Prevalence and molecular characteristics of mcr-1 gene in Salmonella typhimurium in a tertiary hospital of Zhejiang Province

Objectives: mcr-1 gene has been widely reported in the world. This study aimed to analyze the prevalence and molecular characteristics of mcr-1 gene in Salmonella typhimurium from Quzhou People’s Hospital.

Materials and methods: A total of 62 S. typhimurium isolates were isolated and preserved in our laboratory from 2007 to 2016. PCR was used to screen plasmid-mediated colistin resistance gene, mcr-1. For mcr-1-positive isolates, susceptibilities to colistin and other antibiotics were assessed using broth microdilution or agar dilution methods. The genetic location of mcr-1 was determined by analysis of pulsed-field gel electrophoresis profiles of S1-digested genomic DNA and subsequent Southern blot hybridization. The multi-locus sequence type and other drug resistance genes found in the mcr-1-positive isolates were analyzed by performing whole genome sequencing. Genetic environment of mcr-1 gene was analyzed by RAST and Easyfig.

Results: A total of three S. typhimurium isolates were identified to be mcr-1 positive, with the prevalence rate of 4.8% (3/62). The minimum inhibitory concentration values of colistin for all these isolates were 8 µg/mL. The three mcr-1-positive isolates carried mcr-1 gene on two different types of plasmids having the sizes of ~54.7–78.2 kb and 310.1 kb, respectively. All the three isolates belonged to ST34 and carried various resistant genes.

Conclusion: Colistin-resistant, mcr-1-positive S. typhimurium isolates belonging to ST34 have been isolated from Quzhou People’s Hospital. Surveillance needs to be strengthened to identify colistin resistance and prevent the spread of drug-resistant bacteria in the hospital.

Keywords: Salmonella typhimurium, colistin, mcr-1

Introduction
Polymyxins, including polymyxin B and E (colistins), are generally regarded as the last-resort therapy for infections caused by multidrug resistant (MDR) Gram-negative bacilli, especially carbapenem-resistant Enterobacteriaceae. In recent years, polymyxin resistance has gained wide attention in the field of global medical research due to the increasing reports of polymyxin-resistant bacteria. In late 2015, Chinese researchers reported the first plasmid-mediated colistin resistance gene, mcr-1, and since then, it has been reported in other continents as well, including Asia, Europe, America, Africa, and Australia, as well as in several provinces (Zhejiang, Sichuan, Beijing, Guangdong, etc) in China. The discovery of mcr-1 gene makes it possible for the horizontal transmission of polymyxin resistance in Enterobacteriaceae, which may in turn lead to a rapid increase in polymyxin resistance. So far, mcr-1 gene has been found only in Enterobacteriaceae, such as Escherichia coli, Klebsiella pneumoniae, Salmonella spp.,
Enterobacter spp., Klyvera ascorbata, Raoultella ornitholytica, Citrobacter braakii, etc.4,6,10,11

Studies focusing on the mcr-1 gene-carrying E. coli and K. pneumonia strains are common, while the studies on prevalence and molecular characteristics of the mcr-1 gene in Salmonella spp. are still lacking. Salmonella typhimurium is an important zoonotic pathogen that usually causes foodborne diseases, and humans, especially infants, are highly susceptible to this infection.12 Furthermore, the occurrence of MDR isolates of S. typhimurium have become common now and have had great impact on the effectiveness of current strategies to prevent and control foodborne diseases.13 This study aims to analyze the prevalence and molecular characteristics of mcr-1 gene in S. typhimurium strains isolated from Quzhou People’s Hospital and provide a basis for the prevention and control of polymyxin resistance in the hospital strains of S. typhimurium.

Materials and methods

Bacterial isolates
A total of 62 S. typhimurium isolates were collected from Quzhou People’s Hospital from 2007 to 2016. All the strains were isolated from patients who visited the hospital during the period. Isolates were identified using the automated Vitek 2 system (BioMérieux, Marcy l’Etoile, France).

Screening for mcr-1 gene
All the isolates were screened for the presence of mcr-1 gene by PCR with primers mcr-1-F (5′-GCTCGTACGTCGTTGTG-3′) and mcr-1-R (5′-GAATGCGGTGGCTCTTT-3′), and positive amplicons were subsequently sequenced. All the sequences were further analyzed on the BLAST server (http://blast.ncbi.nlm.nih.gov/).

Antimicrobial susceptibility testing
Minimum inhibitory concentrations (MICs) of colistin and other ten antimicrobial agents (including levofloxacin, ciprofloxacin, cefotaxime, cefepime, cefoperazone/sulbactam, imipenem, meropenem, amikacin, tigecycline, and aztreonam) were determined for the mcr-1-positive isolates by the broth microdilution method, while the MICs of fosfomycin and sulfamethoxazole/trimethoprim were evaluated by the agar dilution method according to the guidelines of Clinical and Laboratory Standards Institute (CLSI). The results were interpreted in accordance with the CLSI and European Committee on Antimicrobial Susceptibility Testing (for colistin, tigecycline, and fosfomycin) breakpoints (http://www.eucast.org/clinical_breakpoints).

Southern blot analysis
To determine the plasmid location of the mcr-1 gene, genomic DNA digested with S1 nuclease (TaKaRa, Tokyo, Japan) was electrophoresed on a CHEF-mapper XA pulsed-field gel electrophoresis system (Bio-Rad Laboratories Inc., Hercules, CA, USA) for 22 hours at 14°C with run conditions of 6 V/cm and pulse times from 2.16 seconds to 63.8 seconds. The DNA fragments were transferred to a positively charged nylon membrane (EMD Millipore, Billerica, MA, USA) and then hybridized with a digoxigenin-labeled mcr-1-specific probe. The fragments were then detected using a NBT/BCIP color detection kit (Hoffman-La Roche Ltd., Basel, Switzerland).

Whole genome sequencing (WGS)
The total genomes of the mcr-1-positive isolates were extracted and then sequenced on an Illumina-Hiseq™ 2000 sequencing system (Illumina Inc, San Diego, CA, USA) using a paired-end 2×100 bp protocol. Sequence reads were assembled using CLC Genomics Workbench software package (CLC Bio 8.0, Aarhus, Denmark). The multi-locus sequence type (MLST) and other resistant genes were analyzed on the website of Center of Genomics Epidemiology (http://www.genomicsepidemiology.org/). Gene prediction and annotation were performed using RAST (http://rast.nmpdr.org/). Sequence comparison was performed using BLAST (http://blast.ncbi.nlm.nih.gov), and physical maps were generated by using Easyfig.14

Ethics approval
The clinical isolates were part of the routine hospital laboratory procedure. The Ethics Committee of the Quzhou People’s Hospital approved this study as it mainly focused on bacteria, and not the patients.

Results
Epidemiology data and characteristics of mcr-1-positive isolates
A total of three mcr-1-positive isolates of S. typhimurium were identified (16–541, 16–573, and 16–623), with the prevalence rate of 4.8% (3/62). All the three strains were isolated from feces of patients with infectious diarrhea diseases in 2016. Two patients were infants and the other was 15 years old (male =1, female =2). No underlying diseases were found in all the three patients, and all of them were eventually cured (Table 1).
Antimicrobial susceptibility of mcr-1-positive isolates
All the three mcr-1-positive S. typhimurium strains were resistant to colistin, with the MIC of 8 µg/mL. Moreover, they were all resistant to the third/fourth-generation cephalosporins (ceftaxime and cefepime) and sulfamethoxazole/trimethoprim, while imipenem, meropenem, amikacin, tigecycline, and fosfomycin showed great activity against these mcr-1-positive isolates (Table 2).

mcr-1 gene locations
S1-nuclease digestion and Southern blot analysis indicated that all three mcr-1 genes were located on plasmids. mcr-1 genes of isolates 16–541 and 16–623 were located on the same-size plasmids of ~310.1 kb, while the one of isolate 16–573 was located on a ~60 kb plasmid (Figure 1).

WGS analysis
The whole genomes of the three S. typhimurium strains were sequenced and analyzed.

Other mechanisms associated with antimicrobial resistance were analyzed by using ResFinder. In addition to mcr-1, all the three isolates carried a variety of resistance genes to different antibiotics, including aminoglycosides, β-lactams, fluoroquinolones, sulfonamides, tetracyclines, and trimethoprim. In addition, isolate 16–573 carried fosA3 gene, which induced fosfomycin resistance, while isolates 16–541 and 16–623 carried ARR-3 gene, which induced rifampicin resistance (Table 3).

Genetic environment of mcr-1 gene
One of the three mcr-1-carrying plasmids (16-573) was greatly similar to pEc20COE13 (accession number: KY012274), which belonged to plasmid type IncI2 (Figure 2A). No ISApI1 elements were identified at the upstream or downstream of mcr-1 gene.

Discussion
Since the first report of mcr-1 gene, it has been widely reported all over the world, and can be isolated from animals, food, environment, and humans (patients and healthy people). Apart from the common strains like E. coli and K. pneumonia, mcr-1 gene has also been reported from Enterobacter aerogenes and Enterobacter cloacae.15 Salmonella spp., especially S. typhimurium, is one of the main hosts of mcr-1 gene. Although many countries, such as Britain, Italy, the Netherlands, and Portugal, have reported mcr-1-carrying S. typhimurium isolates, most of them were of animal origin.16–19

This study analyzed the prevalence and molecular characteristics of mcr-1 gene in S. typhimurium isolates from 2007 to 2016 retrospectively, which were preserved in the laboratory of Quzhou People’s Hospital. The results showed that the detection rate of mcr-1 gene was 4.8%, which was slightly higher than that reported previously (0.06%–1.55%).16,20 It is observed that mcr-1-positive S. typhimurium were

Table 1 Characteristics of mcr-1-positive isolates

<table>
<thead>
<tr>
<th>Isolates</th>
<th>Age</th>
<th>Sex</th>
<th>Living place</th>
<th>Underlying disease</th>
<th>Outcome</th>
<th>Department</th>
<th>Samples</th>
<th>Isolated date</th>
</tr>
</thead>
<tbody>
<tr>
<td>16–541</td>
<td>15 years</td>
<td>Female</td>
<td>Village</td>
<td>None</td>
<td>Cured</td>
<td>Gastroenterology department</td>
<td>Feces</td>
<td>8/27/2016</td>
</tr>
<tr>
<td>16–573</td>
<td>8 months</td>
<td>Female</td>
<td>City</td>
<td>None</td>
<td>Cured</td>
<td>Pediatric department</td>
<td>Feces</td>
<td>9/20/2016</td>
</tr>
<tr>
<td>16–623</td>
<td>10 months</td>
<td>Male</td>
<td>Village</td>
<td>None</td>
<td>Cured</td>
<td>Pediatric department</td>
<td>Feces</td>
<td>11/2/2016</td>
</tr>
</tbody>
</table>

Table 2 MICs of mcr-1-positive Salmonella typhimurium isolates to colistin and other antibiotics (µg/mL)

<table>
<thead>
<tr>
<th>Antibiotics</th>
<th>16–541</th>
<th>16–573</th>
<th>16–623</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colistin</td>
<td>8 (R)</td>
<td>8 (R)</td>
<td>8 (R)</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>4 (I)</td>
<td>0.25 (S)</td>
<td>4 (I)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>8 (R)</td>
<td>0.125 (S)</td>
<td>8 (R)</td>
</tr>
<tr>
<td>Cefotaxime</td>
<td>&gt;256 (R)</td>
<td>&gt;256 (R)</td>
<td>&gt;256 (R)</td>
</tr>
<tr>
<td>Cefepime</td>
<td>128 (R)</td>
<td>64 (R)</td>
<td>128 (R)</td>
</tr>
<tr>
<td>Cefoperazone/</td>
<td>32 (I)</td>
<td>16 (S)</td>
<td>32 (I)</td>
</tr>
<tr>
<td>sulfactam</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Imipenem</td>
<td>0.5 (S)</td>
<td>0.5 (S)</td>
<td>1 (S)</td>
</tr>
<tr>
<td>Meropenem</td>
<td>0.0625 (S)</td>
<td>0.0625 (S)</td>
<td>0.0625 (S)</td>
</tr>
<tr>
<td>Amikacin</td>
<td>8 (S)</td>
<td>4 (S)</td>
<td>16 (S)</td>
</tr>
<tr>
<td>Tigecycline</td>
<td>1 (S)</td>
<td>0.5 (S)</td>
<td>1 (S)</td>
</tr>
<tr>
<td>Fosfomycin</td>
<td>0.25 (S)</td>
<td>64 (R)</td>
<td>0.25 (S)</td>
</tr>
<tr>
<td>Sulfamethoxazole/trimethoprim</td>
<td>&gt;32 (R)</td>
<td>&gt;32 (R)</td>
<td>&gt;32 (R)</td>
</tr>
<tr>
<td>Aztreonam</td>
<td>8 (I)</td>
<td>4 (S)</td>
<td>16 (R)</td>
</tr>
</tbody>
</table>

Abbreviations: MIC, minimum inhibitory concentration; I, intermediate; R, resistant; S, susceptible.
not detected until 2016. Furthermore, all the mcr-1 genes were located on plasmids. One of the three mcr-1-carrying plasmids belonged to plasmid type IncI2, and the other two belonged to IncHI2, which was the same as the recently reported mcr-1-harbored plasmid of ST34 S. typhimurium isolated from pigs in China. All these results suggest that mcr-1 gene may play an important role in polymyxin resistance of clinically isolated S. typhimurium strains and lead to the rapid increase of polymyxin resistance in these bacteria.

S. typhimurium is a common clinical pathogenic serotype of Salmonella spp. In recent years, there has been an increase in the incidence of antimicrobial resistance among the Salmonella spp., which can be attributed to the irrational use of antibiotics in clinics as well as the randomly discharged stools of poultry which can contain the residues of antibiotics. According to the previously reported study, mcr-1-positive isolates usually remain susceptible to many other antibiotics. In this study, mcr-1-positive strains were resistant to colistin as well as to third/fourth-generation cephalosporins and sulfamethoxazole/trimethoprim. WGS analysis showed that these isolates were all CTX-M-14-type extended-spectrum beta-lactamase producers.

In Table 3, the resistant genes of mcr-1-positive S. typhimurium isolates are shown. The most prevalent resistant gene is the blal gene, which is responsible for aminoglycoside resistance. Additionally, the blacTX-M-14 gene is also present in all the isolates, contributing to the resistance to beta-lactam antibiotics. The fosA gene is present in isolates 16–541 and 16–573, conferring resistance to fluoroquinolones. The rifampicin resistance is conferred by the arr-3 gene, and the sulfonamide resistance is due to the sul1, sul2, and sul3 genes. The tet genes are also present, conferring resistance to tetracyclines, with tet(A) and tet(B) being the most common. The dfrA genes are present in all isolates, contributing to the resistance to sulfonamides and trimethoprim.
β-lactamase producing strains and carried sulfonamide and trimethoprim resistance genes, which were in accordance to the resistant phenotype. The MIC of fosfomycin of isolate 16–573 was 64 µg/mL, which was far higher than the MIC of other two isolates (0.25 µg/mL). It was due to the co-expression of fosA3 in isolate 16–573. In addition, although the isolate also carried quinolone-resistance genes oqxA and oqxB, it was susceptible to both levofloxacin and ciprofloxacin, which might be due to the non-expression of the two genes.

In China, the most common ST of S. typhimurium, especially MDR S. typhimurium, is ST34,13 which is also prevalent in Europe.24 In this study, all the three S. typhimurium isolates belonged to ST34. At the same time, most of the S. typhimurium strains carrying mcr-1 gene were isolated from animals and belonged to ST34,21,25 which suggested that ST34 was closely related to antimicrobial resistance and the spread of this clone would pose a great threat to the prevention and control of clinical S. typhimurium infections.

Conclusion
In conclusion, colistin-resistant mcr-1-positive S. typhimurium strains have emerged in Quzhou People’s Hospital and belong to the most common sequence type ST34, which is associated with MDR S. typhimurium. It is necessary to strengthen the surveillance of polymyxin resistance rate in our hospital to prevent the spread of resistant bacteria.

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Disclosure
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References