The isolation and genome sequencing of ammonia-oxidizing bacteria (AOB) remain vital to our understanding of the potential roles these organisms play in the global nitrogen cycle. To complement physiological studies on AOB, complete-genome sequences provide insight into how inventory relates to metabolic capacity and environmental niche. The AOB Nitrosomonas ureae Nm10 was first isolated from soils in Sardinia, Italy (1), and is an oligotrophic aerobic betaproteobacterium belonging to Nitrosonomas cluster 6a (2).

The genome of N. ureae was sequenced at the University of Washington, WA, using the PacBio RSII platform; 300,584 raw reads resulted in 166,852 quality-filtered trimmed reads yielding 1,340 Mb, with a mean genome-wide coverage of 311X. The filtered reads were assembled at the University of Alberta, Alberta, Canada, using HGAP version 2.3 (3), and resulted in a 1-contig scaffold. Annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (4). The genome is 3.3 Mbp, with a mean G+C content of 44.5% and 2,897 predicted protein-coding genes. The genome includes 40 tRNA genes and a single copy of the 16S-23S-5S rRNA operon. Gene prediction analysis and comparative genomics were performed with IMG (5). The closest neighbor of N. ureae is Nitrosonomas sp. strain AL212 (6), with an average nucleotide identity (ANI) (7) of 93.18%.

N. ureae oxidizes ammonia to nitrite as a sole source of energy and reductant. The genome contains 3 operons for ammonia monooxygenase (amoCAB), two of which are followed by the orf4 and orf5 genes that are often found in β-AOB (8). Two orphan amoC genes were also identified, along with a single copy of the AOB-specific red-copper protein nitrosocyanin (9). It is important to note that this is the first report of an AOB containing four complete operons for hydroxyamine dehydrogenase (haoAB-cycAB), as betaproteobacterial AOB usually contain 2 or 3 copies, and one copy often lacks the cycC gene (8).

N. ureae can utilize urea as an alternate nitrogen source (1) and contains both urea carboxylase (EC 6.3.4.6) and a putative allophanate hydrolase (EC 3.5.1.54) genes (10), as well as genes for a complete urease found in some Nitrososira genomes (11). Carbon fixation genes, including two copies of form I RubisCO-encoding genes, were identified with similarity to those of Nitrosonomas sp. strain Is79 (12).

Terrestrial AOB can contribute to nitrogen-oxide release, including the production of nitric and nitrous oxide through nitrifier denitrification (13, 14). The genes in N. ureae that are implicated in this process include a copper-containing nitrite reductase (nirK), NO-responsive regulator NnrS, cytochrome P460 (cytL), and cytochrome c’ beta (cytS). Interestingly, no homologues for nitric oxide reductases were found in the genome, a featured shared by the closely related 6a AOB Nitrosonomas sp. Is79 (12).

The N. ureae genes for iron acquisition and storage include one copy of the ferric uptake regulation protein (FUR) (15), a Streptococcus-like ferric iron ABC transporter (16), two copies of TonB-associated ferric siderophore transporters (17), and two copies of bacterioferritin genes. Two copies of cyanophycin synthetase genes, utilized for nitrogen storage (18), were also identified.

Nucleotide sequence accession numbers. The genome sequence has been deposited in GenBank under the accession no. CP013341. The version described in this paper is the first version, CP013341.1.

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