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.

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 opportunistic 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) | N₅₀ (bp) | No. of contigs | GC content (%) | No. of tRNAs | Total no. of genes | Accession no. |
|-----------|--------------------|------------------|------------------|----------|----------------|----------------|--------------|--------------------|---------------|
| 38.i.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   |
| 204i.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           | 5,353              | NJAC00000000   |
| 322i.h    | 4143               | Human            | 4,965,831        | 185,473  | 79             | 50.78          | 81           | 5,165              | NJAB00000000   |
| 104       | 162                | Chicken          | 4,921,291        | 193,770  | 78             | 50.78          | 79           | 5,237              | 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   |

The reads 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.

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