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Whole Genome Sequencing Analysis of Nontyphoidal
Salmonella enterica of Chicken Meat and Human Origin
Under Surveillance in Sri Lanka

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Abstract
A total of 73 nontyphoidal Salmonella enterica isolates, 33 from raw chicken meat and 40 from routine clinical specimens, were collected between 2015 and 2017 from eight cities in Sri Lanka for a pilot study of whole genome sequencing for Salmonella surveillance. The isolates were characterized by conventional serotyping and whole genome sequencing. The raw sequenced data were assembled and analyzed to predict Salmonella serotypes, determine sequence type (ST) profiles of genome and plasmid, and identify plasmid replicon sequences and antimicrobial resistance (AMR) genes. The most common serovar isolated from chicken meat was Salmonella enterica serovar Agona of ST13 (n = 16), in contrast to Salmonella enterica serovar Enteritidis of ST11 (n = 21) in human. Salmonella enterica serovar Corvallis is the only serovar that was overlapping between human and chicken meat. The level of agreement between serotyping and serotype prediction results was 100%. Among the 33 chicken isolates, multidrug resistance (MDR) was observed in five isolates, including two Salmonella enterica serovar Kentucky ST314, which harbored six different classes of AMR determinants. Among the 40 human isolates, MDR was detected in two Salmonella enterica serovar Chester (ST2063) isolates containing five different antibiotic classes of AMR determinants. Out of 73 isolates, the only human Salmonella enterica serovar Typhimurium strain of ST36 was found to possess extended-spectrum beta-lactamase (ESBL) gene, blaCTX-M-15, and it was positive for ESBL production. In summary, this study identified S. enterica serovars that were dominating in chicken meat and human and showed the genomic differences among the chicken meat and human strains. It should be noted that the limited number of isolates and sampling at a different time period means that thorough source attribution is not possible. To the best of our knowledge, this is the first report on the use of whole genome sequencing analysis of nontyphoidal S. enterica isolated from chicken meat and human in Sri Lanka.

Keywords: Salmonella enterica, CTX-M-15, whole genome sequencing, Sri Lanka, human, chicken meat, surveillance

Short Report/Case Study

Salmonella enterica, a common foodborne pathogen worldwide, has >2600 serovars that can cause infections of varying severity to human and animal. The nontyphoidal Salmonella (NTS) strains may be host generalist with broad host specificity that colonizes or infect a wide range of vertebrate animals or may be restricted to particular animal species (Feasey et al., 2012). NTS infections usually cause mild to moderate self-limiting gastroenteritis in young adults, and no antibiotic treatment is required. However, in ~6% of the gastroenteritis cases, bacteria may proceed to cause an
invasive extraintestinal disease leading to bacteremia and focal infection in the young, elderly, and immunocompromised humans, and ciprofloxacin and extended-spectrum cephalosporin are commonly prescribed to treat such invasive disease (Rowe et al., 1997). Globally, an increasing prevalence of ciprofloxacin and extended-spectrum cephalosporin resistance have been reported in clinical NTS strains (Crump et al., 2015), and it is thought to be associated with the use of fluoroquinolones and beta-lactams as a growth promoter in food-producing animals. NTS is transmitted through animal products (mainly through eggs, meats, and poultry products) and produce contaminated with animal feces and/or human sewage, and contact with animals and animal environment (Crump et al., 2015).

Ministry of Health in Sri Lanka reported an overall decreasing trend in the incidence of dysentery, enteric fever, and food poisoning for the period of 2007–2017 (MoH, 2018). The number of aforementioned foodborne illness cases that can be attributed to S. enterica in Sri Lanka is unknown. Similarly, the transmission pattern of S. enterica in Sri Lanka remains unclear, and there is no published data characterizing the molecular epidemiology of S. enterica in human and poultry production. In Sri Lanka, both fluoroquinolones and beta-lactams are used to treat human Salmonella infection and are banned for growth promotion purposes (personal communication from Dr. Palika Fernando, National AMR steering committee member, Head Department of Bacteriology, Veterinary Research Institute, Sri Lanka). Given the public health significance of Salmonella, this pilot cross-sectional genomic-based surveillance study is done to provide the NTS situation in humans and raw chicken meats from eight cities in Sri Lanka. It is important to note that this study is not designed to compare the prevalence between the different cities. On the contrary, this study aims to provide a molecular snapshot of genetic variability among the collected Salmonella strains.

A total of 73 nontyphoidal S. enterica isolates, 33 from raw chicken meat and 40 from clinical specimens (i.e., stool, blood, and joint fluid) were collected from eight cities in Sri Lanka, namely Abissawella, Badulla, Colombo, Galle, Jaffna, Kandy, Peradeniya, and Ragama between 2015 and 2017 (Table 1). Genomic DNA extraction, library construction, and sequencing were performed as previously described (Guo et al., 2019). Sequence data were deposited into GenBank under BioProject accession number PRJNA504925. GenBank accession numbers for individual isolates are listed in Table 1. De novo assembly of draft genome (Afgan et al., 2018), assessment of draft genome assembly quality (Gurvich et al., 2013), and genomic analyses (Larsen et al., 2012; Zankari et al., 2012; Carattoli et al., 2014; Zhang et al., 2015; Alikhan et al., 2018) were performed as previously described (Tay et al., 2019). Conventional serotyping according to Kauffman–White scheme was done in-house at the Enteric Reference Laboratory in Medical Research Institute with antisera purchased from S&A Reagents Lab Ltd., Part. (Thailand).

Genomic analyses showed that Salmonella enterica serovar Agona of ST13 (n = 16) and Salmonella enterica serovar Enteritidis of ST11 (n = 21) were the most prevalent serovars that were observed among chicken meat and human isolates, respectively. Salmonella enterica serovar Corvallis ST1541 is the only serovar that was overlapping between human and chicken meat in this study. There was 100% concordance between conventional serotyping by Kauffman–White scheme and genotypic serotype prediction by SeqSero (Zhang et al., 2015). Discrepancy was observed for four human isolates; they were serotyped to be Paratyphi B var java (henceforth Java) but were predicted to be Paratyphi B. They have identical serological formula and Java is considered a variant of Paratyphi B that can ferment d-tartrate, whereas Paratyphi B cannot due to a single nucleotide change in the start codon of the STM3356 gene (Malorny et al., 2003). Hence, when the draft genome of these four isolates were blasted against the STM3356 gene of Java strain NCTC5706 (GenBank accession number: LT571437.1), the start codon was ATG (data not shown). In addition, these isolates were phenotypically tested to be positive for d-tartrate fermentation (data not shown). Altogether, this indicates the isolates are able to ferment d-tartrate and they are indeed Paratyphi B var. Java, which tallies with the serotyping result. Hence, this suggests that additional genetic loci or alleles should be taken into consideration for prediction of a certain serotype from sequence data. More than two-thirds (50/73) of the isolates contained plasmid replicons. The commonly seen plasmid replicons were IncFII(S) andIncFIB(S), of sequence type [F-:A16:B22] and were found in 16 Salmonella Enteritidis strains. Among the chicken meat isolates, 87.9% (29/33) of them had at least one resistance gene and multidrug resistance (MDR; defined as resistance to three or more classes of antibiotics) was observed in 15.2% of them (5/33), including two Salmonella enterica serovar Kentucky ST314 strains, which harbored six different classes of antimicrobial resistance (AMR) determinants. In contrast, among the human isolates, 17.5% (7/40) of them had at least one resistance gene and only two isolates (5%, 2/40) were found to be MDR, which were both Salmonella enterica serovar Chester ST2063 strain that contained five AMR determinants, belonging to five different antibiotic classes. It is worth mentioning that out of 73 isolates, only one human isolate contained extended-spectrum beta-lactamase (ESBL) gene, blaconf07 As expected, when we performed the double-disc synergy test (Guo et al., 2019), the strain was tested to be positive for ESBL production. Among all the identified AMR genes, the most frequent resistance genotype was fosA7 and was found in all 16 Salmonella Agona (ST13) strains from different chicken meat samples. We did not test the phenotypic resistance of these isolates to fosfomycin, and hence we do not know if fosA7 gene confers phenotypic resistance to fosfomycin. When a whole genome single nucleotide polymorphism (SNP) analysis with CFASNP SNP Pipeline (Davis et al., 2015) that was installed on Galaxy-Trakr (https://www.galaxytrakr.org) (Afgan et al., 2018) was performed on the 16 Salmonella Agona isolates, the minimum and maximum SNP differences were 0 and 36, respectively (data not shown). Upon construction of the best-scoring maximum likelihood (ML) SNP tree with randomized accelerated ML (RAxML) using a GTRGAMMA model of evolution and default parameters (Stamatakis, 2014), it appears that some isolates are phylogenetically related due to 0 SNP difference, but they may not be epidemiologically related due to lack of information on sampling source.

The investigation has identified the S. enterica serovars that were dominating in chicken meat and human, and showed the genomics differences among the chicken meat
| Laboratory identifier | Isolate | Sample type | Location | Sample isolation date | MLST<sup>a</sup> | Serotyping<sup>b</sup> | Predicted serotype(s)<sup>f</sup> | Resistance genes<sup>d</sup> | Point mutation relating to resistance<sup>d</sup> | Plasmid replicons<sup>e</sup> | pMLST<sup>i</sup> | GenBank accession | No. of Contigs (≥500 bp)<sup>g</sup> | Total length (≥500 bp)<sup>g</sup> |
|----------------------|---------|-------------|----------|-----------------------|-----------------|------------------|-----------------------------------|-----------------|----------------------------------------|----------------|-----------|-----------------|------------------|------------------|
| 1 NAFTEC00025 SL_1_03 | Raw chicken | Colombo | January 5, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 2 NAFTEC00026 SL_2_05 | Raw chicken | Colombo | January 5, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 3 NAFTEC00027 SL_3_07 | Raw chicken | Colombo | January 5, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 4 NAFTEC00028 SL_4_08 | Raw chicken | Colombo | January 5, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 5 NAFTEC00029 SL_5_09 | Raw chicken | Colombo | January 5, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 6 NAFTEC00030 SL_6_10 | Raw chicken | Colombo | January 12, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 7 NAFTEC00031 SL_7_12 | Raw chicken | Colombo | January 12, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 8 NAFTEC00032 SL_8_13 | Raw chicken | Colombo | January 12, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 9 NAFTEC00033 SL_9_15 | Raw chicken | Colombo | January 12, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 10 NAFTEC00034 SL_10_20 | Raw chicken | Colombo | January 12, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 11 NAFTEC00035 SL_11_62 | Raw chicken | Colombo | January 12, 2015 | 314 | Kentucky | Kentucky | aph(6)-Id, tet(A), blmTEM-1B, qnrS1, sul3 | | | | | | |
| 12 NAFTEC00036 SL_12_81 | Raw chicken | Colombo | February 16, 2015 | 1541 | Corvalis | Corvalis or Chailey | qepS1 | | | | | | |
| 13 NAFTEC00037 SL_13_91 | Raw chicken | Colombo | February 16, 2015 | 1541 | Corvalis | Corvalis or Chailey | qepS1 | | | | | | |
| 14 NAFTEC00038 SL_14_93 | Raw chicken | Colombo | February 16, 2015 | 1541 | Corvalis | Corvalis or Chailey | qepS1 | | | | | | |
| 15 NAFTEC00039 SL_15_94 | Raw chicken | Colombo | February 16, 2015 | 1541 | Corvalis | Corvalis or Chailey | qepS1 | | | | | | |
| 16 NAFTEC00040 SL_16_97 | Raw chicken | Colombo | February 16, 2015 | 1541 | Corvalis | Corvalis or Chailey | qepS1 | | | | | | |
| 17 NAFTEC00041 SL_17_98 | Raw chicken | Colombo | February 16, 2015 | 1541 | Corvalis | Corvalis or Chailey | qepS1 | | | | | | |
| 18 NAFTEC00042 SL_18_102 | Raw chicken | Colombo | February 16, 2015 | 1541 | Corvalis | Corvalis or Chailey | qepS1 | | | | | | |
| 19 NAFTEC00043 SL_19_103 | Raw chicken | Colombo | February 23, 2015 | 1541 | Corvalis | Corvalis or Chailey | qepS1 | | | | | | |

(continued)
| Laboratory identifier | Isolate | Sample type | Location | Sample isolation date | MLST<sup>a</sup> | Serotyping<sup>b</sup> | Predicted serotype(s)<sup>c</sup> | Resistance genes<sup>d</sup> | Plasmid replicons<sup>e</sup> | pMLST<sup>f</sup> | GenBank accession | No. of Contigs (<500 bp)<sup>g</sup> | Total length (<500 bp)<sup>h</sup> |
|----------------------|---------|-------------|----------|-----------------------|-----------------|-----------------|-----------------|-----------------|-------------------|---------------|-----------------|-----------------|-----------------|
| 20 NAFTEC00044 SL_20_107 Raw chicken | Colombo | February 23, 2015 | 1541 | Corvalis | Corvalis or Chailey | gyrS1 | qnrS1 | IncI1 | ST-284 | SMPG00000000 | 35 | 4984004 |
| 21 NAFTEC00045 SL_21_109 Raw chicken | Colombo | February 23, 2015 | 13 | Agona | Agona | fosA7 | | | | SMPI00000000 | 30 | 4838095 |
| 22 NAFTEC00046 SL_22_111 Raw chicken | Colombo | February 23, 2015 | 31 | Newport | Newport | | | | | SMPK00000000 | 20 | 4660707 |
| 23 NAFTEC00047 SL_23_112 Raw chicken | Colombo | February 23, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 24 NAFTEC00048 SL_24_113 Raw chicken | Colombo | February 23, 2015 | 31 | Newport | Newport | | | | | | | |
| 25 NAFTEC00049 SL_25_114 Raw chicken | Colombo | February 23, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 26 NAFTEC00050 SL_26_115 Raw chicken | Colombo | February 23, 2015 | 1541 | Corvalis | Corvalis or Chailey | gyrS1 | | | | | | |
| 27 NAFTEC00051 SL_27_116 Raw chicken | Colombo | February 23, 2015 | 31 | Newport | Newport | | | | | | | |
| 28 NAFTEC00052 SL_28_117 Raw chicken | Colombo | February 23, 2015 | 314 | Kentucky | Kentucky | aph(6)-Id, tet(A), blaTEM-1B, qnrS1, sul3, dfrA14 | | | IncX1 | | | | |
| 29 NAFTEC00053 SL_29_118 Raw chicken | Colombo | February 23, 2015 | 1541 | Corvalis | Corvalis or Chailey | gyrS1 | | | | | | |
| 30 NAFTEC00054 SL_30_119 Raw chicken | Colombo | February 23, 2015 | 314 | Kentucky | Kentucky | aph(6)-Id, tet(A), blaTEM-1B, qnrS1, sul3, dfrA14 | | | IncX1 | | | | |
| 31 NAFTEC00055 SL_31_120 Raw chicken | Colombo | February 23, 2015 | 31 | Newport | Newport | | | | | | | |
| 32 NAFTEC00056 SL_32_126 Raw chicken | Colombo | March 2, 2015 | 314 | Kentucky | Kentucky | aph(6)-Id, tet(A), blaTEM-1B, qnrS1, sul3, dfrA14 | | | IncX1 | | | | |
| 33 NAFTEC00057 SL_33_127 Raw chicken | Colombo | March 2, 2015 | 13 | Agona | Agona | fosA7 | | | | | | |
| 34 NAFTEC00058 SL_35_S91 Human (blood) | Colombo | July 11, 2016 | 1541 | Corvalis | Corvalis or Chailey | gyrS1 | | | | | | |
| 35 NAFTEC00059 SL_36_S106 Human (stool) | Jaffna | October 3, 2016 | 11 | Enteritidis | Enteritidis | | | | | | | |
| 36 NAFTEC00060 SL_37_S111 Human (stool) | Colombo | October 3, 2016 | 2063 | Chester | Chester | | | | | | | |
| 37 NAFTEC00061 SL_38_S112 Human (blood) | Colombo | February 25, 2016 | 365 | Weltevreden | Weltevreden | | | | IncFII(S) | | | | |

(continued)
| Laboratory identifier | Isolate | Sample type | Location | Sample isolation date | MLST | Serotyping | Predicted serotype(s) | Resistance genes | Point mutation relating to resistance | Plasmid replicons | pMLST[^1] | GenBank accession | No. of Contigs (≥500 bp) | Total length (≥500 bp) |
|----------------------|---------|-------------|----------|-----------------------|------|------------|----------------------|-----------------|--------------------------------------|-----------------|-----------|------------------|----------------------|----------------------|
| NAFTEC00062 SL_39_S118 | Human (stool) | Jaffna | October 3, 2016 | 1541 | Corvalis | Corvalis or Chailey | gyrS1 | | | | SMPY00000000 | 32 | 4855244 |
| NAFTEC00063 SL_40_S180 | Human (blood) | Jaffna | October 13, 2016 | 11 | Enteritidis | Enteritidis | | | | IncFIB(S), IncFII(S) | SMZ00000000 | 25 | 4705099 |
| NAFTEC00064 SL_41_S215 | Human (blood) | Jaffna | October 5, 2016 | 11 | Enteritidis | Enteritidis | | | | IncFIB(S), IncFII(S) | SMQ00000000 | 26 | 4705085 |
| NAFTEC00065 SL_42_S216 | Human (blood) | Jaffna | October 5, 2016 | 3771 | Weltevreden | Weltevreden | D87G | | IncFIB(S), IncFII(S) | SMQ00000000 | 62 | 4916302 |
| NAFTEC00066 SL_43_S218 | Human (blood) | Colombo | October 15, 2016 | 11 | Enteritidis | Enteritidis | | | | IncFIB(S), IncFII(S) | SMQ00000000 | 24 | 4707867 |
| NAFTEC00067 SL_44_S232 | Human (stool) | Colombo | October 13, 2016 | 11 | Enteritidis | Enteritidis | | | | IncFIB(S), IncFII(S) | SMQ00000000 | 27 | 4738730 |
| NAFTEC00069 SL_46_S250 | Human (blood) | Colombo | October 9, 2016 | 11 | Enteritidis | Enteritidis | D87Y | | IncFIB(S), IncFII(S) | SMQ00000000 | 25 | 4646372 |
| NAFTEC00070 SL_47_S271 | Human (blood) | Galle | October 9, 2016 | 11 | Enteritidis | Enteritidis | D87Y | | IncFIB(S), IncFII(S) | SMQ00000000 | 23 | 4704679 |
| NAFTEC00071 SL_48_S290 | Human (stool) | Ragama | October 24, 2016 | 43 | Paratyphi B var java | | | | Paratyphi B | SMQ00000000 | 24 | 4729267 |
| NAFTEC00073 SL_50_S294 | Human (blood) | Colombo | October 24, 2016 | 11 | Enteritidis | Enteritidis | | | | IncFIB(S), IncFII(S) | SMQ00000000 | 37 | 4753025 |
| NAFTEC00074 SL_51_S295 | Human (blood) | Colombo | October 24, 2016 | 11 | Enteritidis | Enteritidis | IncFIB(S), IncFII(S) | | | SMQ00000000 | 25 | 4729886 |
| NAFTEC00076 SL_52_S304 | Human (blood) | Ragama | November | 11 | Enteritidis | Enteritidis | | | | IncFIB(S), IncFII(S) | SMQ00000000 | 24 | 4729267 |
| NAFTEC00077 SL_53_S307 | Human (blood) | Colombo | November 7, 2016 | 287 | Mountpleasant | Mountpleasant | fosA7 | | | | SMQM00000000 | 30 | 4645898 |
| NAFTEC00078 SL_55_S309 | Human (blood) | Colombo | November 10, 2016 | 43 | Paratyphi B var java | Paratyphi B | | | | | SMQN00000000 | 38 | 4753099 |
| NAFTEC00079 SL_57_S315 | Human (blood) | Kandy | November 24, 2016 | 11 | Enteritidis | Enteritidis | D87G | | IncFIB(S), IncFII(S) | [F:A16:B22] | SMQ00000000 | 24 | 4707889 |
| NAFTEC00080 SL_58_S327 | Human (stool) | Jaffna | November 29, 2016 | 3771 | Weltevreden | Weltevreden | IncFIB(S) | | [S1:A:-:B-] | SMQ00000000 | 68 | 4932856 |
| NAFTEC00081 SL_59_S329 | Human (blood) | Colombo | November 30, 2016 | 3771 | Weltevreden | Weltevreden | IncFIB(S) | | [F:A16:B] | SMQ00000000 | 68 | 4916026 |
| NAFTEC00082 SL_61_S333 | Human (blood) | Colombo | December | 11 | Enteritidis | Enteritidis | IncFIB(S), IncFII(S) | | [F:A16:B22] | SMQ00000000 | 26 | 4705042 |
| NAFTEC00083 SL_62_S353 | Human (blood) | Colombo | December | 1541 | Corvalis | Corvalis or Chailey | | | | | SMQT00000000 | 31 | 4894143 |
| NAFTEC00084 SL_63_S360 | Human (blood) | Ragama | December | 1602 | Mbundaka | Mbundaka | | | | | SMQU00000000 | 36 | 4722738 |
| Laboratory identifier | Isolate ID | Sample type | Location | MLST | Serotyping | Predicted serotype(s) | Resistance genes | Plasmid replicons | pMLST | GenBank accession | No. of Contigs (≥500 bp) | Total length (≥500 bp) |
|----------------------|------------|-------------|----------|------|------------|----------------------|------------------|-------------------|--------|-----------------|------------------------|-------------------------|
| 61 NAFTEC00085 SL_64_D94 Human (stool) | Colombo | December 30, 2016 | 2063 Chester Chester | aph(6)-Id, blaTEM-1B, qnrS1, sul3, dfrA14 | IncX1 | SMQV00000000 | 33 | 4586888 |
| 62 NAFTEC00086 SL_65_D912 Human (stool) | Awissawella | December 30, 2016 | 2063 Chester Chester | aph(6)-Id, blaTEM-1B, qnrS1, sul3, dfrA14 | IncX1 | SMQW00000000 | 35 | 4587278 |
| 63 NAFTEC00087 SL_66_D001 Human (stool) | Colombo | January 5, 2017 | 29 Stanley Stanley | E466D | IncFIB(S), IncFH(S) | [F-:A16:B22] | SMQX00000000 | 24 | 4633473 |
| 64 NAFTEC00088 SL_67_S04 Human (stool) | Peradeniya | January 9, 2017 | 36 Typhimurium Typhimurium | IncFIB(S), IncFH(S) | SMQY00000000 | 26 | 4706648 |
| 66 NAFTEC00090 SL_69_S11 Human (stool) | Jaffna | January 9, 2017 | 5309 Vancouver Vancouver | IncFIB(S), IncFH(S) | SMQW00000000 | 26 | 4723314 |
| 67 NAFTEC00091 SL_70_W02 Human (stool) | Galle | February 13, 2017 | 11 Enteritidis Enteritidis | IncFIB(S), IncFH(S) | SMRE00000000 | 25 | 4705684 |
| 68 NAFTEC00092 SL_71_W03 Human (stool) | Galle | February 13, 2017 | 11 Enteritidis Enteritidis | IncFIB(S), IncFH(S) | SMRE00000000 | 25 | 4705684 |
| 69 NAFTEC00093 SL_72_S24 Human (stool) | Badulla | February 13, 2017 | 11 Enteritidis Enteritidis | IncFIB(S), IncFH(S) | SMRE00000000 | 25 | 4705684 |
| 70 NAFTEC00094 SL_73_S41 Human (stool) | Galle | February 25, 2017 | 43 Paratyphi B Paratyphi B | IncFIB(S), IncFH(S) | SMRF00000000 | 38 | 4753322 |
| 71 NAFTEC00095 SL_74_D64 Human (stool) | Kandy | February 13, 2017 | 43 Paratyphi B Paratyphi B | IncFIB(S), IncFH(S) | SMRG00000000 | 37 | 4753109 |
| 72 NAFTEC00096 SL_75_D66 Human (stool) | Colombo | February 13, 2017 | 43 Paratyphi B Paratyphi B | IncFIB(S), IncFH(S) | SMRG00000000 | 37 | 4753109 |
| 75 NAFTEC00099 SL_78_S58 Human (stool) | Colombo | February 13, 2017 | 11 Enteritidis Enteritidis | IncFIB(S), IncFH(S) | SMRG00000000 | 37 | 4753109 |
| 76 NAFTEC00100 SL_79_S78 Human (stool) | Kandy | February 27, 2017 | 11 Enteritidis Enteritidis | IncFIB(S), IncFH(S) | SMRG00000000 | 37 | 4753109 |
| 77 NAFTEC00101 SL_80_S79 Human (stool) | Kandy | February 27, 2017 | 11 Enteritidis Enteritidis | IncFIB(S), IncFH(S) | SMRG00000000 | 37 | 4753109 |
| 79 NAFTEC00103 SL_82_D95 Human (stool) | Awissawella | February 27, 2017 | 11 Enteritidis Enteritidis | IncFIB(S), IncFH(S) | SMRG00000000 | 37 | 4753109 |

*aUsing MLST v2.0.
*bPerformed serological identification according to Kauffman–White scheme.
*cUsing SeqSero v1.0.
*dUsing ResFinder v2.3 (minimum percentage identity of 90% and minimum length of 60%).
*eUsing PlasmidFinder 1.3 (minimum percentage identity of 95% and minimum length of 60%).
*fUsing pMLST v2.0.
*gUsing Quast v4.6.3.
*hIsolate with new ST being assigned by EnteroBase.
MLST, Multilocus sequence typing; ST, sequence type.
and human strains. Since it is a retrospective study, it is limited by the absence of adequate (≥50) and regular sampling at indicated cities/locations for a longer period of time (≥21 year), within the same time period for both chicken meat and human samples. Hence, it is not possible to draw any conclusion about the correlation between the clinical isolates and the chicken reservoir. Nevertheless, the generated data do provide very rough details about Salmonella serotypes and resistance traits in chicken meat and human in studied cites, and contribute to the design of sampling framework for prospective Salmonella and AMR surveillance.

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Authors’ Contributions

M.Y.F.T. performed bioinformatics analysis, analyzed and interpreted the data, and drafted and coordinated the article writing. S.P. analyzed and interpreted the data, and contributed to article writing. L.C. performed bioinformatics analysis. U.W. did meat sampling and performed bacterial isolation and identification. N.S., K.D.K.W., and L.R.D.C.L. worked on the human isolates. K.L.G.S. performed DNA extraction. R.S.H., M.T.T., and J.S. contributed to article writing and provided scientific advice.

Disclosure Statement

No competing financial interests exist.

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