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PacBio Genome Sequences of *Escherichia coli* Serotype O157:H7, Diffusely Adherent *E. coli*, and *Salmonella enterica* Strains, All Carrying Plasmids with an *mcr-1* Resistance Gene

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Abstract

We report here Illumina-corrected PacBio whole-genome sequences of an *Escherichia coli* serotype O157:H7 strain (2017C-4109), an *E. coli* serotype O[undetermined]:H2 strain (2017C-4173W12), and a *Salmonella enterica* subsp. *enterica* serovar Enteritidis strain (2017K-0021), all of which carried the *mcr-1* resistance gene on an IncI2 or IncX4 plasmid. We also determined that pMCR-1-CTSe is identical to a previously published plasmid, pMCR-1-CT.

Plasmid-mediated colistin resistance, mediated by the mcr-1 gene, has been identified in *Escherichia coli*, *Salmonella enterica*, and other *Enterobacteriaceae* strains worldwide. The *mcr-1* gene was initially described in an *E. coli* IncI2 plasmid isolated from a pig in China (1). In 2016, the first case of *mcr-1* in a U.S. isolate was reported (2,3). So far in the United States, 49 *mcr-1*-positive isolates, including 47 from human samples, have been reported and are routinely tracked by the CDC (https://www.cdc.gov/drugresistance/biggest-threats/tracking/mcr.html). Here, we report the availability of three whole-genome sequence assemblies generated by PacBio sequencing and corrected with Illumina reads. Additionally, 2017K-0021 was verified using the strain's whole-genome map (WGM).

Strains were grown on blood agar (Becton, Dickinson and Co., USA), and DNA was extracted using the Promega Wizard genomic DNA purification kit (Promega Corp., USA). PacBio and Illumina sequencing, assembly, finishing, and optical mapping were performed as previously described, except where noted (4). Following the manufacturers' protocols,

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Data availability. he whole-genome sequences reported here have been deposited in DDBJ/ENA/GenBank under the accession numbers listed in Table 1. The versions described in this paper are the first versions.

sequencing libraries were prepared with a Nextera XT library prep kit (Illumina, USA) or a NEBNext Ultra library prep kit (New England BioLabs, USA) and sequenced on the MiSeq platform (4). PacBio sequence reads were filtered and assembled *de novo* utilizing the PacBio Hierarchical Genome Assembly Process (HGAP) version 3 and polished using Quiver (5). PacBio sequences were further corrected with Illumina sequencing reads using Pilon (6). WGMs were generated for 2017K-0021 according to the OpGen protocol, as previously described (4). The final assembly yielded single-chromosome sequences for all three isolates. Resistance genes and plasmid replicons were detected using the ResFinder and PlasmidFinder databases, respectively (http://www.genomicepidemiology.org) IncF replicon sequence types were determined as previously described (7).

E. coli strain 2017C-4109 (Table 1) carried genes for serotype O157:H7. Additionally, virulence factors *stx*$_2$ (*stx*$_{2a}$ and *stx*$_{2c}$), *eae*, and *ehxA* were identified. Two plasmids were identified in this isolate, an IncI2 plasmid (pMCR-1) carrying the *mcr-1* gene and an IncFII/FIB plasmid (p2017C-4109, replicon sequence type F23:A-:B3) carrying no known resistance genes.

E. coli strain 2017C-4173W12 (Table 1) did not carry a described O serotype gene but carried genes for H2 and *afaC*, a marker for diffusely adherent *E. coli* (DAEC) (8). Two plasmids were identified in this isolate, an IncI2 plasmid (pMCR-1_2017C-4173W12) carrying the *mcr-1* gene and a second IncFII/FIB plasmid (p2017C-4173W12, replicon sequence type F29:A-:B10), with additional replicons IncQ and Col156, carrying the following resistance genes: *bla*$_{TEM-1b}$, *sul1*, *sul2*, *strA*, *strB*, *aadA5*, *mphA*, and *dfrA17*.

Salmonella enterica subsp. *enterica* serovar Enteritidis strain 2017K-0021 (Table 1) carried the expected serotype genes. Two plasmids were identified in this isolate, an IncX4 plasmid (pMCR-1-CTSe) carrying the *mcr-1* gene and an IncFII/FIB plasmid (p2017K-0021, replicon sequence type S1:A-:B22) carrying no known resistance genes. IncX4 plasmid pMCR-1-CTSe (GenBank accession number CP030795) was aligned to the previously described plasmid pMCR-1-CT (CP018773), and they were determined to be identical (4).

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TABLE 1

NCBI/GenBank accession numbers, assembly metrics, and associated plasmids

Strain	Assignment	NCBI accession no.	Length (bp)	GC content (%)	Complete and circular
2017C-4109	Chromosome	CP030767	5,384,880	50.5	Yes
pMCR-1	Plasmid	CP030766	59,808	42.4	Yes
p2017C-4109	Plasmid	CP030765	93,169	47.9	Yes
2017K-0021	Chromosome	CP030794	4,685,707	52.2	Yes
pMCR-1-CTSe	Plasmid	CP030795	33,304	41.8	Yes
p2017K-0021	Plasmid	CP030796	59,371	51.9	Yes
2017C-4173W12	Chromosome	CP030768	5,300,308	50.7	Yes
pMCR-1_2017C-4173W12	Plasmid	CP030769	149,680	52.4	Yes
p2017C-4173W12	Plasmid	CP030770	27,128	42.5	No