Draft Genome Sequence of an Ammonia-Oxidizing Archaeon, “*Candidatus Nitrosopumilus koreensis*” AR1, from Marine Sediment

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Ammonia-oxidizing archaea (AOA) are ubiquitous in various marine environments and play important roles in the global nitrogen and carbon cycles. We here present a high-quality draft genome sequence of an ammonia-oxidizing archaeon, “*Candidatus Nitrosopumilus koreensis*” AR1, which was found to dominate an ammonia-oxidizing enrichment culture in marine sediment off Svalbard, the Arctic Circle. Despite a significant number of nonoverlapping genes (ca. 30%), similarities of this strain to “*Candidatus Nitrosopumilus maritimus*” were revealed by core genes for archaeal ammonia oxidation and carbon fixation, G+C content, and extensive synteny conservation.

Some lineages of *Thaumarchaeota* inhabiting various environments, including marine water, freshwater, and hot springs, have been proposed for use as ammonia-oxidizing archaea (AOA) (5, 9, 11). These microbes are capable of using ammonia as an energy source and of performing carbon fixation through the 3-hydroxypropionate/4-hydroxybutyrate pathway (1). But, despite their important contributions to the biogeochemical nitrogen cycle, there remain many unanswered questions on their physiology and ecology. Recently, the genome sequence of “*Candidatus Nitrosopumilus maritimus*” strain SCM1, an ammonia-oxidizing archaeon initially isolated in an aquarium, was published (3, 12). More recently still, AOA in 78-m-deep marine sediment off Svalbard, the Arctic Circle, were enriched using ammonia as an electron donor (8). One such AOA was identified as “*Candidatus Nitrosopumilus koreensis*” strain AR1, the genome of which was analyzed in the present study.

The AR1 genome was sequenced by shotgun and mate-paired (about 8-kb, insert library) end-sequencing methods using a 454 GS-FLX Titanium platform (Roche Applied Science). Preparation and sequencing of the sample as well as analytical processing were performed according to the manufacturer's instructions at the National Instrument Center for Environmental Management (NICEM), Seoul National University, Republic of Korea. To increase the quality of the metagenomic sequences, we removed sequencing artifacts and short sequences. Assembly was performed using the Roche GS *de novo* assembler (Newbler assembler v.2.3).

The draft genome of “*Ca. Nitrosopumilus koreensis*” AR1 is approximately 1.63 Mbp in length and has a G+C content of 34.2%. Putative coding sequences (CDSs) were predicted using the MetaGeneAnnotator, COG, Pfam, and RAST (2, 6, 7, 10). Of the 1,986 predicted CDSs in the genome, most of them (71.9%) showed homology to “*Ca. Nitrosopumilus maritimus*” genes. Despite the similarities among the G+C and gene contents and synteny conservations, the average nucleotide identity of strain AR1 to “*Ca. Nitrosopumilus maritimus*” SCM1 was only about 85%; thus, it was considered to be a novel species of the genus “*Ca. Nitrosopumilus*” (4).

The genome contains core genes that are involved in lithotrophic growth through ammonia oxidation and that code for am-

monia monooxygenase and ammonium transporter. Genes for multicopper oxidase and blue-copper-domain-containing proteins potentially involved in energy conservation through ammonia oxidation were less enriched than those of “*Ca. Nitrosopumilus*.” The absence of the hydroxylamine oxidoreductase gene indicates a novel ammonia oxidation pathway in strain AR1, as in the other AOA. The genome contains genes of the 3-hydroxypropionate/4-hydroxybutyrate pathway for carbon fixation. Despite these core genes, unique genes (ca. 30%) of AR1 might offer the genetic potential for sedimentary-AOA niche differentiation. For example, a high-affinity phosphate uptake operon found in the genome of “*Ca. Nitrosopumilus maritimus*” was not detected in the AR1 genome.

Nucleotide sequence accession number. The draft genome sequence of “*Ca. Nitrosopumilus koreensis*” AR1 is available in the GenBank database (NCBI) under the accession number CP003842.

ACKNOWLEDGMENTS

This work was supported by the Basic Science Research Program (20090087901 to S.-K.R. and 2012039639 to S.-J.P.) through the National Research Foundation of Korea (NRF) funded by the Ministry of Education, Science and Technology and by the Marine and Extreme Genome Research Center Program of the Ministry of Land, Transport, and Maritime Affairs.

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Received 27 September 2012 Accepted 1 October 2012

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doi:10.1128/JB.01857-12

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