

# Draft Genome Sequence of a Taxonomically Unique *Neisseria* Strain Isolated from a Greater White-Fronted Goose (*Anser albifrons*) Egg on the North Slope of Alaska

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**We report here the draft genome sequence of a unique *Neisseria* strain that was isolated from a greater white-fronted goose (*Anser albifrons*) egg. The sequencing was performed with an Illumina MiSeq system, and the sequence consists of 275 contigs. The total genome is 2,397,978 bp long and has a G+C content of 46.4%.**

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The order *Neisseriales* consists of 32 genera, including the important pathogens *Neisseria gonorrhoeae* and *Neisseria meningitidis* (1). Other species of *Neisseriales* are sometimes isolated from human and animal specimens (2, 3). There are reports of *Neisseria* species being isolated from a sheldrake liver (4), the cloaca and phallus of domestic geese (5), and duck feces (6), and there is one report of *Neisseria animalis* being isolated from a mallard (*Anas platyrhynchos*) egg (7).

During the summer of 2013, we isolated a *Neisseria* species from the contents of 21 nonviable greater white-fronted goose (*Anser albifrons*) eggs on the North Slope of Alaska (8). We identified the DNA of this same species in an additional 2 nonviable eggs. Here, we report the draft genome sequence of a unique *Neisseria* strain (KH1503) isolated from the contents of an addled greater white-fronted goose egg. Based on our sequencing of the 16S rRNA gene and chaperonin 60 gene, this isolate seems to be most closely related to *Neisseria canis*, *Neisseria animaloris*, or *Neisseria shayeganii*. The identity scores for full-length (>1,400 bp) 16S rRNA gene sequences are  $\leq 97\%$ .

A pure culture was obtained by growing the isolate on blood agar plates at 37°. Bacteria were grown overnight in tryptic soy broth and pelleted by centrifugation at  $5,000 \times g$  for 10 min, and genomic DNA was extracted using a Wizard genomic DNA purification kit (Promega, Madison, WI). Genomic DNA was used to prepare a sequencing library using a Nextera DNA sample preparation kit (Illumina, San Diego, CA). Sequencing was performed on an Illumina MiSeq version 2 system and generated 24 to 30 million paired-end reads ( $2 \times 250$  bp), for a total of 7.4 Gbp.

We assembled the bacterial genome *de novo* using SPAdes version 2.5.1 (9). The assembled contigs totaled 2,397,978 bp. The assembly consisted of 275 contigs, ranging in size from 209 bp to 242,609 bp (median, 244 bp; mean, 8,720 bp) with a G+C content of 46.4%. We annotated the genome assembly using the NCBI Prokaryotic Genomes Annotation Pipeline (10). There are 2,334 putative genes, 2,159 coding sequences (CDSs), 122 pseudogenes, 3 rRNAs, 49 tRNAs, and 1 noncoding RNA. The genome sequence

of this organism will allow for its further characterization and assessment of pathogen potential.

**Nucleotide sequence accession numbers.** The draft genome sequence of *Neisseria* sp. KH1503 has been deposited at DDBJ/EMBL/GenBank under the accession no. [JTDO00000000](https://www.ncbi.nlm.nih.gov/nuccore/JTDO00000000). The version described in this paper is version JTDO01000000.

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