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GENOME SEQUENCES

Draft Genome Sequences of Sixteen Fluoroquinolone-Resistant Extraintestinal *Escherichia coli* Isolates from Human Patients

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ABSTRACT We report here the draft genome sequences of 16 fluoroquinolone-resistant extraintestinal *Escherichia coli* isolates from human patients. These isolates had high MICs (32 to 256 μg/mL) for ciprofloxacin and contained point mutations in the quinolone resistance-determining region (QRDR) of both *gyrA* and *parC* that confer resistance to fluoroquinolone. The whole-genome sequence data provide a better understanding of the fluoroquinolone resistance mechanisms in these isolates and would be beneficial in source tracking these pathogens during pandemic outbreaks.

Urinary tract infection (UTI) is an extremely common bacterial infection of the bladder and/or kidney. It affects more than a billion women worldwide (1) and about 8 million women in the United States, resulting in approximately 100,000 hospitalizations (1–3). Untreated UTI can lead to septic shock and death and contributes to preterm labor, agitation, or delirium in the elderly (1). The incidence of UTI increases with age and sexual activity. UTI is commonly treated with antibiotics such as ciprofloxacin, trimethoprim-sulfamethoxazole, cephalosporins, and nitrofurans (3–5).

Most community-acquired UTI episodes (80%) are caused by *Escherichia coli*, and most UTI-causing *E. coli* strains are uropathogenic *E. coli* (UPEC). UPEC strains have distinctive virulence capabilities that distinguish them from diarrheagenic and commensal *E. coli* and allow the UPEC strains to colonize, invade, injure, and trigger inflammation at extraintestinal sites, thereby producing disease.

Most UPEC strains belong to *E. coli* phylogenetic group B2 or D and are often clonal; the leading sequence types (STs) isolated worldwide are ST69, ST73, ST95, and ST131 (5–7). These clones are a major contributor to hospital- and community-acquired UTIs and bloodstream infections and are multidrug resistant (MDR), including having resistance to fluoroquinolones (5–7), and are a major public health concern (5–10).

The *E. coli* strains used in this study were isolated by streaking urine samples on MacConkey agar plates incubated at 37°C. These strains were isolated by the Department of Veteran's Affairs (VA), Minneapolis, Minnesota, after approval from their institutional review board (IRB). Presumptive positive colonies of *E. coli* were identified by the Vitek GNI+ card with VTK-RO7.01 software (bioMérieux Vitek, Hazelwood, MO). Sixteen *E. coli* strains were resistant to fluoroquinolone (FQ). All 16 FQ-resistant isolates had MICs of 128 to 256 μg/mL for nalidixic acid and 32 to 256 μg/mL for ciprofloxacin. The genome sequences of these isolates will be useful for further understanding the mechanism of FQ resistance, virulence properties, and source tracking of these isolates during pandemic outbreaks.

Genomic DNA was extracted from overnight cultures on MacConkey agar plates using the DNeasy blood and tissue kit (Qiagen, Valencia, CA). DNA libraries were

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TABLE 1 Summary of genome sequence analysis of extraintestinal *Escherichia coli* isolates from human patients

Isolate	N_{50} (bp)	No. of contigs	Total no. of reads	Genome length (bp)	Genome coverage (×)	No. of CDSs[a]	G+C content (%)	SRA accession no.	GenBank accession no.
Escherichia coli MVAST4410	73,614	181	5,238,611	5,239,854	50	4,988	50.55	SRX9748648	JAEMEI000000000
Escherichia coli MVAST2986	191,314	107	5,093,752	5,095,001	50	4,904	50.73	SRX9748649	JAEMEJ000000000
Escherichia coli MVAST3079	44,133	280	5,083,391	5,083,391	50	4,930	50.86	SRX9748656	JAEMEK000000000
Escherichia coli MVAST3385	190,966	124	5,284,823	5,282,826	50	5,146	50.88	SRX9748657	JAEMEL000000000
Escherichia coli MVAST3887	55,163	242	5,282,995	5,279,786	50	5,063	50.58	SRX9748658	JAEMEM000000000
Escherichia coli MVAST2284	158,975	120	5,267,684	5,267,772	50	5,130	50.67	SRX9748659	JAEMEN000000000
Escherichia coli MVAST4331	191,083	110	5,093,752	5,095,354	50	4,930	50.76	SRX9748660	JAEMEO000000000
Escherichia coli MVAST2842	110,606	175	5,166,958	5,166,958	50	5,024	50.82	SRX9748661	JAEMEP000000000
Escherichia coli MVAST2624	74,671	196	5,111,376	5,117,732	50	4,966	50.80	SRX9748662	JAEMEQ000000000
Escherichia coli MVAST3604	190,899	86	5,242,655	5,242,655	50	5,062	50.68	SRX9748663	JAEMER000000000
Escherichia coli MVAST4169	103,745	142	5,022,955	5,022,955	50	4,823	50.62	SRX9748650	JAEMES000000000
Escherichia coli MVAST2250	130,178	114	5,136,438	5,136,438	50	4,854	50.54	SRX9748651	JAEMET000000000
Escherichia coli MVAST3636	105,677	140	5,141,629	5,141,629	50	4,949	50.62	SRX9748652	JAEMEU000000000
Escherichia coli MVAST2316	64,078	212	5,029,007	5,029,007	50	4,861	50.79	SRX9748653	JAEMEV000000000
Escherichia coli MVAST3575	147,709	137	5,414,888	5,414,888	50	5,312	50.60	SRX9748654	JAEMEW000000000
Escherichia coli MVAST4715	140,083	130	5,062,858	5,062,858	50	4,869	50.59	SRX9748655	JAEMEX000000000

[a]CDS, coding DNA sequence.

constructed by using the Nextera XT library prep kit (Illumina). The whole-genome sequence was performed using an Illumina MiSeq platform (Illumina, San Diego, CA) with 2 × 251-bp paired-end reads. Trimming and assembly were performed by using the CLC Genomics Workbench 21.0.4 (Qiagen).

Draft genomes were annotated initially using the Pathosystems Resources Integration Center (PATRIC) software version 3.6.12. and the data were submitted to the NCBI for final annotation to the Prokaryotic Genome Annotation Pipeline (PGAP) (11) under the accession numbers shown in Table 1. Default parameters were used for all software unless otherwise specified. The average G+C content of these strains was estimated to be approximately 50.69% as estimated by the PATRIC database, which was annotated using default parameters. Table 1 shows the number of contigs, sequence assembly size, coding sequences, and functional coding sequences for the respective strains.

Data availability. SRA submissions of FASTQ files and the draft genome sequences for these 16 UPEC strains have been deposited at DDBJ/ENA/GenBank under accession numbers given in Table 1 (BioProject accession number PRJNA669151).

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