmented species (3). The pigmented species tend to produce bioactive compounds, while the nonpigmented species generally have broader environmental tolerance than the pigmented ones (3). Currently, the genome sequences of over 10 strains are available in public databases (2, 7, 9–11). However, among the sequenced strains, only two (*P. tunicata* D2^T [10] and *P. rubra* ATCC 29570^T [11], both belonging to the pigmented clade) are type strains of *Pseudoalteromonas* species. Here, we present the genome sequences of seven type strains, including three from the pigmented clade (*P. citrea* NCIMB 1889^T, *P. piscicida* JCM 20779^T, and *P. spongiae* UST010723-006^T) and four from the nonpigmented clade (*P. arctica* A 37-1-2^T, *P. haloplanktis* ATCC 14393^T, *P. marina* mano4^T, and *P. undina* NCIMB 2128^T).

Genomes were sequenced using Illumina Solexa technology (1). A 500-bp Illumina paired-end library was prepared for each strain. The sequencing generated 520 Mb to 540 Mb of clean data for each strain. The average sequencing coverage ranged from 100-fold to 130-fold. Reads (read length, 90 bp) of each strain were assembled using SOAPdenovo, version 1.05 (6). Numbers of large contigs (>500 bp) were 114 for NCIMB 1889^T, 73 for JCM 20779^T, 14 for UST010723-006^T, 68 for A 37-1-2^T, 56 for ATCC 14393^T, 31 for mano4^T, and 20 for NCIMB 2128^T. The protein-coding open reading frames (ORFs) were predicted using Glimmer, version 3.02 (4) and were annotated using the Swiss-Prot, NCBI nr, and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases (8).

The genome sizes are 5.34 Mb for *P. citrea* NCIMB 1889^T (4,677 ORFs), 5.28 Mb for *P. piscicida* JCM 20779^T (4,782 ORFs), 4.72 Mb for *P. spongiae* UST010723-006^T (4,331 ORFs), 4.63 Mb for *P. arctica* A 37-1-2^T (4,242 ORFs), 5.02 Mb for *P. haloplanktis* ATCC 14393^T (4,441 ORFs), 4.18 Mb for *P. marina* mano4^T (3,863 ORFs), and 4.00 Mb for *P. undina* NCIMB 2128^T (3,689 ORFs). The G+C content ranges from 39.04% (*P. arctica* A 37-1-2^T) to 43.24% (*P. piscicida* JCM 20779^T). Comparisons of all sequenced *Pseudoalteromonas* genomes showed that, on average, the genomes of the pigmented strains (5.53 ± 0.57 Mb for 7 strains) were larger than those of the nonpigmented ones (4.39 ± 0.45 Mb for 15 strains).

The sequenced genomes of the type strains not only facilitate the study of the physiology, adaptation, and evolution of this genus but also provide a good resource for the study of the synthesis of the bioactive compounds by this genus.

Nucleotide sequence accession numbers. The genome sequences of the seven strains were deposited in GenBank under accession numbers AHBY00000000, AHBZ00000000, AHCA00000000, AHCB00000000, AHCC00000000, AHCE00000000, and AHCF00000000.

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REFERENCES

1. **Bennett S.** 2004. Solexa Ltd. Pharmacogenomics **5**:433–438.
2. **Bian F, et al.** 2012. Genome sequences of six *Pseudoalteromonas* strains isolated from Arctic sea ice. J. Bacteriol. **194**:908–909.
3. **Bowman JP.** 2007. Bioactive compound synthetic capacity and ecological significance of marine bacterial genus *Pseudoalteromonas*. Mar. Drugs 5:220–241.
4. **Delcher AL, Bratke KA, Powers EC, Salzberg SL.** 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics 23:673–679.
5. **Gauthier G, Gauthier M, Christen R.** 1995. Phylogenetic analysis of the genera *Alteromonas*, *Shewanella*, and *Moritella* using genes coding for small-subunit rRNA sequences and division of the genus *Alteromonas* into two gen-

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era, *Alteromonas* (emended) and *Pseudoalteromonas* gen. nov., and proposal of twelve new species combinations. Int. J. Syst. Bacteriol. **45**:755–761.

6. **Li R, et al.** 2010. De novo assembly of human genomes with massively parallel short read sequencing. Genome Res. **20**:265–272.
7. **Médigue C, et al.** 2005. Coping with cold: the genome of the versatile marine Antarctica bacterium *Pseudoalteromonas haloplanktis* TAC125. Genome Res. **15**:1325–1335.
8. **Ogata H, et al.** 1999. KEGG: Kyoto encyclopedia of genes and genomes. Nucleic Acids Res. **27**:29–34.
9. **Qin QL, et al.** 2011. Comparative genomics reveals a deep-sea sediment-adapted life style of *Pseudoalteromonas* sp. SM9913. ISME J. **5**:274–284.
10. **Thomas T, et al.** 2008. Analysis of the *Pseudoalteromonas tunicata* genome reveals properties of a surface-associated life style in the marine environment. PLoS One **3**:e3252.
11. **Xie BB, et al.** 9 January 2012, posting date. Genome sequence of the cycloprodigiosin-producing bacterial strain *Pseudoalteromonas rubra* ATCC 29570^T. J. Bacteriol. **194**:1637–1638. doi:10.1128/JB.06822-11.