

Investigation of an enteritis outbreak caused by *Salmonella enterica* serovar Aberdeen in China

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Salmonella Aberdeen is a ubiquitous pathogen that can cause severe gastroenteritis and plays an important role in food-borne illness and international food-trade dispute.^[1] However, the molecular biological characteristics of this organism have been rarely studied. This study was conducted in accordance with the Declaration of Helsinki and aimed to assess the epidemiological and clinical characteristics of a food-borne outbreak caused by *Salmonella* Aberdeen. Furthermore, the molecular biological characteristics of the outbreak isolates were detected and analyzed. From June 10 to 12, 2018, an enteritis outbreak affected 75 employees in the Fushan district of Yantai, Shandong province, China, including 33 males and 42 females. The mean age of the patients was 34.2 ± 5.3 years. An epidemiological investigation revealed that all infected employees had eaten the lunch provided by a catering company on June 9, 2018. In total, 22 samples, including four feces samples, five surplus food samples, eight cooking utensils used by the catering company, and five samples of chicken and eggs from the market where the food raw materials were purchased, were collected.^[2] Of the 22 samples, six (27.2%) were tested positive for *Salmonella* Aberdeen (O11:Hi;1,2), including three isolates from feces (3/4, 75%) and three from surplus foods (3/5, 60%). Pulsed-field gel electrophoresis (PFGE) results showed the highly close correlation among the isolates, which were digested using the restriction enzyme nucleases XbaI (96.8%) and BlnI (100%) (Takara, Dalian, Liaoning, China) according to the PulseNet standardized PFGE protocol.^[3] The PFGE patterns were analyzed using BioNumerics, Version 6.0 (Applied Maths, Kortrijk, Belgium).

Nine virulence genes, including *Salmonella* enterotoxin genes (*stn*), pilus gene Fimbrin (*fimA*), virulence island

genes (*invA*, *mgtC*, *siiE*, *sseL*, *sopB*), virulence plasmid genes (*spvC*) and *virK*, were detected in *Salmonella*, and their primers were designed according to GenBank. The results showed that six virulence genes, namely *stn*, *fimA*, *virK*, *invA*, *mgtC*, and *siiE* rather than *sseL*, *sopB*, and *spvC*, were detected in all six isolates.

Fifteen different antibiotic drugs, for example, ampicillin, ceftazidime, ampicillin-sulbactam, imipenem, tetracycline, nalidixic, erythromycin, cefoxitin, chloramphenicol, cefotaxime (CTX), cefazolin (CFZ), gentamicin, compound sulfamethoxazole, azithromycin, and ciprofloxacin, were tested for antimicrobial susceptibility with the broth microdilution method of the Clinical and Laboratory Standards Institute. The results showed that all six isolates were sensitive to all tested drugs except CFZ. Thirteen drug-resistant genes of *Salmonella*, including *BlaTEM*, *BlaSHV*, *BlaOXA-1*, *BlaOXA-2*, *BlaPER*, *BlaCMY*, CTX-M group I, CTX-M group II, CTX-M group III, CTX-M group IV, *Mcr-1*, *Mcr-2*, and *InvA* genes, were detected using polymerase chain reaction in capillary gel electrophoresis (QIAXcel Advanced, Hilden, Germany). The results showed that the CTX-M group II (351 bp) and CTX-M group IV (474 bp) were in all isolates.

The epidemiological investigation showed the shortest, longest, and average incubation periods were 1, 88, and 14 h, respectively. The clinical symptoms of the 75 workers mainly included diarrhea (89.3%, 67/75), abdominal pain (89.3%, 67/75), increased C-reactive protein (CRP) level (77.3%, 58/75), nausea (65.3%, 49/75), fever (52.0%, 39/75), and vomiting (45.3%, 34/75).

Salmonella Aberdeen is rarely reported and does not cause typical food-borne outbreaks abroad. In China, the first food poisoning caused by Aberdeen was reported in

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1964.^[4] During 1976 to 1980, Aberdeen detection rate was 0.39% (105/27183) in *Salmonella enterica*. There was 3% of Aberdeen in 807 *Salmonella* strains isolated from 24,895 fecal samples during 2006 to 2007 as China joined WHO Global Salm-Surv.^[1]

The same serotypes were isolated from the retained food and patient stool samples of the outbreak, and the PFGE results showed that the isolated strain had a high similarity ($\geq 96.8\%$); thus, this food-borne outbreak was typically caused by *Salmonella* Aberdeen. According to epidemiological evidence, the outbreak occurred because the food processing environment of the catering was poor and raw and cooked foods were not kept separate during processing, thus allowing for cross-contamination.

The incubation period of Aberdeen infection is similar to that of other *Salmonella enterica*, including *Salmonella typhimurium/enteritidis*. The clinical symptoms mainly include diarrhea, fever, abdominal pain, nausea, vomiting, and increased CRP levels. We confirmed that the isolates contained *stn*, *fimA*, *virK*, *invA* (*salmonella* pathogenicity island [SPI]-1), *mgtC* (SPI-3), and *siiE* (SPI-4). *Stn* is an enterotoxin gene and is an important virulence factor encoding products that can induce intestinal juice secretion as the study of *Salmonella typhimurium* infection mechanism indicated. *FimA* as a fimbriae gene helps bacteria adhesion to animal cells and promotes its colonization. *VirK* is a regulatory gene that mainly facilitates diffusion of bacterial toxins in the host. *InvA* plays an important role in the invasion of *Salmonella* into intestinal M cells. *MgtC* is a virulence factor located in SPI-3 and allows bacteria to survive in macrophages and low-magnesium environments. *SiiE* is located in SPI-4 and it aids bacterial adhesion to the epithelium. Diarrhea and abdominal pain are the main symptoms for diagnosis of *Salmonella* Aberdeen infection, and CRP levels should be widely tested in routine blood tests.

All patients with severe symptoms showed remarkable improvement following CTX and levofloxacin injections

after 3 to 7 days. In order to analyze the relationship between their phenotypes and genotypes, the antimicrobial resistance and the resistance genes of the isolates were investigated. The results showed that all six isolates were resistant to CFZ, but resistance genes showed they all contained CTX-M group II and CTX-M group IV. The results of this study are consistent with the results of widespread distribution and prevalence of the CTX-M gene sub-type in *Salmonella* in China.^[5] CTX-M type extended spectrum β -lactamases (ESBLs) is a new type of ESBL gradually recognized and with increasingly large family members. Its main phenotype shows elevated level resistance to cephalosporin antibiotics. The resistance of *Salmonella* Aberdeen to first-generation CFZ should be a wide concern for all healthcare professionals.

Conflicts of interest

None.

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