



Genome Sequences of Five Multidrug-Resistant *Escherichia coli* Sequence Type 117 Isolates Recovered from Dairy Calves

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ABSTRACT *Escherichia coli* sequence type 117 (ST117) strains have been recovered from poultry with colibacillosis, as well as from urinary tract infections and fatal septic infections in humans. To further investigate ST117 isolates recovered from non-poultry food animals, we sequenced the genomes of five ST117 isolates from dairy calves in Pennsylvania.

Escherichia coli sequence type 117 (ST117) encompasses a group of multiserotype avian pathogenic *E. coli* (APEC) and extraintestinal pathogenic *E. coli* (ExPEC) strains of phylogenetic group D (1–5). Recent studies have indicated that poultry may be a reservoir of *E. coli* strains that frequently cause extraintestinal infections in humans (1–5). However, the literature suggests that these strains are infrequently isolated from dairy and beef cattle. During an ongoing study focused on the prevalence of antibiotic resistance in *E. coli* recovered from dairy calves, we isolated five ST117 strains with various levels of resistance. ST117 represented 4% of a subset of *E. coli* isolates selected for whole-genome sequencing. These data indicate that some lineages associated with human extraintestinal infections, particularly ST117, may be occasionally isolated from cattle and that their prevalence among nonavian food-producing animals has not been adequately evaluated. To further evaluate the genomic characteristics and the phylogeny of these strains, we sequenced the genomes of these five ST117 isolates.

The *E. coli* isolates were originally recovered from dairy calf feces enriched in buffered peptone water and subsequently streaked onto CHROMagar EC plates (Hardy Diagnostics, France). DNA was extracted from purified colonies grown in Luria-Bertani (LB) broth. To sequence the genomes of these isolates, libraries were constructed using the Nextera XT library prep kit (Illumina, La Jolla, CA), which were then sequenced using a high-output version 2.0 flow cell on a NextSeq 500 platform (Illumina). Raw reads were cleaned and trimmed using DeconSeq (6) and Trimmomatic (7) and assembled using SPAdes version 3.8.0 (8). After assembly, the genomes were analyzed *in silico* using the Center for Genomic Epidemiology Web server (<http://www.genomicepidemiology.org/>).

Two isolates were serotyped *in silico* as O119:H4 (ARS-CC9640 and ARS-CC9604), and three were individually serotyped as O161:H4 (ARS-CC9622), O114:H4 (ARS-CC9624), and O33:H4 (ARS-CC9591). Strains of each of these serotypes have been previously isolated from human-derived samples (<http://enterobase.warwick.ac.uk/>). Antibiotic resistance genes were variably distributed among the isolates. ARS-CC9591 contained the β -lactamase *bla*_{CTX-M-14}, *bla*_{TEM-1B}, and *bla*_{CMY-2} genes. ARS-CC9624 contained both a *bla*_{CMY-2} and a *bla*_{TEM-1C} gene. ARS-CC9640 contained a *bla*_{CMY-2} gene. The sulfonamide resistance genes *sul1* and *sul2* or *sul2*-like were detected in two (ARS-CC9624 and ARS-CC9591) and four strains (ARS-CC9624, ARS-CC9640, ARS-CC9604, and ARS-

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TABLE 1 Accession numbers and metadata for the *E. coli* strains sequenced in this study

Isolate ID ^a	Source	Serotype ^b	AMR profile ^c	AMR gene(s) ^b	Virulence profile ^b	GenBank accession no.
ARS-CC9624	Dairy calf	O114:H4	AMP, AUG, AXO, CEP, CTX (FOT), FIS, FOX, SXT, TET	<i>aadA1</i> , <i>bla_{CMY-2}</i> , <i>bla_{TEM-1C}</i> , <i>dfrA1</i> , <i>sul1</i> , <i>sul2</i> -like, <i>tet(A)</i> , <i>tet(B)</i>	<i>espP</i> , <i>ireA</i> , <i>iss</i> , <i>lplfA</i> , <i>mchB</i> , <i>mchC</i> , <i>mchF</i> , <i>pic</i> , <i>vat</i>	NBYY000000000
ARS-CC9640	Dairy calf	O119:H4	AMP, AUG, AXO, CEP, CTX (FOT), FIS, FOX	<i>aph(3')</i> -Ic-like, <i>bla_{CMY-2}</i> , <i>sul2</i>	<i>espP</i> , <i>ireA</i> , <i>iss</i> , <i>lplfA</i> , <i>vat</i>	NBXX000000000
ARS-CC9604	Dairy calf	O119:H4	AMP, AUG, AXO, CEP, CHL, CTX (FOT), FIS, FOX, STR, TET, TIO	<i>aph(3')</i> -Ic-like, <i>bla_{CMY-2}</i> , <i>floR</i> -like, <i>strA</i> , <i>strB</i> , <i>sul2</i> , <i>tet(A)</i> -like, <i>tet(B)</i>	<i>espP</i> , <i>gad</i> , <i>ireA</i> , <i>iroN</i> , <i>iss</i> , <i>lplfA</i> , <i>mchB</i> , <i>mchC</i> , <i>mchF</i> , <i>pic</i>	NBWW000000000
ARS-CC9622	Dairy calf	O161:H4	TET	<i>tet(B)</i>	<i>iroN</i> , <i>iss</i> , <i>lplfA</i> , <i>pic</i> , <i>vat</i>	NBYV000000000
ARS-CC9591	Dairy calf	O33:H4	AMP, AUG, AXO, CEP, CHL, CTX (FOT), FIS, FOX, STR, SXT, TET, TIO	<i>aadA1</i> , <i>aph(3')</i> -Ic-like, <i>bla_{CMY-2}</i> , <i>bla_{CTX-M-14}</i> , <i>bla_{TEM-1B'}</i> , <i>catA1</i> -like, <i>dfrA1</i> , <i>strA</i> , <i>strB</i> , <i>sul1</i> , <i>sul2</i> , <i>tet(B)</i> -like	<i>espP</i> , <i>ireA</i> , <i>iss</i> , <i>lplfA</i> , <i>pic</i> , <i>vat</i>	NBVT000000000

^aID, identification.

^bDetermined *in silico* using the Center for Genomic Epidemiology Web server (<http://www.genomicepidemiology.org/>).

^cAntibiotic susceptibility was determined using a Sensititre automated antimicrobial susceptibility system (Trek Diagnostic Systems, Westlake, OH) with specialty plates CVM3AGNF and ESB1F. AMP, ampicillin; AMR, antimicrobial resistance; AUG, augmentin; AXO, ceftiofur; CEP, cefepime; CTX (FOT), cefotaxime; FIS, sulfisoxazole; FOX, ceftiofur; SXT, trimethoprim-sulfamethoxazole; TET, tetracycline; CHL, chloramphenicol; STR, streptomycin; TIO, ceftiofur.

CC9591), respectively. A *floR*-like and a *catA1*-like phenicol resistance gene were each detected in two separate strains (ARS-CC9604 and ARS-CC9591, respectively).

In a single-nucleotide polymorphism (SNP)-based neighbor-joining phylogenetic analysis of 295 *E. coli* ST117 genomes deposited in GenBank, the study isolates were scattered across the tree and nested within clades that contain poultry and human-derived isolates, indicating that cattle may be a reservoir of strains involved in human infections. However, this remains yet to be studied in-depth. Future research should investigate the role of cattle and other livestock as reservoirs of APEC and ExPEC strains.

Accession number(s). The genome sequences of these five isolates of *E. coli* have been deposited in GenBank under the accession numbers listed in Table 1.

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