Genome Sequence of Neisseria meningitidis serogroup B
strain H44/76

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Neisseria meningitidis is an obligate human pathogen. While it is a frequent commensal of the upper respiratory tract, in some individuals the bacterium spreads to the bloodstream causing meningitis and/or sepsis, serious conditions with high morbidity and mortality. Here we report the availability of the genome sequence of the widely used serogroup B laboratory strain H44/76.

Neisseria meningitidis resides in the nasopharynx of approximately 10 to 30% of the human population. However, in some individuals this pathogen results in invasive disease leading to life-threatening septicemia and meningitis (4,14). The reasons
triggering meningococcal pathogenic outbreaks have not yet been elucidated, but several host and bacterium factors have been proposed (2,8,13).

To date 7 complete \textit{N. meningitidis} genomes are deposited at GenBank (1,10-12,15) of which only one is serogroup B. Here we present the sequence of \textit{N. meningitidis} serogroup B strain H44/76, related to the sequenced serogroup B strain MC58 (GenBank accession no. AE002098), belonging to the same clonal complex 32 (16). \textit{N. meningitidis} H44/76 is widely used in molecular genetic studies, including those related to serogroup B vaccine development, because of its favorable natural transformation efficiency.

Whole genomic DNA of a H44/76 culture that only had 6 plate-culture passages since its isolation from a patient in Norway in 1976 was sequenced (5). Sequencing was performed using shotgun 454 Titanium (Roche) pyrosequencing, according to the manufacturer’s recommendations. The coverage was 20-fold with a median read length of 403 nucleotides. \textit{De novo} and reference mapping assemblies were performed with Newbler (version 2.3). The final assembly, containing 46 contigs, was obtained by combining both assemblies using CodonCode Aligner software (version 3.5, CodonCode Corporation, Dedham, MA). Investigation of the regions surrounding contig boundaries showed that further reduction of the number of contigs was hampered due to misassembly of repetitive sequences and duplicated genes like transposases, rRNA/tRNA regions, two partner secretion systems, and Type IV pili(9).

Annotation was performed using the annotation engine at the Institute for Genome Sciences (University of Maryland, Baltimore, MD [http://ae.igs.umaryland.edu/cgi/index.cgi]). We compared the sequences of 21 gene
fragments of abcZ, adk, aroE, fumC, gdh, pdhC, pgm, aspA, carB, dhpS, glnA, gpm, mtgA, pilA, pip, ppk, pykA, rpiA, serC, talA, porA and porB of the currently sequenced H44/76 genome with those of H44/76 previously submitted to the Neisseria Multi Locus Sequence Typing database (6). All 11,549 compared nucleotides were identical, indicating a high quality of our H44/76 genome. Comparative genome analysis of strain H44/76 and MC58 (recently re-annotated (12)) was performed using BLAT (7) and progressiveMauve (3).

The genome size of H44/76 is 2.18 Mb and 2480 ORFs were annotated, compared to 2.27 Mb and 2465 ORFs in MC58. Both strains have a GC content of 51.5%. Comparative analysis showed that 4 genes are uniquely present in H44/76 and 9 genes are only present in MC58. Of all ORFs in H44/76, 2317 (93%) show more than 99% sequence identity. Of the 18 least similar genes (90-95% sequence identity), 3 (hmbR, tbp1 and an iron(III) ABC transporter) are associated with iron acquisition from the host.

In the genome sequence of MC58, a ~32 Kb region (NMB1124 to NMB1159), is duplicated (NMB1162 to NMB1197) while this region occurs only once in H44/76 (verified by PCR and 454 read coverage analysis) Obviously, the erythromycin cassette that truncates the siaD gene in MC58 (17) is not present in H44/76.

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession AEQZ00000000.

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Footnotes

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