Typhoid fever, caused by Salmonella enterica serovar typhi (S. Typhi), was rarely identified in Taiwan and approximately one third of the cases were imported from Southeast Asia. The transmission source of the indigenous cases and their relatedness to the imported cases remained unknown. The study aimed to delineate the demographics and clinical features of typhoid fever in Taiwan and clarify the relatedness between the imported and the indigenous cases.

Materials and Methods

During 2001 and 2014, patients with any site culture positive for S. Typhi were identified in LINKOU CHANG GUNG MEMORIAL HOSPITAL in Taiwan. The demographic data, clinical manifestations and outcomes were collected by chart review. An imported case was defined as: (1) an isolate recovered from patients within 90 days of their arrival at or returning to Taiwan or (2) an isolate from a patient with foreign ethnicity. The isolates, if available, were determined for antibiotic susceptibilities by disc diffusion method and interpreted according to the Clinical and Laboratory Standards Institute (CLSI) protocols.[1] Further genotyping of the isolates were done by Pulsed-field gel electrophoresis (PFGE) and single nucleotide polymorphism (SNP) typing.

Pulsed-field Gel Electrophoresis Chromosomal DNA was digested with 40 units of XbaI in CutSmart® Buffer. PFGE was carried out with a CHEF Mapper XA System (Bio-Rad Laboratories). The DNA fingerprints generated by PFGE were compared using BIONUMERICS software (Applied Maths, Kortrijk, Belgium).

SNP Typing SNP typing was conducted with hairpin real-time PCR according to the method proposed by Octavia et al.[2] with modification. SNPs in seven alleles were used in the current study, including STY0961, STY1397, STY2331, STY2629, STY3196, STY3622 and STY4105.

Data were analyzed with IBM SPSS® Statistics software (v21.0.0.0; IBM SPSS, Armonk, NY). Analysis was performed using Student t test or Mann–Whitney U test for quantitative variables and χ² test or Fisher test for qualitative variables when appropriate.

Results

A total of 64 patients were identified from 2001 to 2014. Male accounted for 31 (48.4%) cases and the mean and median age was 28.8 ± 18.9 and 25.0 years (range, 1–77 years), respectively. 17 cases (26.6%) were considered imported. (Table 1)

Clinical Features

Clinical manifestations among indigenous and imported groups were similar. Most of the patients had fever (97.8% vs. 94.1%) and gastrointestinal symptoms, including abdominal pain (57.8% vs. 70.6%), nausea or vomiting (34.1% vs. 35.3%), diarrhea (46.7% vs. 58.8%), blood or mucus in stool (28.9% vs. 11.8%), constipation (4.4% vs. 5.9%), hepatomegaly (17.8% vs. 23.5%), splenomegaly (35.6% vs. 41.2%) and jaundice (15.6% vs. 11.8%)[P > 0.05 for all]. Intestinal haemorrhage and shock occurred in 20.5% and 4.5% of indigenous cases, which were not significantly different from those of imported cases (12.5% and 0%). Elevated C-reactive protein was noted in both groups.

Conclusion

The indigenous cases of typhoid fever in northern Taiwan shared similar clinical manifestations and had indistinguishable bacterial antibiograms and genotypes as the imported cases. Migrants and travellers from Southeast Asia, especially Indonesia, can be an important source of S. Typhi transmission in this region.

Reference

1. CLSI. Performance Standards for Antimicrobial Susceptibility Testing. 27th ed. CLSI Supplement M100 Wayne PA: Clinical and Laboratory Standards Institute; 2017

Microbiological Features

The antibiotic susceptibilities were similar between the indigenous and the imported isolates. (Table 2). The PFGE patterns were indistinguishable from the isolates imported and indigenous cases (Figure 1). The SNP typing also revealed that the two groups were phylogenetically related. (Figure 2)