Draft Genome Sequences for a Diverse Set of Isolates from 10 Neisseria Species

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ABSTRACT Neisseria is a diverse genus that includes commensal and pathogenic species that pose a public health threat. While the pathogenic species have been studied extensively, many of the commensals have limited genomic information available. Here, we present draft genome sequences for a diverse set of 37 isolates from 10 Neisseria species.

Neisseria is a broad and genetically diverse genus consisting of Gram-negative betaproteobacteria that make up a large part of the normal flora in humans and animals, colonizing the mucosal membranes of the upper respiratory, gastrointestinal, and genitourinary tracts (1). The genus is largely composed of commensal species but also includes several rare zoonotic pathogens, as well as two important human pathogens, N. meningitidis and N. gonorrhoeae. These two species are of considerable significance due to their ability to cause serious illness in humans, such as meningitis, sepsis, and gonococcal infections (2). Additionally, several rare zoonotic pathogens, such as N. animaloris, have been associated with human wound infections from dog and cat bites (1). While the pathogenic species have been studied extensively and have a large collection of available genomic data, the commensal species have been studied far less extensively, and many only have limited available genomic information. To supplement the existing Neisseria genomic collection, we present genomic data for isolates from 10 Neisseria species: N. animaloris, N. bergeri, N. cinerea, N. elongata, N. mucosa, N. polysaccharea, N. sicca, N. subflava, N. wadsworthii, and N. weaveri.

Bacteria were isolated from clinical specimens collected in Minnesota from 2004 to 2015 and cultivated on tryptic soy blood agar. The cultures were incubated for 24 to 48 hours at 35°C and 5% CO₂. Bacterial DNA was extracted using the QIAamp DNA blood minikit on the Qiagen QIAcube, according to the manufacturer’s guidelines, and DNA concentrations were quantitated using the Qubit double-stranded-DNA (dsDNA) high-sensitivity (HS) assay kit (Thermo Fisher Scientific). Samples were prepared for whole-genome sequencing according to the Nextera XT DNA library preparation protocol and manufacturer’s (Illumina) guidelines. Barcoded libraries were then pooled and loaded onto the Illumina MiSeq platform using 500-cycle V2 chemistries for multiplexed 250-bp paired-end sequencing. The Illumina reads were then trimmed using cutadapt 1.8 (3) and assembled using SPAdes 3.10.1 (4).

In both clinical and research settings, it is essential to accurately identify the pathogenic Neisseria species in order to effectively provide treatment. However, Neisseria spp. have historically been characterized by conventional identification methods, which has left them prone to species misidentification, as not all members of the genus are easily and clearly distinguishable by their phenotypic and biochemical properties alone (5). The high rate of horizontal gene transfer that occurs within and between
species due to the coccolization of pathogens and commensals in the body (2) has also contributed to species misidentification and taxonomic confusion. Alternatively, the use of ribosomal multilocus sequence typing (rMLST) has been shown to be effective at delineating between species (6) and has led to the discussion of species reclassification within the genus. Of particular interest is the proposed reclassification of the most diverse variant of \textit{N. polysaccharea} as a separate species, with the suggested name \textit{N. bergeri} (3). The genomic sequences for isolates from 10 \textit{Neisseria} species in this study will provide data for future studies examining species delineation among \textit{Neisseria} spp., especially for those that previously had limited available genomic information.

**Accession number(s).** The draft genome sequences have been deposited in GenBank under the accession numbers listed in Table 1.

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### TABLE 1 Metadata and GenBank accession numbers for draft genome assemblies reported in this study

| Isolate name | GenBank accession no. | Species | Collection yr | Isolation source | \( N_{sp} \) (bp) | Avg coverage (x) |
|--------------|-----------------------|---------|---------------|------------------|------------------|-----------------|
| C2015003240  | POYC000000000         | \textit{N. animaloris} | 2015          | Swab             | 307,764          | 24              |
| C2014021188  | POYB000000000         | \textit{N. subflava}    | 2014          | Bronchial wash   | 343,438          | 22              |
| C2014019557  | POYA000000000         | \textit{N. cinerea}     | 2014          | Urine            | 252,188          | 12              |
| C2014013859  | POXZ000000000         | \textit{N. cinerea}     | 2014          | Blood            | 366,008          | 18              |
| C2014032421  | POXY000000000         | \textit{N. elongata}    | 2014          | Abdominal wound  | 110,032          | 20              |
| C201402478   | POXK000000000         | \textit{N. sicca}      | 2014          | Eye              | 51,187           | 17              |
| C201302421   | POXW000000000         | \textit{N. cinerea}     | 2013          | Blood            | 207,528          | 14              |
| C2013018262  | POXV000000000         | \textit{N. elongata}    | 2013          | Endotracheal tube| 92,876           | 10              |
| C2013013825  | POUX000000000         | \textit{N. weaveri}     | 2013          | Leg wound        | 207,454          | 18              |
| C2013011231  | POXT000000000         | \textit{N. polysaccharea} | 2013         | Throat swab     | 131,026          | 23              |
| C2013010062  | POXS000000000         | \textit{N. elongata}    | 2013          | Endotracheal tube| 98,407           | 35              |
| C2012029644  | POXR000000000         | \textit{N. animaloris} | 2012          | Swab             | 684,286          | 23              |
| C2012028592  | POXQ000000000         | \textit{N. cinerea}     | 2012          | Sputum           | 285,815          | 31              |
| C2012011976  | POXP000000000         | \textit{N. subflava}    | 2012          | Sputum           | 1,167,507        | 42              |
| C2011033015  | POXX000000000         | \textit{N. subflava}    | 2011          | Blood            | 231,464          | 26              |
| C2011020199  | POXN000000000         | \textit{N. subflava}    | 2011          | Sputum           | 264,440          | 17              |
| C2011020198  | POXM000000000         | \textit{N. subflava}    | 2011          | Sputum           | 342,533          | 47              |
| C2011009653  | POXL000000000         | \textit{N. subflava}    | 2011          | Urine            | 217,621          | 16              |
| C2011009460  | POXK000000000         | \textit{N. subflava}    | 2011          | Sputum           | 378,795          | 19              |
| C2011003085  | POXJ000000000         | \textit{N. elongata}    | 2011          | Swab             | 116,473          | 32              |
| C2010015191  | POXI000000000         | \textit{N. weaveri}     | 2010          | Hand             | 290,757          | 62              |
| C2010010207  | POXH000000000         | \textit{N. elongata}    | 2010          | Peritoneal fluid | 123,763          | 19              |
| C2010005502  | POXG000000000         | \textit{N. sicca}      | 2010          | Sputum           | 553,284          | 23              |
| C2009035459  | POXF000000000         | \textit{N. weaveri}     | 2009          | Leg tissue       | 203,342          | 67              |
| C2009028987  | POXE000000000         | \textit{N. weaveri}     | 2009          | Wound            | 165,690          | 31              |
| C2009010520  | POXD000000000         | \textit{N. subflava}    | 2009          | Blood            | 308,740          | 49              |
| C2008002238  | POXC000000000         | \textit{N. subflava}    | 2008          | Knee             | 222,323          | 35              |
| C2008001664  | POXB000000000         | \textit{N. subflava}    | 2008          | Jejunostomy      | 131,757          | 65              |
| C2008000421  | POXA000000000         | \textit{N. dawsworthii} | 2008         | Finger           | 83,929           | 25              |
| C2008000329  | POWZ000000000         | \textit{N. bergeri}     | 2008          | Meninges         | 135,935          | 27              |
| C2008000328  | POWY000000000         | \textit{N. bergeri}     | 2008          | Lung             | 124,886          | 36              |
| C2008000159  | POWX000000000         | \textit{N. mucosa}      | 2008          | CSF\textsuperscript{a} | 123,178        | 31              |
| C2007003584  | POWW000000000         | \textit{N. sicca}      | 2007          | Blood            | 211,701          | 35              |
| C2007002879  | POWV000000000         | \textit{N. subflava}    | 2007          | Sputum           | 209,740          | 36              |
| C2006001571  | PQVC000000000         | \textit{N. sicca}      | 2006          | Blood            | 62,634           | 27              |
| C2005001510  | POWU000000000         | \textit{N. subflava}    | 2005          | Sinus            | 295,777          | 29              |
| C2004002444  | POWT000000000         | \textit{N. mucosa}      | 2004          | Eye              | 46,652           | 17              |

\textsuperscript{a}CSF, cerebrospinal fluid.
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