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GENOME ANNOUNCEMENT

Genome Sequence of "*Candidatus* Nitrosoarchaeum limnia" BG20, a Low-Salinity Ammonia-Oxidizing Archaeon from the San Francisco Bay Estuary

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Here, we present the draft genome sequence of "*Candidatus* Nitrosoarchaeum limnia" BG20, an ammonia-oxidizing archaeon enriched in culture from low-salinity sediments of the San Francisco Bay estuary. The genome sequence revealed many similarities to the previously sequenced genome of "*Ca.* Nitrosoarchaeum limnia" SFB1 (enriched from a nearby site in San Francisco Bay) and is representative of a clade of ammonia-oxidizing archaea (AOA) found in low-salinity habitats worldwide.

Ammonia-oxidizing microorganisms play quantitatively important roles in the removal of nitrogen from aquatic and terrestrial ecosystems. The oxidation of ammonia to nitrite links the production of fixed nitrogen (via nitrogen-fixing bacteria or through external inputs from wastewater or fertilizer runoff) to nitrogen removal pathways (denitrification and anammox). Ammonia-oxidizing archaea (AOA) appear to be the dominant ammonia oxidizers in many systems, based on abundance of ammonia monooxygenase (*amoA*) genes (e.g., see reference 14 and references therein).

Enrichment cultures targeting AOA were initiated from sediments in the San Francisco Bay estuary. "*Candidatus* Nitrosoarchaeum limnia" BG20 dominated cultures from site BG20 in the low-salinity, riverine region of San Francisco Bay. The AOA grew chemoautotrophically by aerobic ammonia oxidation to nitrite. "*Ca.* Nitrosoarchaeum limnia" BG20 was closely related (99% 16S rRNA identity and 99% *amoA* identity) to the low-salinity AOA "*Ca.* Nitrosoarchaeum limnia" SFB1 enriched from a nearby site in San Francisco Bay (4, 10). Molecular surveys in San Francisco Bay showed that AOA were more abundant than ammonia-oxidizing bacteria (AOB) in sediments where "*Ca.* Nitrosoarchaeum limnia" BG20 was enriched (11). Genomic sequencing, assembly, and annotation of "*Ca.* Nitrosoarchaeum limnia" BG20 were performed by the J. Craig Venter Institute, supported by the Gordon and Betty Moore Foundation Marine Microbiology Initiative (http://camera.calit2.net/microgenome/).

The draft genome of "*Ca.* Nitrosoarchaeum limnia" BG20 is 1,855,559 bp in length and has a G+C content of 33%. The genome was sequenced with a half plate of a 454 FLX Titanium run and assembled with Newbler version 2.23. The final assembly resulted in 343 contigs with an N_{50} size of 16,259 bp, an average contig size of 5,409 bp, and a coverage depth of 125×.

The genome contains 2,636 protein-coding genes, of which 46% are assigned predicted functions. The genome has 39 tRNA genes and single copies of the 5S, 16S, and 23S rRNA genes. The 5S rRNA gene is distantly located from the 16S and 23S rRNA genes, as seen in other AOA genomes (8, 16). No clustered regularly interspaced short palindromic repeats (CRISPRs) were identified (5, 6), but several phage integrase proteins were observed in the genome.

To estimate the extent of genome completeness, predicted protein sequences were searched against a set of 53 highly conserved core gene functions previously identified as universally present in all archaeal genomes based on COG annotations (13). All 53 COGs were identified in the "*Ca.* Nitrosoarchaeum limnia" BG20 genome, suggesting near complete coverage.

The "*Ca.* Nitrosoarchaeum limnia" BG20 genome contains genes of the modified 3-hydroxypropionate/4-hydroxybutyrate pathway for carbon fixation (1–3, 7, 16). The genome codes for proteins putatively involved in ammonia oxidation, including ammonia monooxygenase, ammonium transporter, nitrite reductase, and several multicopper oxidase and blue copper domain-containing proteins. Interestingly, "*Ca.* Nitrosoarchaeum limnia" BG20 is predicted to have a urea transporter protein similar to *Cenarchaeum symbiosum* A (7), but no urease enzymes were identified.

The draft genome of "*Ca.* Nitrosoarchaeum limnia" BG20 contained genes coding for both the FtsZ and Cdv cell division systems, a feature unique to the *Thaumarchaeota* (9, 15), although recent evidence suggests that Cdv is the primary division system in the *Nitrosopumilus maritimus* (12). The draft genome was missing ectoine biosynthesis genes used to tolerate salt stress in *N. maritimus* (16) but did contain mechanosensitive ion channel genes. Similar to "*Ca.* Nitrosoarchaeum limnia" SFB1 (4), "*Ca.* Nitrosoarchaeum limnia" BG20 had a large number of chemotaxis and flagellar genes associated with motility, which are absent in *N. maritimus*.

Nucleotide sequence accession numbers. The draft genome sequence of "*Ca.* Nitrosoarchaeum limnia" BG20 is available in the NCBI GenBank database under accession number AHJG00000000. The raw sequence reads are available in the NCBI SRA database under accession number PRJNA50027.

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