An ongoing outbreak of multidrug-resistant _Salmonella enterica_ serovar _Anatum_ began in Taiwan in 2015. Pork and poultry were identified as vehicles for transmission. Contaminated meat contributed to the high rate of infections among children. Nearly identical _Salmonella Anatum_ strains have been identified in the United Kingdom, the United States, and the Philippines.

Non-typhoidal _Salmonella_ (NTS) is a major cause for foodborne diseases worldwide. In Taiwan, the ambient climate and flourishing pig-raising industry makes NTS infections rampant. As in other countries, salmonellosis was primarily caused by _Salmonella enterica_ serovars Enteritidis and Typhimurium in Taiwan (1), but rare serovars such as _Salmonella_ Goldcoast have appeared in recent years (2). Recommended antimicrobial treatment options for salmonellosis include fluoroquinolones and extended-spectrum cephalosporins (1). However, resistance to these antibiotics has been emerging in many countries, leading to increased disease prevalence, disease severity, and death and the requirement of last-line antimicrobial drugs (e.g., carbapenems) (3–5).

Since 2015, northern Taiwan has seen an increase in _Salmonella_ infections, caused by previously rare _Salmonella Anatum_. The infections were also reported in central Taiwan, indicating that this outbreak had already prevailed throughout the entire island (6). Co-resistance to ceftriaxone and ciprofloxacin are the main feature of the outbreak clone. Evidence from epidemiologic, laboratory, and supply-chain investigations identified raw pork and poultry as the vehicle for spread of this strain. More important, genomic comparisons against the global public database indicated that this clone has appeared in Europe, Asia, and America. Given the increasing globalization of foodstuffs, these findings prompt an urgent global sharing of whole-genome sequencing (WGS) data to facilitate disease surveillance and early recognition of international foodborne outbreaks (7,8).

### The Study
Chang Gung Memorial Hospital is a main referral hospital for cities in northern Taiwan, including Taipei, New Taipei, and Taoyuan. The population in this region is ≈7 million. In 2012, the hospital’s clinical microbiology laboratory launched a program to monitor the NTS serovars causing human infections. All _Salmonella_ isolates from patients were collected and serotyped. Before 2015, very few _Salmonella Anatum_ isolates were recovered, and most were susceptible to antimicrobial agents. Since then, an increase has been observed, peaking in 2017 (Figure 1, panel A). As of June 2019, a total of 319 nonrepetitive isolates have been identified; of these, 197 (61.8%) isolates were ceftriaxone-resistant (MIC ≥2 µg/mL), 301 (94.4%) were ciprofloxacin-resistant (MIC ≥0.12 µg/mL), and 197 (61.8%) were resistant to both. In addition, 292 (91.5%) isolates were resistant to chloramphenic, and 295 (92.5%) were resistant to trimethoprim/
sulfamethoxazole. A positive correlation was found between higher temperatures and the infections ($r = 0.4; p<0.05$) (Figure 1, panel B); however, no notable effects on Salmonella. Anatum infections have been associated with precipitation or humidity ($r<0.3; p>0.05$).

Detailed methods are described in the Appendix (https://wwwnc.cdc.gov/EID/article/26/12/20-0147-App1.pdf). We first reviewed the clinical and laboratory characteristics of 278 patients from 2015–2018. Most patients had acute gastroenteritis, whereas a few (14/278, 5%) had invasive diseases, such as bacteremia and sepsis. In terms of age distribution, the highest number of cases were in young children (Figure 1, panel C). Pediatric patients (n = 169) had significantly higher rates than adult patients (n = 109) for hospitalization (79.2% vs. 55.0%; $p<0.05$), diarrhea (89.9% vs. 68.8%; $p<0.05$), and fever (89.2% vs. 58.1%; $p<0.05$).

Multilocus sequence typing indicated that the entire collection of clinical Salmonella Anatum isolates belonged to sequence type 64. We randomly selected 54 clinical isolates for WGS (Appendix Table 1). Both core genome multilocus sequence typing and whole-genome single-nucleotide polymorphism analyses, performed by using the BacWGSTdb database (9), further divided these isolates into 3 clades (Figure 2, panel A, B). Clades I and II were more closely related to each other; their most recent common ancestor occurred >21 years ago.
Clade III was more distantly connected to these 2 clades. Typing based on PCR assay was performed on the unsequenced isolates. Clade I accounted for 95.6% (305/319) of all isolates, suggesting it was the cause of the outbreak. The isolates resistant to ceftriaxone, ciprofloxacin, or both clustered within clade I, whereas the isolates of clades II and III were more susceptible. Most of the clade I isolates harbored a 90-kb IncA/C plasmid carrying \textit{bla\textsubscript{DHA-1}} (encoding a class C \(\beta\)-lactamase) and \textit{qnrB} (confering resistance to quinolones). A conjugation assay demonstrated that this plasmid conferred ceftriaxone and ciprofloxacin resistance. In addition, 31 (9.7%) clinical isolates carried \textit{bla\textsubscript{CMY-2}}, which was located within a >100-kb IncI1 plasmid and also encoded a class C \(\beta\)-lactamase. These 31 isolates carried \textit{bla\textsubscript{DHA-1}} simultaneously. In 11 of them, the \textit{bla\textsubscript{DHA-1}}-carrying and \textit{bla\textsubscript{CMY-2}}-carrying plasmids were fused into 1 large plasmid (Figure 2, panel C).

By comparing these findings against sequences in GenBank, we found nearly identical genomic sequences for isolates in the United Kingdom, the

\textbf{Figure 2.} Genomic analysis of the outbreak caused by \textit{Salmonella enterica} serotype Anatum, Taiwan. A) Dated phylogeny for \textit{Salmonella} Anatum clinical isolates and food and environmental isolates. All isolates were divided into 3 clades, shown at right. The nodes’ colors represent the geo source; nodes with black rings were from meat or the environment, and the remainder were derived from the patients. The right heatmap represents the presence (in black) or absence (in gray) of key antimicrobial-resistance genes (1, \textit{bla\textsubscript{DHA-1}}; 2, \textit{qnrB4}; 3, \textit{bla\textsubscript{CMY-2}}). B) Minimal spanning tree based on alleles identified through core genome multilocus sequence typing. Dots with black circles represent food isolates; the others are clinical isolates. The collection date for the 6 US isolates in panel B was missing in GenBank and therefore not included in panel A. Scale bar indicates 5 single nucleotide polymorphisms. C) Gene structure of multidrug-resistant plasmids in \textit{Salmonella} Anatum in Taiwan compared with international isolates. Two types of plasmids were identified in the clade I \textit{Salmonella} Anatum isolates in Taiwan. One carried \textit{bla\textsubscript{CMY-2}}, with its structure being shown by pSal-5091\_CMY. A similar plasmid, pCMY2 (GenBank accession no. LC019731.1), is shown. The other carried \textit{bla\textsubscript{DHA-1}}; its structure is shown by pSal-5091\_DHA. International isolates shown in the figure, whose genomes also were downloaded from GenBank (Appendix Table 1, https://wwwnc.cdc.gov/EID/article/26/12/20-0147-App1.pdf), possess very similar plasmids. In certain isolates, the 2 plasmids can integrate into 1 large plasmid, with its structure shown by pSal-3973\_DHA\_CMY. Red genes represent antimicrobial-resistance genes; blue genes represent transposase/integrase genes; and yellow genes represent Inc-determinant genes.
United States, and the Philippines. The collection time for these isolates also occurred during 2015–2019, which nearly coincided with the outbreak in Taiwan. These international Salmonella Anatum isolates also carried the 90-kb IncA/C plasmid (Figure 2, panel A, C); therefore, they were likely ceftriaxone- and ciprofloxacin-resistant concomitantly. The only distinction of these international isolates was their lack of the bla\textsubscript{CMY-2}–carrying plasmid. Accordingly, we speculated that the Salmonella Anatum clone had arrived in Taiwan through food trade and later acquired the bla\textsubscript{CMY-2}–carrying plasmid.

To trace the source of Salmonella Anatum, we investigated food samples from supermarkets and traditional markets of 8 districts with high density of Salmonella patients in New Taipei City and Taoyuan City, Taiwan (Appendix Figure 1). A total of 11 Salmonella Anatum isolates were collected from pork, 4 from poultry, and 1 from beef in these regions (Appendix Table 2, Figure 1). WGS showed that they all belonged to clades I and II, providing strong evidence that raw meats were the outbreak vehicle. All 16 isolates harbored the bla\textsubscript{DHA-1}–carrying IncA/C plasmid. Other Salmonella serovars also were detected in this investigation. The overall Salmonella isolation rate from retail meats was significantly higher in traditional markets than in the supermarkets (p<0.001) (Appendix Table 3). In Taiwan, pork in the supermarkets is usually provided through the cold transportation chain, whereas for traditional markets pork is usually provided through the traditional chain, with notable differences. Temperatures were much lower in the cutting factory and butcher shop in the cold chain than in the traditional chain (Appendix Figure 2). Furthermore, pork was wrapped by plastic tissue and bags in the cold chain, but the traditional chain did not do any wrapping or packaging during transportation.

To clarify the contradictory findings that most infections occurred in young children even though pork is not a major food for infants, we conducted a questionnaire survey among parents of 20 infants (<1 year of age) with NTS infections and 80 parents of infants without (controls) (Appendix). Parents of the infected infants more often touched, rinsed, and cooked meat before feeding other foods to their infants (Appendix Table 4). Moreover, these parents were more willing to purchase meat from traditional markets rather than supermarkets. A possibility is that they bought meat from the traditional markets, then their frequent rinsing flushed the Salmonella on the surface of the meats, cutting boards and knives, and sinks, and finally onto fresh vegetables, fruit, and other ready-to-eat foods that were cross-contaminated and reached the infants through parents or other caregivers. This transmission mode is of particular importance in infants and has already been reported for other bacterial pathogens such as Yersinia enterocolitica (I0).

Conclusions

Our study sought to describe an outbreak in Taiwan caused by a multidrug-resistant Salmonella Anatum clone. The questionnaire and supply-chain investigations we conducted found that the infection cases were closely associated with improper packaging during transportation and unhygienic food handling in the customers’ kitchen. The high similarity of genomic sequence between the Taiwan isolates and international isolates indicates the global dissemination of this clone and highlights the public health value of multicountry sharing of epidemiologic, trace-back, microbiologic, genomic, and food trade data.

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Characterization and Source Investigation of Multidrug-Resistant *Salmonella* Anatum from a Sustained Outbreak, Taiwan

Appendix

Supplementary Methods

Patients and Setting

Chang Gung Memorial Hospital (CGMH) is a main referral hospital for cities in northern Taiwan, including Taipei, New Taipei, and Taoyuan. The population in this region is approximately seven million. The Clinical Microbiology Laboratory has launched a program to monitor the serovars of NTS causing human infections since 2012. All *Salmonella* isolates from patients were collected and serotyped. Antimicrobial susceptibility testing was performed using the disc diffusion method specified in the Clinical and Laboratory Standards Institute (CLSI) guidelines (1). *S.* Anatum is a relatively uncommonly recorded serovar for human infections. Prior to 2015, very few *S.* Anatum isolate was recovered and most of the isolates were susceptible to antimicrobial agents. However, since 2015, culture-confirmed infections caused by *S.* Anatum has been increasing (Figure 1, https://wwwnc.cdc.gov/EID/article/26/12/20-0147-F1.htm). A review on the clinical manifestations of the patients with *S.* Anatum infection from 2015 to 2018 was carried out. This study was approved by the Institutional Review Board of CGMH (201601804B0 and 201702155B0).

Serogrouping and serotyping was conducted as described previously (2). The MIC of CIP and CRO on these isolates was determined by E-test and interpreted according to the recommendations provided by CLSI (1).

To trace the source of *S.* Anatum, we investigated food samples from supermarkets and traditional markets of eight districts with high density of *Salmonella* patients in New Taipei City, and Taoyuan City in Taiwan (Appendix Figure 1). All the *Salmonella* isolates derived from food
samples were further examined for their serogroups, serovars, and their antimicrobial susceptibility to CRO and CIP.

Meteorological data, including temperature, humidity and precipitation in Northern Taiwan, were collected from the Taiwan Central Weather Bureau, which is available at: https://e-service.cwb.gov.tw/HistoryDataQuery/index.jsp. The correlation and lag effect of case number and temperature were analyzed using bivariate correlation and linear regression softwares in IBM SPSS Statistics version 20.0 (IBM Corp., Armonk, NY), and significance was set at p < 0.05.

**Meat Processing and Transport**

To clarify the discrepancy of *Salmonella* detection rate between different markets, and to further investigate suspicious contamination nodes during meat processing and transportation, we designed an experiment to contrast cold chain with traditional chain transportation of the meat. Four nodes at each of the transportation lines were investigated: slaughter houses (samples obtained from the carcass surfaces), cutting factories and pre-cooling chambers, where the pig carcass were cut into large pieces (samples from the environmental and meat surfaces), transport vehicles (samples from the environment), and butcher shops, where the large pork chunks were cut into small pieces for consumer purchase (samples from the environment and meat surfaces). We collected carcass surface samples and environment samples from floor, hook, conveyor belt, meat grinder, basket, kitchen knife, chopping board and workers’ hands surface in slaughterhouse, cutting factory, transport vehicle and butcher shop. Each sampling surface area of the carcass and environment samples was 100 cm². In addition, each of the meat samples was collected over 25 g in cutting factory and butcher shop. Meat isolation and identification followed the method of Taiwan Food and Drug Administration. Carcass surface and environment sampling followed USDA Laboratory Guidebook (https://www.fsis.usda.gov) with a sensitivity of $1.4 \times 10^1$ CFU/100 cm². All investigated samples were collected with sterilized sponges, bags, gloves and templates (Nasco Whirl-Pak, USA).

**Whole-Genome Sequencing and Conjugation**

A total of 76 isolates were subjected to whole genome sequencing (WGS), that was performed using the Illumina Miseq platform (Illumina, CA, USA) and/or MinION Sequencer (Nanopore, Oxford, UK). The genome assembly and comparative analysis followed the methods
as described previously (2). The genomic sequences were deposited into the GenBank database, with the accession numbers being listed in Appendix Table 1. The NCBI Pathogen Detection Service (https://www.ncbi.nlm.nih.gov/pathogens) was searched for S. Anatum genomes that were highly similar to the genome sequences collected in Taiwan. Multilocus sequence typing was performed on all S. Anatum isolates (2,3).

To investigate the transferability of the resistance plasmids identified in the genome sequencing, we carried out a conjugation assay using *E. coli* J53 (a sodium-azide-resistant strain) as the recipient and outbreak S. Anatum isolates as the donor (Sal-4377 and Sal-4162). The conjugation assay was conducted following the protocol described in a previous study (2).

**Questionnaire Investigation**

Caregivers of children with culture-confirmed S. Anatum infection were invited to complete a questionnaire. The questionnaire is designed based on a WHO protocol (https://www.who.int/immunization/diseases/rotavirus/generic_protocols/en/). The total number of the questionnaire completed was 100, and the ratio of the patient to healthy controls was 1:4, namely 20 children in the patient group and 80 in the healthy group. The healthy children were recruited from well-baby clinics. Ages (<1y) were matched between the case and control groups. Chi-square test was used to analyze all questionnaire data using IBM SPSS Statistics version 20.0 (IBM Corp., Armonk, NY). The false-discovery rate (FDR) correction was made for multiple comparisons, with 0.1 as the significance threshold.

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### Appendix Table 1. Accession numbers of the genomic sequences sequenced and analyzed in this study

| Strain/Isolate | Collection Date | Country/Region | Source | Accession | Note                  |
|----------------|-----------------|----------------|--------|-----------|-----------------------|
| GB10           | 2019/7/3        | Taiwan         | food/environment | WHYQ000000000 | sequenced in this study |
| GC94-2         | 2019/7/3        | Taiwan         | food/environment | WHYP000000000 | sequenced in this study |
| GC66           | 2019/7/3        | Taiwan         | food/environment | WHYO000000000 | sequenced in this study |
| GC67-2         | 2019/7/3        | Taiwan         | food/environment | WHYN000000000 | sequenced in this study |
| GC68-1         | 2019/7/3        | Taiwan         | food/environment | WHYM000000000 | sequenced in this study |
| M-2589         | 2018/8/21       | Taiwan         | food/environment | WHYL000000000 | sequenced in this study |
| M-2592         | 2018/8/21       | Taiwan         | food/environment | WHYK000000000 | sequenced in this study |
| M-3471         | 2018/3/31       | Taiwan         | food/environment | CP045458-CP045460 | sequenced in this study |
| M-3851         | 2017/6/15       | Taiwan         | food/environment | CP045461-CP045463 | sequenced in this study |
| M-3853         | 2017/6/15       | Taiwan         | food/environment | WHYJ000000000 | sequenced in this study |
| M-4763         | 2019/7/3        | Taiwan         | food/environment | WHYI000000000 | sequenced in this study |
| M-4947         | 2018/10/3       | Taiwan         | food/environment | WHYH000000000 | sequenced in this study |
| M-4949         | 2018/1/11       | Taiwan         | food/environment | WHYG000000000 | sequenced in this study |
| M-5351         | 2017/8/3        | Taiwan         | food/environment | WHYF000000000 | sequenced in this study |
| M-5360         | 2017/8/3        | Taiwan         | food/environment | CP045509-CP045512 | sequenced in this study |
| M-5365         | 2017/8/3        | Taiwan         | food/environment | WHYE000000000 | sequenced in this study |
| M-6525         | 2019/7/25       | Taiwan         | food/environment | WHYD000000000 | sequenced in this study |
| M-6697         | 2018/4/16       | Taiwan         | food/environment | WHYC000000000 | sequenced in this study |
| M-6699         | 2018/4/16       | Taiwan         | food/environment | WHYB000000000 | sequenced in this study |
| M-7537         | 2018/8/2        | Taiwan         | food/environment | WHYA000000000 | sequenced in this study |
| M-9196         | 2017/8/18       | Taiwan         | food/environment | WHXK000000000 | sequenced in this study |
| M-9750         | 2019/8/13       | Taiwan         | food/environment | WHXY000000000 | sequenced in this study |
| Sal-1135       | 2012/6/15       | Taiwan         | human        | CP045456   | sequenced in this study |
| Sal-2097       | 2013/11/1       | Taiwan         | human        | CP045456   | sequenced in this study |
| Sal-2955       | 2015/6/13       | Taiwan         | human        | WHXX000000000 | sequenced in this study |
| Sal-3348       | 2015/12/5       | Taiwan         | human        | WHXW000000000 | sequenced in this study |
| Sal-3381       | 2015/12/19      | Taiwan         | human        | WHXV000000000 | sequenced in this study |
| Sal-3386       | 2015/12/21      | Taiwan         | human        | WHXU000000000 | sequenced in this study |
| Sal-3389       | 2015/12/21      | Taiwan         | human        | WHXT000000000 | sequenced in this study |
| Sal-3343       | 2015/12/3       | Taiwan         | human        | WHXS000000000 | sequenced in this study |
| Sal-3660       | 2016/6/29       | Taiwan         | human        | WHXR000000000 | sequenced in this study |
| Sal-3805       | 2016/7/23       | Taiwan         | human        | WHXQ000000000 | sequenced in this study |
| Sal-3824       | 2016/7/28       | Taiwan         | human        | WHXP000000000 | sequenced in this study |
| Sal-3892       | 2016/8/17       | Taiwan         | human        | WHXO000000000 | sequenced in this study |
| Sal-3897       | 2016/8/20       | Taiwan         | human        | WHXN000000000 | sequenced in this study |
| Sal-3930       | 2016/9/1        | Taiwan         | human        | WHXM000000000 | sequenced in this study |
| Sal-3944       | 2016/9/5        | Taiwan         | human        | WHXL000000000 | sequenced in this study |
| Sal-3948       | 2016/8/6        | Taiwan         | human        | CP045513-CP045514 | sequenced in this study |
| Sal-3973       | 2016/9/15       | Taiwan         | human        | CP045466-CP045467 | sequenced in this study |
| Sal-3985       | 2016/9/10       | Taiwan         | human        | WHXK000000000 | sequenced in this study |
| Sal-3991       | 2016/9/19       | Taiwan         | human        | WHXJ000000000 | sequenced in this study |
| Sal-3993       | 2016/9/11       | Taiwan         | human        | WHXI000000000 | sequenced in this study |
| Sal-3997       | 2016/9/13       | Taiwan         | human        | WHXH000000000 | sequenced in this study |
| Sal-4162       | 2016/10/25      | Taiwan         | human        | WHXG000000000 | sequenced in this study |
| Sal-4179       | 2016/10/20      | Taiwan         | human        | WHXF000000000 | sequenced in this study |
| Strain/Isolate | Collection Date | Country/Region | Source | Accession | Note |
|---------------|-----------------|----------------|--------|-----------|------|
| Sal-4221      | 2016/11/23      | Taiwan         | human  | WHXE00000000 | sequenced in this study |
| Sal-4295      | 2017/1/11       | Taiwan         | human  | CP045515   | sequenced in this study |
| Sal-4377      | 2017/3/26       | Taiwan         | human  | WHXD00000000 | sequenced in this study |
| Sal-4420      | 2017/5/5        | Taiwan         | human  | WHXC00000000 | sequenced in this study |
| Sal-4478      | 2017/5/22       | Taiwan         | human  | WHXB00000000 | sequenced in this study |
| Sal-4494      | 2017/5/31       | Taiwan         | human  | WHXA00000000 | sequenced in this study |
| Sal-4499      | 2017/6/2        | Taiwan         | human  | WHW200000000 | sequenced in this study |
| Sal-4518      | 2017/6/4        | Taiwan         | human  | WHWX00000000 | sequenced in this study |
| Sal-4550      | 2017/6/16       | Taiwan         | human  | WHWY00000000 | sequenced in this study |
| Sal-4567      | 2017/6/21       | Taiwan         | human  | WHWW00000000 | sequenced in this study |
| Sal-4583      | 2017/6/28       | Taiwan         | human  | WHWV00000000 | sequenced in this study |
| Sal-4627      | 2017/7/14       | Taiwan         | human  | WHWU00000000 | sequenced in this study |
| Sal-4698      | 2017/8/3        | Taiwan         | human  | WHWT00000000 | sequenced in this study |
| Sal-4737      | 2017/8/17       | Taiwan         | human  | CP045516-CP045517 | sequenced in this study |
| Sal-4762      | 2017/8/21       | Taiwan         | human  | WHWS00000000 | sequenced in this study |
| Sal-4873      | 2017/9/15       | Taiwan         | human  | WHWR00000000 | sequenced in this study |
| Sal-4995      | 2017/10/16      | Taiwan         | human  | WHWQ00000000 | sequenced in this study |
| Sal-5087      | 2017/11/16      | Taiwan         | human  | WHWP00000000 | sequenced in this study |
| Sal-5091      | 2017/11/24      | Taiwan         | human  | CP045518-CP045521 | sequenced in this study |
| Sal-5131      | 2017/12/6       | Taiwan         | human  | WHWO00000000 | sequenced in this study |
| Sal-5147      | 2017/12/14      | Taiwan         | human  | WHWN00000000 | sequenced in this study |
| Sal-5186      | 2018/1/10       | Taiwan         | human  | WHWM00000000 | sequenced in this study |
| Sal-5191      | 2018/1/10       | Taiwan         | human  | WHWL00000000 | sequenced in this study |
| Sal-5196      | 2018/1/19       | Taiwan         | human  | WHWK00000000 | sequenced in this study |
| Sal-5200      | 2018/1/22       | Taiwan         | human  | WHWJ00000000 | sequenced in this study |
| Sal-5217      | 2018/2/22       | Taiwan         | human  | WHWI00000000 | sequenced in this study |
| Sal-5226      | 2018/2/27       | Taiwan         | human  | WHWH00000000 | sequenced in this study |
| Sal-5240      | 2018/3/16       | Taiwan         | human  | WHWG00000000 | sequenced in this study |
| Sal-5242      | 2018/3/19       | Taiwan         | human  | WHWF00000000 | sequenced in this study |
| Sal-5328      | 2018/5/21       | Taiwan         | human  | WHWE00000000 | sequenced in this study |
| Sal-5379      | 2018/6/7        | Taiwan         | human  | WHWD00000000 | sequenced in this study |
| 795421        | Aug. 2019       | United Kingdom | human  | AAKCLH01   | downloaded from public database |
| 300980        | Sep. 2016       | United Kingdom | human  | AAHNES01   | downloaded from public database |
| PNUAS010879   | Missing         | USA            | human  | AAHES01    | downloaded from public database |
| PNUAS011492   | Missing         | USA            | human  | AAES01     | downloaded from public database |
| PNUAS038936   | Missing         | USA            | human  | AAIC01     | downloaded from public database |
| PNUAS051059   | Missing         | USA            | human  | AADNYC01   | downloaded from public database |
| PNUAS051057   | Missing         | USA            | human  | AAADV01    | downloaded from public database |
| PNUAS068759   | Missing         | USA            | human  | AADTUF01   | downloaded from public database |
| FDA00008841   | 2015/2/20       | Philippines    | food/environment | AAGLBT01 | downloaded from public database |
| 227024        | Feb. 2016       | United Kingdom | human  | AAHNHE01   | downloaded from public database |
**Appendix Table 2.** *Salmonella* serovars isolated from 438 food samples obtained from traditional markets and supermarkets in northern Taiwan in 2017–2019.

| Food     | Positive Rate | Serotype (n)                                                                 |
|----------|---------------|-------------------------------------------------------------------------------|
| Raw Pork | 50.7% (75/148) | S. Agona (10); S. Anatum (11); S. Corvallis (1); S. Derby (16); S. Give (5); S. Goldcoast (1); S. Kentucky (3); S. Livingstone (3); S. London (8); S. Mbondaka (2); S. Muenster (4); S. Newport (2); S. Potsdam (1); S. Rissen (1); S. Typhimurium (3); S. Weltevreden (4) |
| Raw Chicken | 36.6% (34/93) | S. Albany (6); S. Anatum (4); S. Brancaster (3); S. Derby (1); S. Enteritidis (4); S. Goldcoast (1); S. Kentucky (6); S. Livingstone (2); S. Muenster (2); S. Schwarzengrund (2); S. Thompson (1); S. Typhimurium (2) |
| Raw Beef  | 3.7% (1/27)   | S. Anatum (1)                                                                 |
| Raw Duck  | 100% (1/1)    | S. Albany (1)                                                                 |
| Egg      | 0% (0/46)     | ND                                                                            |
| Vegetable| 5.2% (5/96)   | S. Albany (1); S. Derby (2); S. Kaitaan (1); S. Zigong (1)                    |
| Seafood  | 6.7% (1/15)   | S. Albany (1)                                                                 |
| Fruit    | 0% (0/12)     | ND                                                                            |

ND, not detected.

**Appendix Table 3.** *Salmonella* isolation rate between supermarkets and traditional markets in northern Taiwan in 2017–2019*

| Sample | Source (n) | Positive (n) | Negative (n) | Positive Rate (%) | P-value |
|--------|------------|--------------|--------------|--------------------|---------|
| Pork   | Supermarket (36) | 4            | 32           | 11.1               | <0.001  |
|        | Traditional Market (112) | 71           | 41           | 63.4               |         |
| Chicken| Supermarket (36)  | 7            | 29           | 19.4               | 0.006   |
|        | Traditional Market (57) | 27           | 30           | 47.4               |         |
| Duck   | Supermarket (0)   | ND           | ND           | ND                 | NA      |
|        | Traditional Market (1) | 1            | 0            | 100                |         |
| Beef   | Supermarket (12)  | 0            | 12           | 0                  | NA      |
|        | Traditional Market (15) | 1            | 14           | 0                  |         |
| Seafood| Supermarket (8)   | 0            | 8            | 0                  | 0.268   |
|        | Traditional Market (7) | 1            | 6            | 14.3               |         |
| Egg    | Supermarket (11)  | 0            | 11           | 0                  | NA      |
|        | Traditional Market (35) | 0            | 35           | 0                  |         |
| Vegetable| Supermarket (37)  | 0            | 37           | 0                  | 0.069   |
|        | Traditional Market (59) | 5            | 54           | 8.5                |         |
| Fruit  | Supermarket (4)   | 0            | 4            | 0                  | NA      |
|        | Traditional Market (8) | 0            | 8            | 0                  |         |

*ND, not detected; NA, not applicable.
### Appendix Table 4. Case-control survey for Salmonella-infected infants under 1 y of age in Chang Gung Memorial Hospital, Taiwan in 2019.

| Items | Salmonella (n = 20) | Healthy (n = 80) | Odds Ratio | 95% Low | 95% High | p-value | FDR* |
|-------|---------------------|------------------|------------|---------|----------|---------|------|
| **Contact** | | | | | | | |
| Share toys with other people | 4 | 20% | 13 | 16% | 1.288 | 0.371 | 4.481 | 0.69 | 0.794 |
| Share pillow, comforter or mattress with other people | 10 | 50% | 35 | 44% | 1.286 | 0.482 | 3.431 | 0.615 | 0.755 |
| **Surroundings** | | | | | | | |
| Purchase bulk eggs without washing | 11 | 55% | 19 | 24% | 3.924 | 1.414 | 10.886 | 0.006 | 0.081 |
| Traditional market as the major pork shopping place | 11 | 55% | 20 | 25% | 3.667 | 1.328 | 10.127 | 0.009 | 0.081 |
| Home cooking/Vegetable | 18 | 90% | 59 | 74% | 3.203 | 0.684 | 14.994 | 0.122 | 0.302 |
| Home cooking/Rice, noodle, other grains | 18 | 90% | 61 | 76% | 2.803 | 0.596 | 13.194 | 0.177 | 0.376 |
| Home cooking/Pork | 14 | 70% | 38 | 48% | 2.579 | 0.900 | 7.386 | 0.072 | 0.249 |
| Cook raw food and delicatessen with the same chop board | 10 | 50% | 23 | 29% | 2.478 | 0.910 | 6.746 | 0.071 | 0.249 |
| Main caregiver are grandparents or other elders | 8 | 40% | 17 | 21% | 2.471 | 0.871 | 7.009 | 0.083 | 0.249 |
| Traditional market as the major egg shopping place | 8 | 40% | 20 | 25% | 2.000 | 0.716 | 5.590 | 0.181 | 0.376 |
| Home cooking/Eggs | 13 | 65% | 46 | 58% | 1.373 | 0.495 | 3.807 | 0.542 | 0.752 |
| **Diet** | | | | | | | |
| Rinse or wash raw meat before cooking | 18 | 90% | 50 | 63% | 5.400 | 1.170 | 24.923 | 0.018 | 0.122 |
| Process raw meat before feeding infants | 10 | 50% | 15 | 19% | 4.333 | 1.530 | 12.271 | 0.004 | 0.081 |
| Eat banana | 5 | 25% | 8 | 10% | 3.000 | 0.861 | 10.452 | 0.074 | 0.249 |
| Eat pork | 6 | 30% | 15 | 19% | 1.857 | 0.613 | 5.629 | 0.269 | 0.484 |
| Eat apple | 7 | 35% | 18 | 23% | 1.855 | 0.644 | 5.343 | 0.248 | 0.478 |
| Use milk powder, rice cereal or malt extract in 30 d | 5 | 25% | 14 | 18% | 1.571 | 0.490 | 5.037 | 0.444 | 0.749 |
| Wash and air-dry scoop after feeding milk powder, rice cereal or malt extract | 11 | 55% | 37 | 46% | 1.420 | 0.531 | 3.802 | 0.484 | 0.752 |
| Use rice cereal | 4 | 20% | 12 | 15% | 1.417 | 0.404 | 4.973 | 0.585 | 0.752 |
| Infants need to be fed by caregivers | 15 | 75% | 55 | 69% | 1.364 | 0.446 | 4.167 | 0.585 | 0.752 |
| Eat shrimp | 7 | 35% | 23 | 29% | 1.334 | 0.472 | 3.770 | 0.585 | 0.752 |
| Drinking water after water filter and boiling | 5 | 25% | 17 | 21% | 1.235 | 0.393 | 3.882 | 0.717 | 0.794 |
| Frequency of handwashing before feeding infants (>75%) | 6 | 30% | 21 | 26% | 1.204 | 0.410 | 3.540 | 0.735 | 0.794 |
| **Diet/Dairy Products** | | | | | | | |
| Milk powder | 17 | 85% | 66 | 83% | 1.202 | 0.310 | 4.665 | 0.790 | 0.820 |
| Breast milk | 3 | 15% | 26 | 33% | 0.367 | 0.099 | 1.363 | 0.123 | 0.302 |
| **Purchase Source** | | | | | | | |
| Traditional markets | 14 | 70% | 34 | 43% | 3.157 | 1.100 | 9.058 | 0.028 | 0.151 |
| Supermarkets | 8 | 40% | 34 | 43% | 0.902 | 0.332 | 2.448 | 0.839 | 0.839 |

*FDR, False Discovery Rate.*
Appendix Figure 1. Food samples surveyed for *Salmonella* from supermarkets and traditional markets of eight districts with higher density of *Salmonella* infection in New Taipei City and Taoyuan City of northern Taiwan. *S. Anatum* were isolated from traditional markets and supermarkets of Linkou District (A17) and Xinzhuang District (A12), and from traditional markets of Taoyuan District (C2), Zhongli District (C7), and Guishan District (C1).
Appendix Figure 2. A comparison of *Salmonella* detection rates between the cold chain and traditional chain. A) Differences of temperature and transportation time between the two transportation chains. B) Different packaging manners employed during transportation. C) A comparison of detection rates of *Salmonella* spp. between the cold and traditional transportation chains.