Complete Genome Sequence of Colistin-Resistant *Escherichia fergusonii* Strain EFCF056

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**ABSTRACT**

Here, we report the complete genome sequence of colistin-resistant *Escherichia fergusonii* strain EFCF056, isolated from chicken feces. This genome contains six plasmids, including a 204,246-bp plasmid harboring the colistin resistance gene *mcr-1*. These results will increase our understanding of plasmid-mediated *mcr-1* gene presence and transmission in *E. fergusonii*.

Of the eight *Escherichia* species (1, 2), *E. fergusonii* and *E. coli* are easily confused during isolation due to their phenotypic and genotypic similarities (1, 3). *E. fergusonii* is pathogenic to both humans and animals (1, 3, 4, 5, 6) and has reportedly acquired multiple-drug resistance (1, 6). Since there is limited research on antimicrobial resistance in *E. fergusonii*, an isolate from chicken feces from Zhejiang Province, China, was examined for antimicrobial resistance. Its whole-genome sequence is described here.

A single colony from a previously cultured isolate was selected and inoculated into 10 ml of LB broth for genomic DNA extraction (QIAprep Spin miniprep kit; Qiagen, Germany). The purity and quantity of the extracted DNA were examined using a NanoDrop One UV-visible (UV-vis) spectrophotometer (Thermo Fisher Scientific, USA) and a Qubit 3.0 fluorometer (Invitrogen, USA), respectively. Libraries were prepared (SQK-LSK109 kit; Oxford Nanopore Technologies [ONT]) and sequenced using FLO-MIN106D R9.4 flow cell (ONT) technology on a GridION sequencer (ONT) and repeated on an Illumina HiSeq platform. All software systems were operated on their default settings. Guppy v3.2.4 (ONT) was used for base calling of raw fast5 data and removal of adapter sequences. An Illumina sequencing library was generated using a NEXTflex DNA sequencing kit (Bioo Scientific, USA). A total of 16,654,064 paired-end reads (2 *×* 150 bp) were checked for quality and trimmed with Trimmomatic v0.36. All low-quality (*Q* < 20) data were filtered out. The 140,754 nanopore reads (total of 3,427,444,055 nucleotides) were assembled *de novo* using Canu v1.7.11 (7), achieving an *N*50 value and mean read size of 33,077 bp and 24,350 bp, respectively. The assembly was circularized using Circulator v1.5.1 and corrected by Illumina reads (497-fold coverage) using Pilon v1.22 software (8). The completed assembly consisted of seven contigs with an *N*50 contig size of 4,576,669 bp. Two clear GC skew shift points were found around the start codon of *dnaA* on the chromosomal sequence.

As shown in Table 1, this genome comprises a chromosome of 4,576,669 bp (GC content, 49.86%) and six plasmids. The gene prediction and annotation of this genome (NCBI Prokaryotic Genome Annotation Pipeline) revealed 5,082 protein-coding sequences (CDSs), 82 tRNA genes, and 7 rRNA operons. No rRNA genes were found in the plasmids. The average nucleotide identity value of genome sequences of *E. fergusonii*...
strains EFCF056 (GenBank accession number CP040805) and ATCC 35469 (accession number NC_011740) (9) was 98.53%.

The acquired antimicrobial resistance genes were predicted via the ResFinder database (10). In addition, there were aac(3)-IId, aadA2, aph(3’)-Ib, aph(6’)-Id, mntB, aac(6’)-Ib-cr, adaA2, mcr-1, qnrS2, aac(6’)-Ib-cr, qepA, aph(3’)-la, floR, catA1, catB3, ARR-3, sul1, sul2, dfrA12, and tet(A).

The results showed that E. fergusonii might be a reservoir for antimicrobial resistance genes. Further studies are required to investigate the MIC distribution and frequency and the importance of the colistin resistance gene mcr-1.

**Data availability.** The complete genome sequence of *Escherichia fergusonii* EFCF056 has been deposited in GenBank/ENA/DBJ under accession numbers CP040805, CP040806, CP040807, CP040808, CP040809, CP040810, and CP040811. The accession numbers of the original read data set in the SRA are SRR9214441 (Nanopore), SRR10686670 (Nanopore), and SRR10718121 (Illumina).

**ACKNOWLEDGMENTS**

This work was financially supported by the National Natural Science Foundation for the Youth (grant 31700007), the Key Research and Development Program of Zhejiang Province (grant 2020C02031), and the State Key Laboratory for Managing Biotic and Chemical Threats to the Quality and Safety of Agro-products (grants 2010DS700124-ZZ1703 and 2010DS700124-ZZ1905).

We have no potential conflicts of interest to declare.

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