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PROKARYOTES

# Draft Genome Sequences of Five Neonatal Meningitis-Causing *Escherichia coli* Isolates (SP-4, SP-5, SP-13, SP-46, and SP-65)

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**ABSTRACT** Neonatal meningitis-causing *Escherichia coli* isolates (SP-4, SP-5, SP-13, SP-46, and SP-65) were recovered between 1989 and 1997 from infants in the Netherlands. Here, we report the draft genome sequences of these five *E. coli* isolates, which are currently being used to validate food safety processing technologies.

Neonatal meningitis-associated *Escherichia coli* (NMEC) strains are one of the leading causes of neonatal bacterial meningitis, associated with 15% to 40% mortality and morbidity rates and severe neurological defects in surviving neonates (1). The pathogenesis of NMEC disease involves cross-contamination from the mother's feces during birth, followed by neonatal gastrointestinal (GI) tract colonization and subsequent neonatal sepsis. NMEC strains are able to survive and multiply to high titers in the bloodstream of neonates, which allows them to invade the central nervous system and cause meningitis (1–3). Of the approximately 180 serogroups of *E. coli*, those preferentially associated with NMEC strains include O1, O7, O12, O18, and O83 (4, 5). The five present study isolates were recovered from the cerebrospinal fluid of neonates with bacterial meningitis in the Netherlands between 1989 and 1997 (6). NMEC-like strains are present in some foods (7), consistent with possible foodborne transmission. These five isolates, along with other extraintestinal pathogenic *Escherichia coli* (ExPEC) types, are currently being used to validate food safety intervention technologies (8).

Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany) and quantified using a Qubit 3.0 fluorometer (Life Technologies, Carlsbad, CA). The genomic DNA library was prepared using the Nextera Flex DNA library prep kit (Illumina, San Diego, CA), which generated ca. 600-bp fragments. Libraries were analyzed for concentration, pooled, and denatured for loading onto a flow cell for cluster generation. Denatured libraries were sequenced on an Illumina MiniSeq platform with 2 × 151-bp reads using a paired-end protocol with 50× coverage. Single or duplicate Illumina reads were assembled *de novo* using SPAdes (version 3.9.0). Virulence factors, antibiotic resistances, sequence types, mRNA, rRNA, tRNA, genes, pseudogenes, and coding sequences (CDSs) were determined using the Illumina Bacterial Analysis Pipeline (version 1.0.4) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP; version 4.3). The accession numbers and assembly metrics are listed in Table 1.

Genomics data are now considered an integral part of risk assessment for food safety and environmental microbiology (9). These genomic data will be useful for understanding NMEC pathogenesis and should provide novel insights regarding the persistence of NMEC strains in foods and effective food safety interventions against such strains.

**Accession number(s).** The whole-genome shotgun projects reported here have been deposited in DDBJ/ENA/GenBank under the accession numbers and BioProject

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**TABLE 1** Accession numbers and assembly metrics of five draft whole-genome sequences for *Escherichia coli*

| Isolate | Serotype | GenBank accession no. | Genome size (bp) | G+C content (%) | BioProject no. |
|---|---|---|---|---|---|
| SP-4 | O18:K1 | PNYE00000000 | 4,894,710 | 50.71 | PRJNA422252 |
| SP-5 | O7:K1 | PNYF00000000 | 5,324,549 | 50.52 | PRJNA422419 |
| SP-13 | O18:K1 | PNYD00000000 | 5,161,293 | 50.59 | PRJNA422418 |
| SP-46 | O7:K1 | POSV00000000 | 5,260,766 | 50.54 | PRJNA429215 |
| SP-65 | O83:K1 | POSW00000000 | 3,911,002 | 50.39 | PRJNA429216 |

numbers listed in Table 1. The versions described in this paper are the second versions, PNYE02000000, PNYF02000000, PNYD02000000, POSV02000000, and POSW02000000.

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