Molecular Relatedness of *Salmonella enterica* Typhimurium Isolates from Feces and an Infected Surgical Wound

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**Purpose:** *Salmonella enterica* serovar Typhimurium infection is common in foodborne diseases, but its isolation from surgical incisions is rare. Our aim in this study was to trace the transmission source of a surgical incision infected with *S. Typhimurium* in a Yunnan Province hospital patient and elucidate the underlying molecular mechanisms of antibiotic resistance.

**Methods:** Primers were designed to amplify the drug-resistance genes using polymerase chain reaction (PCR). Susceptibility to antibiotics was determined using Etest strips. Macrogenic restriction profiles were analyzed using pulsed-field gel electrophoresis (PFGE) and XbaI. The two isolates were characterized using agglutination tests and multilocus sequence typing (MLST).

**Results:** MLST analysis revealed that *S. Typhimurium* isolates SM043 and SM080 belonged to the same genotype, ST34, and PFGE revealed that SM043 and SM080 had high similarity. The isolates were both resistant to third-generation cephalosporins. SM043 harbored the antibiotic resistance genes *blaCTX-M-15*, *blaTEM-1*, *qnrS-1*, *qnrB*, and *acc-3*, whereas *blaCTX-M-15*, *blaTEM-1*, *blaCMY-2*, *qnrS-1*, and *acc-3* were detected in SM080.

**Conclusion:** The surgical incision infection by *S. Typhimurium* may have been hospital-acquired. Thus, it is critical to strengthen hospital sanitation by addressing hand hygiene and sterilization of the operational environment to avoid outbreaks of nosocomial *Salmonella* infections.

**Keywords:** *Salmonella*, healthcare-associated infection, cephalosporins, antibiotic resistance, nosocomial infection

**Introduction**

*Salmonella* is a member of the *Enterobacteriaceae* family, which was originally characterized by the ability of the bacteria to metabolize citrate as a sole carbon source.¹ Members of the genus *Salmonella* cause a well-characterized spectrum of diseases in humans, which range from asymptomatic carriage to fatal typhoid fever. Third-generation cephalosporins are commonly used as first-line antibiotics to treat invasive infections or enteric fevers caused by *Salmonella* spp., owing to their pharmacodynamic properties and the low prevalence of resistance.²,³ Our previous study found that the drug-resistance rate to third-generation cephalosporins was low in the Yunnan Province.⁴ Therefore, the mechanism underlying this resistance in *Salmonella* is still unknown. However, outbreaks or cases of infection caused by *Salmonella* resistance to extended-spectrum cephalosporins have been reported around the world.⁵–⁷ Recently, the growing antibiotic resistance of *S. Typhimurium* has created new challenges in the control and prevention of potentially fatal infections.⁸
**Materials and Methods**

**Bacterial Isolates**

Two S. Typhimurium isolates, SM043 and SM080, resistant to third-generation cephalosporins were isolated from clinical specimens in 2018. SM043 was isolated from the feces of a 9-year-old patient with diarrhea and fever on October 30th 2018. On November 5th 2018, SM080 was isolated from an infected incision secretion from a 4-year-old child after surgery owing to a car accident. The two isolates were identified by the VITEK 2 system (bioMérieux, Lyon, France). Serotypes were detected using the White-Kauffmann-Le Minor (WKL) scheme based on serological detection; a diagnostic serum of *Salmonella* (Statens Serum Institute, Copenhagen, Denmark) was used to determine the serotype.

**Antimicrobial Susceptibility Testing**

Antimicrobial susceptibility was determined by the disk diffusion method and the automated VITEK 2 Compact system with Gram-negative bacteria cards (bioMérieux). The Etest method was employed to verify drug sensitivity to five antibiotics, and the results were interpreted based on CLSI guidelines. 12 Escherichia coli (ATCC 25,922) was used as the quality control strain for antimicrobial susceptibility testing.

**Detection of Drug-Resistant Genes**

Bacterial chromosomal DNA was obtained with a TIANamp Bacterial DNA Kit according to the manufacturer’s instructions (TIANGEN Biotech, Beijing, China). PCR and DNA sequence analysis were performed to confirm the presence of drug-resistance genes. The primers used in this study were described previously. 14–20 The β-lactamase genes included Ambler class A (blaCTX,M, blaTEM, blaSHV, blaKPC, and blaGES), class B (blaNDM), class C (blaCMY, blaACT, and blaDHA), and class D (blaOXA-48). Moreover, genes related to quinolone activity included qnrA, qnrB, and qnrS, and the aac gene was also detected. All amplicon sequences were compared with those in the GenBank nucleotide database (www.ncbi.nlm.nih.gov/blast/).

**Molecular Typing**

The SM043 and SM080 isolates were genotyped using multilocus sequence typing (MLST) and pulsed-field gel electrophoresis (PFGE). Seven housekeeping genes (aroC, dnaN, hemD, hisD, purE, sucA, thrA) were amplified according to the protocol described on the MLST website (https://pubmlst.org). Genotyping was carried out by referring to the molecular typing method of *Salmonella* serotype PFGE in PulsenetChina. *Salmonella* was entrapped with SeaKem Gold Agarose and digested with XbaI. The DNA fragments obtained were separated by PFGE using a Chef Mapper system (Bio-Rad Laboratories, Hercules, CA, USA). Finally, cluster analysis was performed with BioNumerics 7.6 (Applied Maths, Sint-Martens-Latem, Belgium).

**Results**

**Antimicrobial Susceptibility Testing**

The drug-resistance profiles of SM043 and SM080 were consistent, showing high resistance to 3rd- and 4th-generation cephalosporins, including ceftriaxone, cefotaxime, and ceftépime. Minimum inhibitory concentration values for aminoglycoside and tetracycline were also high. The two isolates were susceptible to β-lactam compound drugs, carbapenems, macrolides, and quinolones. These results are summarized in Table 1.

**Drug-Resistance Genes**

A total of 16 drug-resistance genes were amplified, and the two S. Typhimurium isolates carried different genes. The β-lactamase resistance genes blaTEM-1 and blaCTXM-15, quinolone resistance genes qnrB and qnrS-1, and aminoglycoside resistance gene Acc-3 were detected in SM043. The β-lactamase resistance genes blaTEM-1, blaCTXM-15, blaCMY-2, and qnrS-1 were detected in SM080. These results are summarized in Table 1.
Gene Type
MLST analysis showed that SM043 and SM080 were defined as the single sequence type ST34. The two isolates were successfully typed by PFGE and classified into the same PFGE cluster (Figure 1).

Discussion
While *S*. Typhimurium infection is common in foodborne diseases, isolating it from surgical incisions is rare. Two *S*. Typhimurium isolates were isolated from a hospital in the Yunnan province in 2018, one from an outpatient and one from an inpatient. The first isolate, SM043, was isolated from fecal specimens from a pediatric outpatient with diarrhea on October 30th, 2018. The second, SM080, was isolated from a child who developed a surgical wound infection after emergency trauma surgery on November 5th, 2018. PFGE analysis of the two *S*. Typhimurium isolates exhibited an identical macrorestriction profile. Further, MLST analysis defined the two *S*. Typhimurium isolates as the single sequence type ST34. Based on the genotype results of PFGE and MLST analysis, the genetic homology of the two isolates was high.

To reduce the risk of nosocomial transmission, when *S*. Typhimurium was detected in an incision secretion on November 5th, 2018, necessary disinfection and isolation measures were carried out immediately in the Emergency Trauma Surgery Department. The next morning, environmental swabs from bed linens, stethoscopes, and doorknobs as well as hand swabs from doctors and nurses were collected and tested. However, *S*. Typhimurium was not isolated from any of the environmental surfaces, likely because of the preventative measures taken. According to field investigation and analysis, we know that both the Emergency Trauma Surgery Department and Pediatric Outpatient Department of the hospital were located in a temporary building owing to construction. Both the children were confirmed to be patients in the temporary hospital building.

Healthcare-associated infections (HAIs) are known to be key causes of morbidity and mortality in hospitalized patients. Previous studies have suggested that environmental contamination plays a significant role in HAIs and in the unrecognized transmission of pathogens. Cross-transmission of these pathogens can occur via the hands of healthcare workers who become contaminated directly from contact with patients or indirectly by touching contaminated environmental surfaces. *S*. Typhimurium is highly resistant to stress owing to various survival mechanisms, enabling prolonged survival in harsh environments. Unfortunately, in this study, *S*. Typhimurium could not be isolated from the hospital environment. In an earlier *Salmonella* outbreak, epidemiological investigation revealed that the probable

Table 1 Characteristics of the Two *Salmonella* Typhimurium Isolates

| Isolate | MIC (μg/mL) | MLST | Resistance Genes                        |
|---------|-------------|------|----------------------------------------|
|         | Imipenem    | Ceftriaxone | Ampicillin | Ciprofloxacin | Gentamycin |        |
| SM043   | 0.25        | 256  | 256 | 0.094 | 0.38 | ST34 | blaCTX-M-15, blaTEM-1, qnrB, qnrS-1, aae-3 |
| SM080   | 0.25        | 256  | 256 | 0.094 | 0.38 | ST34 | blaCTX-M-15, blaTEM-1, blaCMY-2, qnrS-1, |

Figure 1 Pulsed-field gel electrophoresis patterns of XbaI-digested total DNA from two *S*. Typhimurium isolates.

Abbreviations: MIC, minimum inhibitory concentration; MLST, multilocus sequence typing.
source was leakage of sewage into the water supply system; however, no pathogens were isolated from the water samples. *S. Typhimurium* may remain in environments for a long time, and several studies have shown that microbial contamination of the ward environment can be a source of nosocomial infection transmission.

Closer investigation and inspection of the temporary hospital structure indicated that the distribution of clinical wards and allocation of resources did not comply with prevention measures established during the transition period. First and foremost, the lack of alcohol hand sanitizer, soap, and tissues in the ward negatively impacted the basic hand hygiene practices of patients and their families as well as the compliance of medical personnel in the wards. In this study, surgical incision infections occurred in children as young as 4 years old who were primarily cared for by family members. Secondly, the building layout is inadequate, especially its toilet configuration. The number of toilets in this transition site, which is an old building, is small, and space is very limited, forcing medical staff, patients, and patient families to share toilets. The utilization rate of these toilets was extremely high. Owing to the lack of hand sanitizers, people could not wash their hands after using the toilets. Thirdly, we also found that the janitorial staff only regularly cleaned and disinfected the wards and ward grounds. The beds, door handles, railings, light switches, window edges, toilet door handles, and other environmental surfaces were not being effectively disinfected, which likely contributed to the spread of bacteria in the environment. The hands of healthcare workers are the main source of pathogen transmission in hospitals. It has been reported that 20–40% of nosocomial infections are caused by microorganisms present in the hospital environment that are transmitted directly or through the hands of healthcare workers.\(^{21,25,26}\) Therefore, in this research, we speculate that *S. Typhimurium* was present in the hospital environments, serving as potential reservoirs and posing a serious threat to patients. The surgical incision infection caused by *S. Typhimurium* SM080 was most likely caused by person-to-person transmission. This may have resulted from deteriorating hand hygiene, poor infection control measures, and crowded hospital wards. The nosocomial infection in the Emergency Trauma Surgery Department was finally controlled by the following intervention measures. The most important measure was the uninterrupted provision of hand-washing consumables and improved hand-washing facilities. Second, hand hygiene and nosocomial contact prevention education were provided to patients and staff. Third, the ward custodial team was regularly trained to strengthen cleaning and disinfecting practices. To date, no other nosocomial infections caused by *Salmonella* have been reported.

In China, cephalosporins and fluoroquinolones are commonly used to treat salmonellosis. Resistance to third-generation cephalosporins is increasing in *Salmonella* spp. This mainly results from the production of acquired AmpC β-lactamases and extended-spectrum β-lactamases.\(^{27}\) Both SM043 and SM080 harbored at least one AmpC or extended-spectrum β-lactamase or AmpC gene, which made them resistant to 3rd- and 4th-generation cephalosporins. It is important to continuously monitor antimicrobial resistance and genetic status in *S. Typhimurium* to detect emerging resistance trends. This is the first time that *bla*\(_{TEM-1}\), *bla*\(_{CTX-M-15}\), and *bla*\(_{CMY-2}\) have been detected in *S. Typhimurium* in the Yunnan province.

**Conclusion**

In summary, *S. Typhimurium* spreads not only via the fecal-oral route but also by contact with contaminated hospital environments that serve as potential reservoirs, especially when the strain is resistant to 3rd-generation cephalosporins. Therefore, it is very important to monitor the occurrence of ST34 *S. Typhimurium* in hospital environments and to take appropriate measures for controlling *Salmonella* spp. infections.

**Abbreviations**

PFGE, pulsed-field gel electrophoresis; MLST, multi-locus sequence typing; WKL, White-Kauffmann-Le Minor; HAIs, healthcare-associated infections.

**Data Sharing Statement**

The datasets used and/or analyzed in this study are available from the corresponding author on reasonable request.

**Ethics Statement**

The clinical isolates in this study were specifically isolated for this research. Ethical approval was obtained from the Institutional Ethics Committee (The First People’s Hospital of Yunnan Province, Kunming, Yunnan, China). The study protocol was in accordance with the Declaration of Helsinki for Human Research of 1974 (last modified in 2000). The parents of the two patients provided written informed consent before sample collection.

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