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PROKARYOTES

Draft Genomic Sequencing of Six Potential Extraintestinal Pathogenic *Escherichia coli* Isolates from Retail Chicken Meat

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ABSTRACT Potential extraintestinal pathogenic *Escherichia coli* strains DP254, WH333, WH398, F356, FEX675, and FEX725 were isolated from retail chicken meat products. Here, we report the draft genome sequences for these six *E. coli* isolates, which are currently being used in food safety research.

Extraintestinal pathogenic *Escherichia coli* (ExPEC) strains are responsible for almost 90% of urinary tract infections (UTIs) and many other extraintestinal *E. coli* infections, such as neonatal meningitis, septicemia, abdominal/pelvic infections, and pneumonia (1, 2). ExPEC strains causing colibacillosis in birds carry similar virulence factors to those of human ExPEC (3). Many studies also suggest that ExPEC strains transmitted from food items (e.g., poultry products) could be responsible for some human infections (4–6). The recovery of ExPEC strains from retail food items has been greatest for chicken meat and other animal meat products (7–11). It is possible that control of ExPEC in food and food animals could reduce the incidence of ExPEC-related disease. Toward this end, the present six presumptive ExPEC strains (12), recovered from retail chicken meat, are currently being used in food safety research (13, 14).

Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany) and quantified in a Qubit 3.0 fluorimeter (Life Technologies, Carlsbad, CA). The genomic DNA library was prepared using the Nextera DNA Flex library prep kit (Illumina, San Diego, CA). Libraries were analyzed for concentration, pooled, and denatured for loading onto a flow cell for cluster generation. Denatured libraries were sequenced on an Illumina MiniSeq platform with a 2 × 150-bp-read paired-end protocol with 50× coverage. Two Illumina reads from separate DNA preparations were assembled *de novo* using SPAdes (version 3.9.0). Virulence factors, antibiotic resistance genes, genome size, N_{50} values, multilocus sequence type (MLST), mRNA, rRNA, tRNA, genes, pseudogenes, and coding sequences (CDSs) were determined using the Illumina Bacterial Analysis Pipeline (version 1.0.4) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP, version 4.3). The accession numbers and assembly metrics are listed in Table 1.

Genomic data are now considered an integral part of risk assessment for food safety and environmental microbiology (15). These genomic data will be useful for understanding ExPEC pathogenesis and should provide novel insights regarding the persistence of ExPEC in chicken meat products and effective food safety practices to detect, control, and eliminate such strains.

Accession number(s). The whole-genome shotgun project sequences reported here have been deposited in DDBJ/ENA/GenBank under the accession numbers and BioProject numbers listed in Table 1. The versions described in this paper are the first versions.

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TABLE 1 Accession numbers and assembly metrics of six draft whole-genome sequences

Species	Strain	Serotype	GenBank accession no.	Genome size (bp)	G+C content (%)	BioProject no.
E. coli	DP254	O1:H7	PSNQ00000000	5,235,670	50.41	PRJNA433381
E. coli	WH398	O24:H4	PSNR00000000	5,178,520	50.69	PRJNA433384
E. coli	WH333	O120:H4	PSNS00000000	4,903,012	50.5	PRJNA433490
E. coli	F356	O2:H6	PSNT00000000	5,495,366	50.59	PRJNA433492
E. coli	FEX675	O120:H4	PSNU00000000	5,271,935	50.3	PRJNA433495
E. coli	FEX725	O1:H45	PSOV00000000	5,441,656	50.15	PRJNA433496

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