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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% CO_2. 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

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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_{50} (bp)	Avg coverage (×)
C2015003240	POYC00000000	*N. animaloris*	2015	Swab	307,764	24
C2014021188	POYB00000000	*N. subflava*	2014	Bronchial wash	343,438	22
C2014019557	POYA00000000	*N. cinerea*	2014	Urine	252,188	12
C2014013859	POXZ00000000	*N. cinerea*	2014	Blood	366,008	18
C2014003241	POXY00000000	*N. elongata*	2014	Abdominal wound	110,032	20
C2014002478	POXX00000000	*N. sicca*	2014	Eye	51,187	17
C2013024221	POXW00000000	*N. cinerea*	2013	Blood	207,528	14
C2013018262	POXV00000000	*N. elongata*	2013	Endotracheal tube	92,876	10
C2013013825	POXU00000000	*N. weaveri*	2013	Leg wound	207,454	18
C2013011231	POXT00000000	*N. polysaccharea*	2013	Throat swab	131,026	23
C2013010062	POXS00000000	*N. elongata*	2013	Endotracheal tube	98,407	35
C2012029644	POXR00000000	*N. animaloris*	2012	Swab	684,286	23
C2012028592	POXQ00000000	*N. cinerea*	2012	Sputum	285,815	31
C2012011976	POXP00000000	*N. subflava*	2012	Sputum	1,167,507	42
C2011033015	POXO00000000	*N. subflava*	2011	Blood	231,464	26
C2011020199	POXN00000000	*N. subflava*	2011	Sputum	264,440	17
C2011020198	POXM00000000	*N. subflava*	2011	Sputum	342,535	47
C2011009653	POXL00000000	*N. subflava*	2011	Urine	217,621	16
C2011004960	POXK00000000	*N. subflava*	2011	Sputum	378,795	19
C2011003085	POXJ00000000	*N. elongata*	2011	Swab	116,473	32
C2010015191	POXI00000000	*N. weaveri*	2010	Hand	290,757	62
C2010010207	POXH00000000	*N. elongata*	2010	Peritoneal fluid	123,763	19
C2010005502	POXG00000000	*N. sicca*	2010	Sputum	553,284	23
C2009035459	POXF00000000	*N. weaveri*	2009	Leg tissue	203,342	67
C2009028987	POXE00000000	*N. weaveri*	2009	Wound	165,690	31
C2009010520	POXD00000000	*N. subflava*	2009	Blood	380,740	49
C2008002238	POXC00000000	*N. subflava*	2008	Knee	222,323	35
C2008001664	POXB00000000	*N. subflava*	2008	Jejunostomy	131,757	65
C2008000421	POXA00000000	*N. wadsworthii*	2008	Finger	83,929	25
C2008000329	POWZ00000000	*N. bergeri*	2008	Meninges	135,935	27
C2008000328	POWY00000000	*N. bergeri*	2008	Lung	124,886	36
C2008000159	POWX00000000	*N. mucosa*	2008	CSF[a]	123,178	31
C2007003584	POWW00000000	*N. sicca*	2007	Blood	211,701	35
C2007002879	POWV00000000	*N. subflava*	2007	Sputum	209,740	36
C2006001571	PQVC00000000	*N. sicca*	2006	Blood	62,634	27
C2005001510	POWU00000000	*N. subflava*	2005	Sinus	295,777	29
C2004002444	POWT00000000	*N. mucosa*	2004	Eye	46,652	17

[a]CSF, cerebrospinal fluid.

species due to the cocolonization 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 *N. polysaccharea* as a separate species, with the suggested name *N. bergeri* (3). The genomic sequences for isolates from 10 *Neisseria* species in this study will provide data for future studies examining species delineation among *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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