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Draft Genome Sequence Analysis of Multidrug-Resistant *Escherichia coli* Strains Isolated in 2013 from Humans and Chickens in Nigeria

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ABSTRACT Here, we present the draft genome sequences of nine multidrug-resistant *Escherichia coli* strains isolated from humans ($n = 6$) and chicken carcasses ($n = 3$) from Lagos, Nigeria, in 2013. Multiple extended-spectrum β-lactamase (ESBL) genes were identified in these isolates.

Received 29 August 2017 **Accepted** 1 September 2017 **Published** 5 October 2017

Citation Sharma P, Gupta SK, Adenipekun EO, Barrett JB, Hiott LM, Woodley TA, Iwalokun BA, Oyedeji KS, Oluwadun A, Ramadan H, Frye JG, Jackson CR. 2017. Draft genome sequence analysis of multidrug-resistant *Escherichia coli* strains isolated in 2013 from humans and chickens in Nigeria. Genome Announc 5:e01073-17. https://doi.org/10.1128/genomeA.01073-17.

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The use and misuse of antimicrobials around the world has led to the selection of various multidrug-resistant (MDR) bacteria in humans and animals. In humans, the spread of multidrug-resistant bacteria has increased considerably in hospitals and the community (1, 2). In livestock feeds, antimicrobials have been used to promote growth, as therapeutic agents, and as prophylactics, which has led to the exertion of selective pressure for the emergence of MDR bacteria causing foodborne infections in humans (3–7).

Escherichia coli is a common commensal of the intestinal tract of humans and animals. It is also an opportunist pathogen manifesting in different disease conditions (8–11) and has been associated with illnesses caused by food-producing animals (4). The spread and emergence of MDR *E. coli* have been documented worldwide and thus are a major concern (12). In Nigeria, reports state that infections caused by *E. coli* are increasing (13, 14). In order to effectively treat these infections, it is important to understand the mechanisms of resistance in *E. coli*. As a first step in this study, we report here the draft genome sequences of nine MDR *E. coli* strains isolated from outpatients ($n = 5$), animal handlers ($n = 1$), and chickens ($n = 3$) in Lagos, Nigeria, in 2013 (15, 16).

Genomic DNA from *E. coli* was extracted using the blood and tissue genomic DNA extraction kit (Qiagen, Germantown, MD). Extracted DNA was quantified using the Qubit double-stranded DNA (dsDNA) high-sensitivity (HS) assay kit, according to the manufacturer's instructions (Life Technologies, Inc., Waltham, MA). The Illumina libraries were prepared using the Nextera XT DNA library preparation kit and Nextera XT index primers (Illumina, San Diego, CA). The library fragment size distribution was checked using the Bioanalyzer 2100 using Agilent high-sensitivity DNA kit (Agilent Technologies, Santa Clara, CA) and quantified using the Qubit DNA HS assay kit in a Qubit fluorometer (Thermo Fisher Scientific, USA). The generated libraries were then sequenced using MiSeq reagent kit version 3 with 600 cycles and a paired-end

TABLE 1 Genome assembly statistics for *Escherichia coli* strains

Isolate	Sequence type (15)	Isolation source	Genome size (Mb)	N_{50} (bp)	No. of contigs	GC content (%)	No. of tRNAs	Total no. of genes	Accession no.
38.ii.h	131	Human	5,300,508	200,215	134	50.81	81	5,683	NJAF00000000
129.h	617	Human	4,864,884	126,492	179	50.57	80	5,224	NJAE00000000
204ii.h	542	Human	4,748,637	102,767	127	50.85	80	5,110	NJAD00000000
299.h	398	Human	5,107,667	95,064	161	50.55	80	5,535	NJAC00000000
322i.h	4143	Human	4,920,104	166,962	79	50.78	81	5,165	NJAB00000000
382.h	398	Human	5,108,224	97,665	164	50.55	79	5,545	NJAA00000000
104	162	Chicken	4,921,291	193,770	78	50.78	82	5,166	NIZZ00000000
131i	162	Chicken	4,965,831	185,473	91	50.80	82	5,237	NIZY00000000
141	131	Chicken	5,305,541	230,026	130	50.80	82	5,694	NIZX00000000

read length of 2 × 300 bp on an Illumina MiSeq platform. The quality metrics of the reads were determined by FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc). The sequence data were assembled using the A5-miseq assembler (17), and the genome sequence was annotated via the NCBI Prokaryotic Genome Annotation Pipeline (18). The contigs were reordered with r2cat (19). The genome statistics are shown in Table 1.

Antibiotic resistance genes were identified using ARG-ANNOT (20). All isolates had at least one extended-spectrum β-lactamase (ESBL) resistance gene detected. The isolates also harbored genes conferring resistance to aminoglycosides, tetracycline, trimethoprim, sulfonamides, fluoroquinolones, and chloramphenicol, consistent with their reported phenotypes (15, 16). The detection of circulating antibiotic resistance genes in bacteria from humans and food animals using genome sequencing is useful in predicting emerging resistance, especially in underfunded countries.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under BioProject number PRJNA389301, and the accession numbers are listed in Table 1. The versions described in this paper are the first versions.

ACKNOWLEDGMENTS

We thank Calvin Williams, Carolina Hall, and Latoya Wiggins for their technical support.

This work was supported by U.S. Department of Agriculture (USDA) project 6040-32000-009-00.

The mention of trade names or commercial products in this paper is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture or any of the authors.

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