



HAL
open science

Draft Genome Sequence of a *Neisseria meningitidis* Serogroup C Isolate of Sequence Type 11 Linked to an Outbreak among Men Who Have Sex with Men.

Frédéric J. Veyrier, Eva Hong, Ala-Eddine Deghmane, Muhamed-Kheir Taha

► **To cite this version:**

Frédéric J. Veyrier, Eva Hong, Ala-Eddine Deghmane, Muhamed-Kheir Taha. Draft Genome Sequence of a *Neisseria meningitidis* Serogroup C Isolate of Sequence Type 11 Linked to an Outbreak among Men Who Have Sex with Men.. *Genome Announcements*, 2013, 1 (5), pp.e00795-13. 10.1128/genomeA.00795-13 . pasteur-02073309

HAL Id: pasteur-02073309

<https://pasteur.hal.science/pasteur-02073309>

Submitted on 19 Mar 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

Draft Genome Sequence of a *Neisseria meningitidis* Serogroup C Isolate of Sequence Type 11 Linked to an Outbreak among Men Who Have Sex with Men

Frédéric J. Veyrier, Eva Hong, Ala-Eddine Deghmane, Muhamed-Kheir Taha

Institut Pasteur, Invasive Bacterial Infections Unit and National Reference Centre for Meningococci, Paris, France

Meningococcal disease occurs as sporadic cases in developed countries, with the occasional emergence of new clones of *Neisseria meningitidis*. Here, we report the genome sequence of *N. meningitidis* strain LNP27256, an isolate of sequence type 11 linked to a recent outbreak among men who have sex with men in Europe.

Received 4 September 2013 Accepted 10 September 2013 Published 3 October 2013

Citation Veyrier FJ, Hong E, Deghmane A-E, Taha M-K. 2013. Draft genome sequence of a *Neisseria meningitidis* serogroup C isolate of sequence type 11 linked to an outbreak among men who have sex with men. *Genome Announc.* 1(5):e00795-13. doi:10.1128/genomeA.00795-13.

Copyright © 2013 Veyrier et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Frédéric Veyrier, frederic.veyrier@pasteur.fr, or Muhamed-Kheir Taha, muhamed-kheir.taha@pasteur.fr.

Neisseria meningitidis, a Gram-negative human-specific bacterium, is the agent of severe and life-threatening invasive infections (mainly meningitis and/or septicemia). The incidence of meningococcal disease is region specific (1). However, meningococcal disease is still a major problem in developed countries due to frequent outbreaks that require prompt management, including public health measures (vaccination and chemoprophylaxis). Moreover, major epidemics occur in developing countries, such as those in sub-Saharan Africa. *N. meningitidis* is highly variable due to frequent genetic variations that occur through horizontal DNA exchanges (2). The reports on the increase of meningococcal disease incidence among men who have sex with men (MSM) have raised the question of whether a new clone is emerging in this community (3–5). However, the cases were due to isolates of serogroup C belonging to the clonal complex sequence type 11 (ST11), a genotype that is frequent among cases in the general population. Draft sequencing of isolates from MSM is therefore essential to compare the meningococcal isolates from that population to other isolates from the general population and should prompt a pathophysiological analysis of these isolates.

We announce the draft genome sequence of *N. meningitidis* strain LNP27256, isolated from a blood specimen at the Centre National Recherche Medicale (CNRM) at the Pasteur Institute, Paris, France, from a patient who died of meningitis. Initially, identification of the bacterium to the strain level and confirmation of the identification were carried out by conventional biochemical identification methods, as well as by multilocus sequence typing (MLST). Genomic DNA was extracted using the Genomic-tip 20/G kit (Qiagen) from an overnight culture grown on G2 plates. Whole-genome sequencing was performed using the Illumina HiSeq 2000 sequencer, which generated 100-bp paired reads. The sequencing was done by GATC Biotech using standard protocols as per the manufacturer's instructions. The sequences (8 million reads) were *de novo* assembled using SeqMan NGen (DNASStar, Inc.) using default settings, wherein 223 contigs with 315× aver-

age genome coverage were obtained. The contig N₅₀ was 20 kb, with an average length of 9,775. The contigs were submitted to the NCBI whole-genome shotgun (WGS) submission portal, and the sequences were annotated using the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>).

A more-detailed comparative analysis of this genome with those of other *N. meningitidis* strains will provide further insight into the specific properties related to this strain that are linked to the recent outbreak among men who have sex with men in Europe.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. **AVOU00000000**. The version described in this paper is version AVOU01000000.

ACKNOWLEDGMENTS

This work was supported by the Institut Pasteur and the Institut de Veille Sanitaire.

REFERENCES

1. Harrison LH, Pelton SI, Wilder-Smith A, Holst J, Safadi MA, Vazquez JA, Taha MK, LaForce FM, von Gottberg A, Borrow R, Plotkin SA. 2011. The global meningococcal initiative: recommendations for reducing the global burden of meningococcal disease. *Vaccine* 29:3363–3371.
2. Maiden MC. 1993. Population genetics of a transformable bacterium: the influence of horizontal genetic exchange on the biology of *Neisseria meningitidis*. *FEMS Microbiol. Lett.* 112:243–250.
3. Marcus U, Vogel U, Schubert A, Claus H, Baetzing-Feigenbaum J, Hellenbrand W, Wichmann O. 2013. A cluster of invasive meningococcal disease in young men who have sex with men in Berlin, October 2012 to May 2013. *Euro Surveill.* 18(28):pii=20523. <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20523>.
4. Weiss D, Varma J. 2013. Control of recent community-based outbreaks of invasive meningococcal disease in men who have sex with men in Europe and the United States. *Euro Surveill.* 18(28):pii=20522. <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20522>.
5. Kupferschmidt K. 26 July 2013. Bacterial meningitis finds new niche in gay communities. *Science* 341:328. doi:10.1126/science.341.6144.328.