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Whole-Genome Sequencing of Nontyphoidal *Salmonella enterica* Isolates Obtained from Various Meat Types in Ghana

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**ABSTRACT** Here, we report the draft genome sequences of 16 nontyphoidal *Salmonella enterica* isolates obtained from locally produced meats in Tamale, Ghana, which are commonly consumed by most natives as an important protein source. The draft genomes will help provide a molecular snapshot of *Salmonella enterica* isolates found in these retail meats in Tamale.

Nontyphoidal *Salmonella* (NTS) strains can cause mild to moderate, mostly self-limiting gastroenteritis in humans and can be acquired through many sources, including the consumption of contaminated meat (1). It should be noted that the mortality rate typically reported for NTS strains is 0.1 to 1%, although it could be higher when considering 1-year mortality and/or considering societies with impaired health systems (2). In Ghana, the manner in which meats are handled by butchers in markets could easily expose the meats to *Salmonella* contamination (1, 3). This represents a health risk to Ghanaians since most of them consume locally produced animal meats on a regular basis as an important protein source.

In 2016, a total of 225 locally produced meat samples, namely, beef (*n* = 45), goat (*n* = 45), mutton (*n* = 45), guinea fowl (*n* = 45), and chicken (*n* = 45), were purchased from 5 retail shops in Tamale, the capital city of the northern region of Ghana. One hundred seven *Salmonella enterica* strains were isolated from these meat samples, according to the U.S. FDA bacteriological analytical manual, with slight modification (4). Briefly, meat samples (10 cm²) were swabbed and preenriched in buffered peptone water. Preenriched aliquots were further enriched in Rappaport-Vassiliadis and selenite cystine broths. The enriched aliquots were then streaked on xylose-lysine-deoxycholate and brilliant green agars. Presumptive *Salmonella* colonies were purified and confirmed by biochemical testing, Gram staining, and a *Salmonella* latex agglutination test (Oxoid Ltd., Basingstoke, UK). Overnight Luria-Bertani broth cultures of 16 selected isolates (beef [*n* = 3], goat [*n* = 3], mutton [*n* = 4], guinea fowl [*n* = 3], and chicken [*n* = 3]; Table 1) were subjected to DNA extraction using a QiAamp DNA minikit (Qiagen, Hilden, Germany). Library preparation was performed according to Illumina’s TruSeq Nano DNA sample preparation protocol, which was sequenced on the MiSeq platform (Illumina, CA, USA) with 300-bp paired-end read lengths (5). Raw reads were *de novo* assembled using the Shovill pipeline version 0.9.0 ([https://github.com/tseemann/shovill](https://github.com/tseemann/shovill)) that uses SPAdes version 3.11.0, available in the GalaxyTrakr pipeline ([https://www.galaxytrakr.org](https://www.galaxytrakr.org)). The “trim reads” option was selected, and the list of k-mer sizes to be used was set to “auto.” The draft genome assembly quality was evaluated using
### TABLE 1 Whole-genome sequencing characterization of 16 nontyphoidal *Salmonella enterica* strains that were isolated from various meat samples in Ghana

QUAST version 4.6.3 (7). Draft genomes were analyzed with the following Web-based tools from the Center for Genomic Epidemiology website (http://cge.cbs.dtu.dk/). PlasmidFinder version 2.0 (8) and ResFinder version 3.0 (9) were used to identify plasmid and antimicrobial resistance genes, respectively. MLST version 2.0 (10) and pMLST version 2.0 (8) were used to determine the multilocus sequence typing (MLST) profiles of the genome and plasmid, respectively. Raw reads of isolates with an unknown sequence type (ST) were submitted to EnteroBase (11) (https://enterobase.warwick.ac.uk/) for new ST assignment. Salmonella serovars were predicted from the draft genomes using SeqSero version 1.0 (http://www.denglab.info/SeqSero [12]).

The draft genomes ranged from 4,550,213 to 4,990,760 bp in size, with 52.2% average GC content (Table 1). The number of contigs for each isolate ranged from 17 to 45. Analysis by SeqSero revealed that the isolates belong to seven different serovars. It is noteworthy that all six isolates from poultry were Salmonella enterica subsp. enterica serovar Hato. Eight MLSTs were identified, including two that were newly assigned, ST5307 and ST5308. ResFinder identified only one antimicrobial resistance gene, fosA7 (for fosfomycin), in a Salmonella enterica subsp. enterica serovar Africana strain of mutton origin. Only two plasmid replicon types belonging to IncI1 of Salmonella Hato of chicken and guinea fowl origin and IncFII(S) of Salmonella Africana of mutton origin were seen. The data provided will contribute to understanding the molecular diversity of Salmonella enterica strains found in retail meats in Tamale, the capital city of the northern region of Ghana. It will also be useful in comparative genomic analyses of Salmonella enterica from the meat production chain in Ghana, as well as those from humans when more of such sequence data are deposited into the public database in the future.

**Data availability.** The sequence data were deposited in GenBank under BioProject accession number PRJNA484344. GenBank accession numbers for individual isolates are listed in Table 1.

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F.A. and J.M.T. performed bacterial isolation from meat samples and did phenotypic bacterial identification. K.L.G.S. and M.Y.F.T. performed bacterial culturing and DNA extraction. M.Y.F.T. and S.A.S. performed genomic data analysis. F.A. and M.Y.F.T. drafted the manuscript, and all the other authors helped in the manuscript’s revision.

**REFERENCES**


