

Genome Sequence of an Ammonia-Oxidizing Soil Archaeon, “*Candidatus Nitrosoarchaeum koreensis*” MY1

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Ammonia-oxidizing archaea are ubiquitous microorganisms which play important roles in global nitrogen and carbon cycle on earth. Here we present the high-quality draft genome sequence of an ammonia-oxidizing archaeon, “*Candidatus Nitrosopumilus koreensis*” MY1, that dominated an enrichment culture of a soil sample from the rhizosphere. Its genome contains genes for survival in the rhizosphere environment as well as those for carbon fixation and ammonium oxidation to nitrite.

Ammonia-oxidizing archaea belonging to the archaeal phylum *Thaumarchaeota* are ubiquitous microbes in marine, freshwater, and terrestrial environments (1, 4, 13, 18, 19, 24). They are capable of using ammonia oxidation as an energy source in nutrient-deprived oligotrophic environments and performing carbon fixation through the 3-hydroxypropionate/4-hydroxybutyrate pathway (2, 9, 16, 20, 25). Particularly, increased nitrification in the rhizosphere is reportedly due to ammonia-oxidizing archaea (5, 10).

Despite these significant contributions to the global carbon and nitrogen cycle, many questions about the physiology, metabolism, and ecological niches of the mesophilic ammonia-oxidizing archaea remain unanswered owing to the difficulty of isolation. Only a single species, *Nitrosopumilus maritimus* SCM1, has been isolated from a tropical marine aquarium (15), and no strain in the rhizosphere has been cultured and analyzed.

“*Candidatus Nitrosoarchaeum koreensis*” MY1 dominated an enrichment culture of a soil sample from the rhizosphere of *Caragana sinica* (M.-Y. Jung. et al., submitted for publication). The 16S rRNA gene sequence from MY1 is most closely related to that of “*Candidatus Nitrosoarchaeum limnia*” SFB1 from low-salinity sediments. The genome sequence of MY1 was determined by next generation sequencing technologies.

Paired-end sequences of 2.2 Gb (~1,376-fold genome coverage) were produced from 600-bp and 3-kb genomic libraries with Illumina/Solexa Genome Analyzer Ix (DNA Link, Inc.), and 223.5-Mb single-ended sequences (~139-fold genome coverage) were produced with Roche/454 Genome Sequencer FLX Titanium. Assembly and contig editing were performed with CLC Genomics Workbench (CLC bio, Inc.) and Phred/

Phrap/Consed. A total of 1,945 coding sequences (89.4% coding density) were predicted by Glimmer 3.02 and annotated using the information from GenBank, UniProt, COG, KEGG, Pfam, and RAST (21).

The final assembly consists of a single contig of 1,607,695 bp (32.7% G+C content). The genomes of MY1, SFB1, and SCM1 display a very high degree of synteny. A total of 1,317 protein-coding genes (67.1%) were assigned predicted functions. The genome has one 16S-23S rRNA operon, a distantly located 5S rRNA gene, and 42 tRNA genes. No transposase gene or CRISPR locus was detected. Most of the MY1-specific genes are of unknown functions.

The genome contains genes coding for an ammonia monooxygenase complex and an ammonium transporter for ammonium oxidation, nitrite reductases for ammonium assimilation or NO formation, and a nitric oxide oxidoreductase for denitrification, but like other ammonia-oxidizing archaea, no hydroxylamine oxidase gene was detected (3, 8, 23). MY1 also has an almost complete set of genes of the modified 3-hydroxypropionate/4-hydroxybutyrate pathway for carbon fixation and phosphoenolpyruvate carboxykinase and fructose-1,6-bisphosphatase for gluconeogenesis, though malonate semialdehyde reductase was not detected (2, 6, 8).

Unlike ammonia-oxidizing archaea from the ocean, MY1 is thought to have a citrate transporter for citrate utilization and NiFe-hydrogenase genes related to energy metabolism to survive competition in the rhizosphere (12, 22). Also, instead of genes coding for the ectoine biosynthesis pathway to tolerate salt stress (7, 14), MY1 keeps a number of genes to cope with oxidative stress and antibiotic resistance genes (17).

Nucleotide sequence accession number. The draft genome sequence of “*Candidatus Nitrosoarchaeum koreensis*” MY1 has been deposited in GenBank under accession no. AFPU00000000. The sequence and annotation are also available from the Genome Encyclopedia of Microbes (GEM; <http://www.gem.re.kr>) (11).

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