Multidrug-Resistant Atypical Variants of Shigella flexneri in China

Shaofu Qiu, Yong Wang, Xuebin Xu, Peng Li, Rongzhang Hao, Chaojie Yang, Nan Liu, Zhenjun Li, Zhongqiang Wang, Jian Wang, Zhihao Wu, Wenli Su, Guang Yang, Huiming Jin, Ligui Wang, Yansong Sun, Zhengan Yuan, Liuyu Huang, and Hongbin Song

We identified 3 atypical Shigella flexneri varieties in China, including 92 strains with multidrug resistance, distinct pulse types, and a novel sequence type. Atypical varieties were prevalent mainly in developed regions, and 1 variant has become the dominant Shigella spp. serotype in China. Improved surveillance will help guide the prevention and control of shigellosis.

Each year worldwide, ≈1.5 million children <5 years of age die from diarrheal diseases (1), which is of particular concern in developing countries. Shigella spp. are leading bacterial causes of diarrhea, responsible for ≥80 million cases of bloody diarrhea and 700,000 deaths each year (2), and S. flexneri serotype 2a has been recognized as the most prevalent serotype in China for many years (3). To better understand the etiology of bacterial diarrhea in China and to determine if S. flexneri serotype 2a is still the most prevalent serotype in China, we conducted a study during May 2008–December 2010.

The Study

A total of 10,021 fecal samples were obtained from patients with diarrhea or dysentery at hospitals in 8 provinces within the eastern, southern, western, northern, and central regions of China: Liaoning, Shandong, Jiangsu, Guangdong, Gansu, Sichuan, Xinjiang, and Hebei Provinces. Samples were screened for the presence of Shigella spp. by using API 20E strips (bioMérieux, Marcy l’Etoile, France). Serotyping was performed by using 1) an antisera kit specific for all type- and group-factor antigens (Denka Seiken, Tokyo, Japan) and 2) a panel of monoclonal antibodies against S. flexneri (MASF; Reagensia AB, Stockholm, Sweden). Antimicrobial susceptibility testing was performed by the disk diffusion method as described (4). Genetic relationships were estimated by using multilocus sequence typing, as described (5), and pulsed-field gel electrophoresis (PFGE) (6).

Overall, 1,109 bacterial pathogens were identified. Shigella spp. isolates were the most prevalent, representing 273 (24.6%) of the total. Among the Shigella strains, 92 atypical strains, with 3 different serologic agglutination profiles, were identified (Table 1); 1 of these strains was initially identified as the previously described serotype 4c (7) because it agglutinated with monovalent anti-IV type antiserum and monovalent anti-7,8 group antiserum. This serotype was also serologically indistinguishable from S. flexneri serotype X variant (SFxv), which was recently reported in China (8). However, this serotype could not produce indole, whereas SFxv could. This atypical serotype was provisionally designated S. flexneri X variant (−:7,8, E1037), indole-negative variety. We isolated 73 isolates belonging to this atypical variant, which has become the most frequent serotype in China (Table 1). In 2008, the first 19 S. flexneri X variant (−:7,8, E1037) isolates were detected in Beijing; then in 2009, 26 were detected in Beijing, and in 2010, 23 were detected in Beijing, 3 in Jiangsu Province, and 2 in Shandong Province.

The second atypical serotype reacted with monovalent anti-IV type antiserum but not the group-specific antiserum, and it agglutinated with MASF B–specific and MASF IV-1 E1037–specific antibodies (see online Technical Appendix Table 1). However, this serotype could not produce indole, whereas SFxv could. This atypical serotype was provisionally designated S. flexneri X variant (−:7,8, E1037), indole-negative variety. We isolated 73 isolates belonging to this atypical variant, which has become the most frequent serotype in China (Table 1). In 2008, the first 19 S. flexneri X variant (−:7,8, E1037) isolates were detected in Beijing; then in 2009, 26 were detected in Beijing, and in 2010, 23 were detected in Beijing, 3 in Jiangsu Province, and 2 in Shandong Province.

The third atypical serotype was provisionally designated S. flexneri serotype 2 variant (II:3,4,7,8) because it could agglutinate with monovalent anti-II type antiserum and monovalent anti-3,4 and anti-7,8 group antiserum. It also reacted with type-specific antibody MASF II and group-specific antibodies MASF Y-5 and MASF 7 (online Technical Appendix Table 1). A total of 17 isolates of serotype 2 variant (II:3,4,7,8) have been detected in Jiangsu Province: 10 in 2008, 4 in 2009, and 3 in 2010.

These authors contributed equally to this article.
and 17.6% to cefotaxime. The 2
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...ant to ampicillin, ampicillin/sulbactam, chloramphenicol,
nalidixic acid, and tetracycline; a total of 91.3% were also
resistant to amoxicillin/clavulanic acid, and 84.8% were
resistant to trimethoprim/sulfamethoxazole (Table 2; on-
line Technical Appendix Table 2). The atypical strains
also showed reduced susceptibility to fluoroquinolones and
third-generation cephalosporins. Of the X variant (−:7,8,
E1037), indole-negative variety strains, 82.2% were re-
sistant to norfloxacin, 39.7% to ciprofloxacin, 21.9% to
levofloxacin, and 13.7% to cefotaxime. Of the serotype
2 variant (II:3,4,7,8) strains, 29.4% were resistant to nor-
floxacin, 29.4% to ciprofloxacin, 17.6% to levofloxacin,
and 17.6% to cefotaxime. The 2 S. flexneri untypeable
variant (−:E1037) strains were also resistant to norfloxacin
and ciprofloxacin. Furthermore, 6 of the X variant (−:7,8,
E1037), indole-negative variety strains were also resistant
to ciprofloxacin and ceftoxime.

The atypical serotype strains were all multidrug resis-
tant to ampicillin, ampicillin/subbactam, chloramphenicol,
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and ciprofloxacin. Furthermore, 6 of the X variant (−:7,8,
E1037), indole-negative variety strains were also resistant
to ciprofloxacin and ceftoxime.

Multilocus sequence typing identified all of the vari-
ant strains as a new sequence type (ST), ST100, which
differs from ST18 at the lysP locus only (online Technical
Appendix Figure). Other serotypes (e.g., 1a, 2a, 2b, and Y)
were also identified as ST100. The 73 isolates of X variant
(−:7,8, E1037), indole-negative variety were typed into
29 distinct pulse types (PTs) by PFGE analysis, and the 2
S. flexneri untypeable variant (−:E1037) isolates belonged
to different PTs and had relatively low similarity (online
Technical Appendix Figure). The 17 serotype 2 variant
(II:3,4,7,8) isolates grouped into 17 PTs, showing high
genetic diversity. Several serotype 2 variant (II:3,4,7,8)

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Table 1. Distribution of different Shigella spp. in China during 2008–2010 and 1991–2000

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>S. flexneri</td>
<td>8,082 (86.2)</td>
<td>208 (76.2)</td>
</tr>
<tr>
<td>S. boydii</td>
<td>100.0</td>
<td>100.0</td>
</tr>
<tr>
<td>S. sonnei</td>
<td>1,022 (10.9)</td>
<td>56 (20.5)</td>
</tr>
<tr>
<td>S. dysenteriae</td>
<td>132 (1.4)</td>
<td>6 (2.2)</td>
</tr>
<tr>
<td>S. boydii</td>
<td>139 (1.5)</td>
<td>3 (1.1)</td>
</tr>
</tbody>
</table>

*Data are from (1).

Table 2. Antimicrobial drug resistance profiles of variant serotypes of Shigella flexneri isolates recovered from patients with diarrhea, China, May 2008–December 2010*

<table>
<thead>
<tr>
<th>Antimicrobial drug</th>
<th>X variant (−:7,8, E1037), indole-negative variety, n = 73</th>
<th>Serotype 2 variant (II:3,4,7,8), n = 17</th>
<th>Untypeable variant (−:E1037), n = 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ampicillin</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Ampicillin/subbactam</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Chloramphenicol</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Nalidixic acid</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Amoxicillin/clavulanic acid</td>
<td>91.8 5.5 2.7</td>
<td>88.2 0 11.8</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Trimethoprim/sulfamethoxazole</td>
<td>90.4 9.6 0</td>
<td>58.8 0 41.2</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Norfloxacin</td>
<td>82.2 16.4 1.4</td>
<td>29.4 0 70.6</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>39.7 49.3 11.0</td>
<td>29.4 0 70.6</td>
<td>100.0 0 0</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>21.9 26.0 52.1</td>
<td>17.6 11.8 70.6</td>
<td>0 50.0 50.0</td>
</tr>
<tr>
<td>Cefotaxime</td>
<td>13.7 13.7 72.6</td>
<td>17.6 5.9 76.5</td>
<td>0 0 100.0</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>6.8 0 9.2</td>
<td>5.9 0 94.1</td>
<td>0 0 100.0</td>
</tr>
<tr>
<td>Ceftazidime</td>
<td>5.5 2.7 91.8</td>
<td>0 0 100.0</td>
<td>0 0 100.0</td>
</tr>
<tr>
<td>Imipenem</td>
<td>2.7 0 97.3</td>
<td>0 0 100.0</td>
<td>0 0 100.0</td>
</tr>
</tbody>
</table>

*R, resistant; I, intermediate; S, susceptible.
isolates had greater genetic distance from other serotype 2 isolates. In particular, PT70 had a genetic similarity of <65% with other serotype 2 variant (II:3,4,7,8) isolates.

Conclusions

Three varieties of S. flexneri serotypes, including 92 atypical strains, were identified in this study. The X variant (−:7,8, E1037), indole-negative variety displayed a serologic agglutination profile indistinguishable from that for SFvx, but the indole-negative variety had different biochemical reactions, more serious drug resistance, and different ST and PTs. All variant strains were identified as ST100, a new ST containing multiple other serotypes (e.g., 1a, 2a, 2b, and Y). This finding demonstrates that ST100 is the predominant ST circulating among different S. flexneri serotypes in China. Moreover, the 3 atypical varieties were also genetically distinct by PFGE analysis and showed a relatively high level of genetic diversity; thus, these S. flexneri varieties may have existed for a long time or experienced frequent genetic mutations.

The X variant (−:7,8, E1037), indole-negative variety serotype has supplanted serotype 2a and S. sonnei (3) and represents a new dominant S. flexneri in China; serotype 2 variant (II:3,4,7,8) has become the fifth most common serotype of Shigella spp. in China. The variant strains were prevalent mainly in Beijing and in Jiangsu and Shandong Provinces; these provinces, located in the eastern and northern regions of China, have more developed economies and larger populations compared with the provinces in western China. Industrialization, trade, frequent movement of population, and environmental change can cause the shifting prevalence of diarrheal pathogens and lead to the dissemination of foodborne diseases worldwide (10,11). Therefore, the dynamic change in S. flexneri, especially the emergence of new serotypes, may be attributable to the economy and trade development or to human migration.

Of particular concern is that the atypical strains were completely resistant to several antimicrobial drugs used to treat shigellosis in China (12), and they showed reduced susceptibility to fluoroquinolones and third-generation cephalosporins. The World Health Organization has recommended ciprofloxacin as a first-line antimicrobial drug for shigellosis treatment (12), and third-generation cephalosporins are considered as alternative drug treatments (13). However, the S. flexneri resistance to ciprofloxacin and cefotaxime that we detected in this study was higher than previously reported in China (8,14); this finding raises serious questions regarding the effective treatment of shigellosis in the future.

In conclusion, 3 atypical S. flexneri serotypes with extensive multidrug resistance, distinct PTs, and a novel ST were identified in China. Continuous surveillance should be encouraged to determine the changing trends of these variants in geographic, temporal, phenotypic, and genotypic patterns. Such knowledge will improve our understanding of the actual level of disease and provide guidance for the prevention and control of shigellosis.

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Multidrug-Resistant Atypical Variants of *Shigella flexneri* in China

### Technical Appendix

Technical Appendix Table 1. Agglutination reactions of the variant serotypes of *Shigella flexneri* and reference strains tested during a study of multidrug-resistant atypical variants of *Shigella flexneri* in China. May 2008–December 2010 *

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Serotype</th>
<th>Antisera specific for all type- and group-factor antigens†</th>
<th>Panel of monoclonal antibodies against <em>S. flexneri‡</em></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Typing sera</td>
<td>Grouping sera</td>
</tr>
<tr>
<td></td>
<td></td>
<td>I</td>
<td>II</td>
</tr>
<tr>
<td>SF301</td>
<td>2a</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>ATCC 4a</td>
<td>4a</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>NCTC 4b</td>
<td>4b</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Shig0001</td>
<td>SFxv</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Shig0004</td>
<td>S. flexneri untypeable variant (–:E1037)</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Shig0083</td>
<td>S. flexneri untypeable variant (–:E1037)</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Shig0008</td>
<td>X variant (–:7,8, E1037), indole-negative variety</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Shig0009</td>
<td>X variant (–:7,8, E1037), indole-negative variety</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Shig0190</td>
<td>S. flexneri serotype 2 variant (II:3,4,7,8)</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Shig0191</td>
<td>S. flexneri serotype 2 variant (II:3,4,7,8)</td>
<td>–</td>
<td>+</td>
</tr>
</tbody>
</table>

*SFxv, *S. flexneri* serotype X variant.
†From Denka Seiken, Tokyo, Japan.
‡MASF (Reagensia AB, Stockholm, Sweden).
### Technical Appendix Table 2. Antimicrobial drug resistance of atypical *Shigella* spp. collected during 1991–2000 and 2008–2010, China

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>% Resistant <em>Shigella</em> spp. isolates collected during 1991–2000*</th>
<th>% Resistant <em>S. flexneri</em> variants collected during May 2008–December 2010†</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>S. flexneri X variant (−7,8, E1037), indole-negative variety (n = 73)</td>
<td>S. flexneri serotype 2 (II:3,4,7,8) (n = 17) Untypeable S. flexneri (−E1037) (n = 2) Other S. flexneri (n = 78) S. sonnei (n = 56)</td>
</tr>
<tr>
<td>Ampicillin</td>
<td>53.0</td>
<td>100.0 100.0 100.0 96.2 92.9</td>
</tr>
<tr>
<td>Ampicillin/sulbactam</td>
<td>100.0</td>
<td>100.0 100.0 100.0 73.1 62.5</td>
</tr>
<tr>
<td>Chloramphenicol</td>
<td>18.0</td>
<td>100.0 100.0 100.0 93.6 10.7</td>
</tr>
<tr>
<td>Nalidixic acid</td>
<td>–</td>
<td>100.0 100.0 100.0 100.0 100.0</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>–</td>
<td>91.8 88.2 100.0 94.9 85.7</td>
</tr>
<tr>
<td>Amoxicillin/clavulanic acid</td>
<td>–</td>
<td>91.8 88.2 100.0 94.9 85.7</td>
</tr>
<tr>
<td>Trimethoprim/sulfadiazine</td>
<td>62.0</td>
<td>90.4 58.8 100.0 75.6 89.3</td>
</tr>
<tr>
<td>Norfloxacin</td>
<td>4.9.0</td>
<td>82.2 29.4 100.0 32.1 8.9</td>
</tr>
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<td>Ciprofloxacin</td>
<td>20.0</td>
<td>39.7 29.4 100.0 23.1 5.4</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>–</td>
<td>21.9 17.6 0 15.4 1.8</td>
</tr>
<tr>
<td>Cefotaxime</td>
<td>–</td>
<td>13.7 17.6 0 17.9 25.0</td>
</tr>
<tr>
<td>Ceftazidime</td>
<td>–</td>
<td>5.5 0 0 5.1 8.9</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>13.0</td>
<td>6.8 5.9 0 14.1 85.7</td>
</tr>
<tr>
<td>Imipenem</td>
<td>–</td>
<td>2.7 0 0 0 0</td>
</tr>
</tbody>
</table>

*From (1).
†Variants were collected from patients with diarrhea. –, not detected.
Technical Appendix Figure. Pulsed-field gel electrophoresis dendrogram of *Shigella flexneri* subtypes. The genetic relatedness of atypical and previously known serotypes of *S. flexneri* is shown and was determined by using the unweighted pair group method with arithmetic mean and pairwise Dice coefficients. The strain number, serotype, region, pulse types (PTs), and strain types (STs) are shown for each strain. Serotypes A, B, and C represent the X variant (–7,8, E1037), indole-negative variety; serotype 2 variant (II:3,4,7,8); and *S. flexneri* untypeable variant (–:E1037), respectively.

Reference


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