Draft Genome Sequence of the Commensal *Escherichia coli* Strain F-18

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Here, we report the draft genome sequence of *Escherichia coli* strain F-18, originally isolated from the feces of a healthy individual in 1977. The draft genome is 5,246,829 bp, with a G+C content of 50.50%, and it encodes 4,933 predicted coding sequences (CDSs), 10 rRNAs, and 84 tRNAs.

*E*scherichia coli F-18 is a clinical strain that was originally isolated in the United States in 1977 from the feces of a healthy individual [1]. F-18 contains seven plasmids, is of serotype rough: K1:H5, produces colicin V, and makes type 1 pili. This strain has also been demonstrated to be an excellent colonizer of the streptomycin-treated mouse large intestine [2, 3] and has been used in *in vivo* studies [4]. As *E. coli* F-18 was recovered from a healthy individual, this genome sequence will thus serve as a useful resource for future studies into human intestinal pathogens, as a comparison to pathogenic strains.

Genomic DNA of *E. coli* F-18 was extracted from a freshly grown single colony using an Illumina Nextera XT DNA sample kit, as per the manufacturer's protocol (Illumina, San Diego, CA). Sequencing was performed by Illumina MiSeq using a 2 × 250 paired-end protocol. Read quality analysis and trimming were conducted using Trimmomatic [5] and the quality assessed using in-house scripts combined with SAMtools [6], BedTools, and BWA-MEM [7]. *De novo* assembly was conducted with SPAdes version 3.5 [8], resulting in a total of 101 contigs, with 84 contigs larger than 1,000 bp. The draft genome of *E. coli* F-18 is 5,246,829 bp, with 50.50% G+C content, and it encodes 4,933 coding sequences (CDSs), 10 rRNAs, and 84 tRNA sequences. Bioinformatic prediction of antimicrobial resistance genes using ResFinder (version 2.1) [9] revealed only the sulfonamide resistance gene *sul2*. VirulenceFinder (version 1.5) [10] identified seven genes with potential roles in virulence, including in serum survival and as siderophore receptors.

Accession number(s). This draft genome project has been deposited at DDBJ/EMBL/GenBank under the accession number MLZI00000000 (BioProject PRJNA348710; BioSample SAMN05914511). The version described in this paper is version MLZI01000000.

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