Genome Sequence of a Cold-Adaptable Sulfamethoxazole-Degrading Bacterium, *Pseudomonas psychrophila* HA-4

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***Pseudomonas psychrophila* HA-4 is a cold-adaptable, sulfamethoxazole-degrading bacterium. The genes related to its cold adaptation mechanism and sulfamethoxazole metabolism were unknown. We present the draft genome of strain HA-4. It could provide further insight into the sulfamethoxazole-degrading mechanism of strain HA-4.**

Sulfamethoxazole, a kind of synthetic antibacterial compound, has been frequently detected in the aquatic environment (4). Sulfamethoxazole is difficult to degrade by traditional biological treatment technology, especially at low temperatures (5). In previous reports, the study of the biodegradation of sulfamethoxazole was focused mainly on the isolation and characteristics of sulfamethoxazole-degrading bacteria (2). The genomic information on sulfamethoxazole-degrading bacteria is limited. *Pseudomonas psychrophila* HA-4, isolated from activated sludge from a municipal wastewater treatment plant, is a cold-adaptable, sulfamethoxazole-degrading bacterium that can utilize sulfamethoxazole as its sole source of carbon and energy. The rate of sulfamethoxazole removal could reach 35% after 192 h of cultivation. In order to determine the related genes and mechanism of sulfamethoxazole biodegradation in *P. psychrophila* strain HA-4, its genome has been sequenced.

The genome of strain HA-4 was sequenced with the Illumina High-Seq 2000 system. The reads were assembled into 145 large contigs (>300 bp) using Velvet 1.2.03 (7). The contig N50 is approximately 10.3 kb, and the largest contig assembled is approximately 344.3 kb. The draft sequence consists of 5,235,696 bases with a mean G + C percentage of 56.4%. Annotation of open reading frames was performed by using the RAST annotation server (1) and the NCBI Prokaryotic Genome Annotation Pipeline (6). A total of 4,721 coding sequences and 51 structural RNAs were predicted. There are 525 subsystems in the genome, as determined by the RAST server (1). Comparison with the genome sequences available at the RAST server suggested that the closest neighbor of strain HA-4 is *Pseudomonas fluorescens* PfO-1 (score, 514), followed by *P. fluorescens* PfO-5 (score, 478) and *P. fluorescens* SBW25 (score, 448).

Strain HA-4 is a cold-adaptable microorganism, and its optimal growth temperature is 10°C. In the genome of strain HA-4, we found six cold shock protein-encoding genes. The results indicate that the cold shock protein of strain HA-4 could improve its activity at low temperatures. Meanwhile, 167 genes related to fatty acid, lipid, and isoprenoid metabolism were identified. In our study, the percentage of unsaturated fatty acids in strain HA-4 increased as the temperature decreased. As previously reported, lipid composition, especially the unsaturated fatty acids, plays an important role in maintaining the fluidity and mass transfer of the cell membrane at low temperatures (3). Sulfamethoxazole is an

aromatic compound, and 82 genes related to aromatic compound metabolism have been found in the genome of strain HA-4. These results provide clues for further study of the cold adaptation mechanism and sulfamethoxazole metabolism of strain HA-4.

Nucleotide sequence accession numbers. The *P. psychrophila* strain HA-4 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. [ALJC000000000](#). The version described in this paper is the first version, ALJC01000000.

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