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GENOME ANNOUNCEMENT

Genome Sequence of a *Neisseria meningitidis* Capsule Null Locus Strain from the Clonal Complex of Sequence Type 198

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***Neisseria meningitidis* is a commensal and accidental pathogen exclusively of humans. Although the production of polysaccharide capsules is considered to be essential for meningococcal virulence, there have been reports of constitutively unencapsulated strains causing invasive meningococcal disease (IMD). Here we report the genome sequence of a capsule null locus (*cnl*) strain of sequence type 198 (ST-198), which is found in half of the reported cases of IMD caused by *cnl* meningococcal strains.**

Neisseria meningitidis is a commensal bacterium of humans that occasionally causes severe disease, particularly in infants and young adults (13). Nearly all of the *N. meningitidis* isolates recovered from cases of invasive meningococcal disease (IMD) are encapsulated (3), and the production of a polysaccharide capsule is considered a main virulence factor of meningococci (15). Accordingly, there have been only four reports so far of constitutively unencapsulated *cnl* strains causing IMD (4, 6, 7, 14), although the prevalence of *cnl* strains is 16% in healthy children and young adults (2, 11). Multilocus sequence typing indicated that most *cnl* strains belong to only a very few clonal complexes (CCs) of, among others, sequence type 53 (ST-53) and ST-198 (7). Whereas CC ST-53 *cnl* strains can be found frequently in carriers but almost never in cases of IMD, ST-198 *cnl* strains were found in two of four reported IMD cases caused by *cnl* strains (6, 7). Here we provide the genome sequence of an *N. meningitidis cnl* strain of CC ST-198 and compare it to the genome of *cnl* strain α14 of CC ST-53 (12).

For *de novo* sequencing of the *N. meningitidis* α704 genome at 65-fold coverage, Roche/454 sequencing of 3-kb paired-end libraries using the GS FLX Titanium chemistry (Roche Diagnostics, Penzberg, Germany) was combined with Sanger sequencing of fosmid libraries generated with vector pCC1FOS (EPICENTRE Biotechnologies, Madison, WI) and of PCR products for gap closure on an ABI 3730XL sequencer (Applied Biosystems, Foster City, CA). We used the Roche GS *De Novo* Assembler software for the assembly of the Roche/454 sequence data and the CONSED (5) software package for guidance during the finishing phase and obtained a draft genome consisting of two scaffolds and 41 scaffolded contigs. The *N. meningitidis* α704 scaffolds and 11 unscaffolded contigs were arranged according to the *N. meningitidis* α14 reference genome (12) and concatenated by 12-mer linkers (CTA GCTAGCTAG). Annotation of the *N. meningitidis* α704 genome was performed with GenDB (9) using the NeMeSys annotation of α14 as a reference (10).

The α704 draft genome consists of 1,983,849 bp comprising 1,754 coding sequences and 69 putative pseudogenes. It has 1,744 genes in common with strain α14 (pairwise BLASTN [1] comparisons with an E value of <0.01) with an average nucleotide sequence identity of 97%. Among others, it contains a 25-kb Mu-like prophage absent from α14 and a 50-kb P2-like prophage absent from all of the sequenced meningococcal genomes except that of strain α710 (8). In line with its almost 10-times-higher adhesion and invasion rates, compared with those of strain α14, observed *in vitro* using FaDu nasopharyngeal cell lines (B. Joseph et al., unpublished data), the genome of α704 also harbors a full-length *opc* gene and a second *pilC* gene, which both encode (major) adhesins of meningococci. These genomic differences in particular are likely to contribute to the epidemiologically observed differences between the invasive properties of CC ST-198 and ST-53 *cnl* strains.

Nucleotide sequence accession numbers. The genome sequence of *N. meningitidis* α704 has been assigned GenBank accession numbers CAJS01000001 to CAJS01000042.

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