AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Complete Genome Sequence of the Neonatal Meningitis *Escherichia coli* Serotype O18:K1 Strain NMEC15

Aline L. de Oliveira,[a,c] Timothy J. Johnson,[b] Nicolle L. Barbieri,[c] Lisa K. Nolan,[d] Catherine M. Logue[c]

[a]Department of Microbiology, University of Georgia, Athens, Georgia, USA
[b]Department of Veterinary and Biomedical Sciences, College of Veterinary Medicine, University of Minnesota, Saint Paul, Minnesota, USA
[c]Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA
[d]Department of Infectious Diseases, College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA

ABSTRACT Neonatal meningitis *Escherichia coli* (NMEC) is the second leading cause of sepsis and meningitis in neonates worldwide. Here, we report the genome sequence of NMEC15, belonging to serotype O18:K1, isolated from the cerebrospinal fluid (CSF) of an infant with neonatal bacterial meningitis (NBM) in the Netherlands.

Neonatal meningitis *Escherichia coli* (NMEC) is the second leading cause of sepsis and meningitis in neonates worldwide (1). However, NMEC has emerged as the most common cause of meningitis and sepsis among very-low-birth-weight infants (<1,500 g birth weight) since the 1990s (2–5).

NMEC15 (serotype O18:K1) was isolated from the cerebrospinal fluid (CSF) of a newborn infant (<28 days) with meningitis in the Netherlands as described elsewhere (6, 7). The O serogroup was identified at the *E. coli* Reference Center at Pennsylvania State University. NMEC15 belongs to serotype O18:K1, similar to the prototypic NMEC strain RS218 (8). Here, we present the genome sequence of NMEC15.

NMEC15 was grown on LB agar and subsequently in Luria-Bertani broth at 37°C. Genomic DNA (gDNA) was extracted using the ChargeSwitch gDNA mini bacteria kit (Life Technologies, Carlsbad, CA) for Illumina sequencing. The DNA yields were quantified using a Qubit fluorimeter double-stranded DNA (dsDNA) high-sensitivity (HS) kit (Life Technologies). The QIAseq FX kit (Qiagen, Germantown, MD) was used to prepare the genomic library for Illumina 2 × 300-bp MiSeq sequencing. The raw reads were subjected to quality processing using Trimmomatic v0.40 to remove low-quality reads/regions and Illumina adapters. Unless otherwise stated, all software used default parameters. The reads were then assembled using Shovill (GPLV3) (https://github.com/tseemann/shovill) with the SPAdes v3.15.3 assembler and annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.2 (9). Following trimming, 639,894 reads corresponding to 319,947 matching paired-end reads were used for assembly. The assembly resulted in 252 contigs with an N_{50} value of 192,568 bases and approximately 23.5× average genome coverage. The assembled genome size was 5,288,759 bp, organized into 252 contigs with a 50.57% GC content. The strain harbors the plasmid replicons IncFIB and IncFII, identified using PlasmidFinder v2.1 (Center for Genomic Epidemiology; http://www.genomicepidemiology.org/).

Two clusters for the type 6 secretion system (T6SS) were identified in NMEC15, T6SS1 and T6SS2, using NCBI BLAST analysis of contigs. The T6SS1 cluster is 30.2 kb long, with a GC content of 52.2%. The T6SS2 cluster is 27.9 kb long, with a 52% GC content.

The resistance genes identified using ResFinder v4.1 included *sul1* (sulfonamide) and *aadA1* (aminoglycoside). The *E. coli* virulence factors identified through VirulenceFinder v2.0 included the increased serum survival gene (*iss*), the S-fimbria minor subunit (*sfaS*), and the vacuolating autotransporter toxin (*vat*).

Citation de Oliveira AL, Johnson TJ, Barbieri NL, Nolan LK, Logue CM. 2021. Complete genome sequence of the neonatal meningitis *Escherichia coli* serotype O18:K1 strain NMEC15. Microbiol Resour Announc 10:e00832-21. https://doi.org/10.1128/MRA.00832-21.

Editor David Rasko, University of Maryland School of Medicine

Address correspondence to Catherine M. Logue, Catherine.Logue@uga.edu.

Received 19 August 2021
Accepted 27 August 2021
Published 23 September 2021

Data availability. The genome sequence has been deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under accession number SRX10988923 (NMEC15), BioProject accession number PRJNA732675, BioSample accession number SAMN19334708, and genome accession number JAHTGQ000000000.

REFERENCES

1. Stoll BJ, Hansen N, Fanaroff AA, Wright LL, Carlo WA, Ehrenkranz RA, Lemons JA, Donovan EF, Stark AR, Tyson JE, Oh W, Bauer CR, Korones SB, Shankaran S, Laptook AR, Stevenson DK, Papile L-A, Poole WK. 2004. To tap or not to tap: high likelihood of meningitis without sepsis among very low birth weight infants. Pediatrics 113:1181–1186. https://doi.org/10.1542/peds.113.5.1181.
2. Stoll BJ, Hansen NI, Higgins RD, Fanaroff AA, Duara S, Goldberg R, Laptook A, Walsh M, Oh W, Hale E, National Institute of Child Health and Human Development. 2005. Very low birth weight preterm infants with early onset neonatal sepsis: the predominance of Gram-negative infections continues in the National Institute of Child Health and Human Development Neonatal Research Network, 2002–2003. Pediatr Infect Dis J 24:635–639. https://doi.org/10.1097/01.inf.0000168749.82105.64.
3. Bizzarro MJ, Dembry L-M, Baltimore RS, Gallagher PG. 2008. Changing patterns in neonatal Escherichia coli sepsis and ampicillin resistance in the era of intrapartum antibiotic prophylaxis. Pediatrics 121:689–696. https://doi.org/10.1542/peds.2007-2171.
4. Stoll BJ, Hansen N, Fanaroff AA, Wright LL, Carlo WA, Ehrenkranz RA, Lemons JA, Donovan EF, Stark AR, Tyson JE, Oh W, Bauer CR, Korones SB, Shankaran S, Laptook AR, Stevenson DK, Papile L-A, Poole WK. 2002. Changes in pathogens causing early-onset sepsis in very-low-birth-weight infants. N Engl J Med 347:240–247. https://doi.org/10.1056/NEJMoa012657.
5. Camacho-Gonzalez A, Spearman PW, Stoll BJ. 2013. Neonatal infectious diseases: evaluation of neonatal sepsis. Pediatr Clin North Am 60:367–389. https://doi.org/10.1016/j.pcl.2012.12.003.
6. Johnson JR, Oswald E, O'Bryan TT, Kuskowski MA, Spanjaard L. 2002. Phylogenetic distribution of virulence-associated genes among Escherichia coli isolates associated with neonatal bacterial meningitis in the Netherlands. J Infect Dis 185:774–784. https://doi.org/10.1086/339343.
7. Spanjaard L, Bol P, Ekker W, Zanen HC. 1985. The incidence of bacterial meningitis in the Netherlands—a comparison of three registration systems, 1977–1982. J Infect 11:259–268. https://doi.org/10.1016/S0163-4453(85)93327-4.
8. Wijetunge DSS, Karunathilake KHEM, Chaudhari A, Katani R, Dudley EG, Kapur V, DebRoy C, Kariyawasam S. 2014. Complete nucleotide sequence of pRS218, a large virulence plasmid, that augments pathogenic potential of meningitis-associated Escherichia coli strain RS218. BMC Microbiol 14:203. https://doi.org/10.1186/s12866-014-0203-9.
9. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.