Multidrug-Resistant IncA/C Plasmid in Vibrio cholerae from Haiti

To the Editor: The agents of epidemic cholera are Vibrio cholerae toxic serogroups O1 and O139. Cholera symptoms include watery diarrhea and severe dehydration, which can rapidly result in death unless rehydration therapy is prompt (1). Antimicrobial agents may reduce the severity and duration of disease (1); commonly used are tetracyclines, fluoroquinolones, macrolides, and trimethoprim/sulfamethoxazole (1). However, V. cholerae resistance to antimicrobial drugs is increasing because of the accumulation of genetic mutations and the acquisition of resistance genes, which are usually transferred on mobile genetic elements such as integrating conjugative elements (ICEs) (1).

As of March 12, 2014, the ongoing cholera outbreak that began in Haiti in October 2010 had caused 700,796 cases and 8,548 deaths (2). To characterize infections, the National Public Health Laboratory in Haiti and the US Centers for Disease Control and Prevention (CDC) collaborated to perform standard microbiological and antimicrobial-drug susceptibility testing on isolates from case-patients.

Since October 2010, the National Public Health Laboratory has identified 465 isolates, which were then forwarded to CDC for determination of MICs for 15 antimicrobial agents by broth microdilution (Sensititre; Trek Diagnostics Systems, Cleveland, OH, USA) according to manufacturer’s recommendations (Table). Resistance was defined by the Clinical and Laboratory Standards Institute interpretive standards, when available (3). The typical outbreak strain (2010EL–1786) displayed resistance to streptomycin, sulfisoxazole, trimethoprim/sulfamethoxazole, and nalidixic acid, and decreased susceptibility to ciprofloxacin and chloramphenicol (4). Resistance was caused by mutations in the QRDR regions of the gyrA and parC genes and presence of ICEVchHai1 containing the dfrA1, floR, strAB, and sul2 resistance genes (4).

In April of 2012, the 2 agencies began sentinel laboratory-based surveillance for acute diarrheal disease at 4 hospitals in Haiti (5). As part of this surveillance, fecal specimens were sent to the National Public Health Laboratory for organism isolation, identification, antimicrobial-drug testing, and subsequently to CDC for expanded antimicrobial-drug testing and molecular characterization. One isolate, 2012EL–2176, showed the typical resistance phenotype of the outbreak strain but additional resistance to ampicillin, amoxicillin/clavulanic acid, cefoxitin, ceftriaxone, cefotiofur; the tetracycline MIC was intermediate (Table).

Analysis of this isolate by serotype, pulsed-field gel electrophoresis, multilocus variable number–tandem repeat analysis, and whole-genome sequencing confirmed that the isolate was similar to outbreak isolates (data not shown) (6). PCR and whole-genome sequencing analysis by use of ResFinder (http://www.genomicepidemiology.org/) identified the original outbreak resistance determinants and additional determinants (aac(3)-IIa, blaCMY-2, blaCTX-M-2*, blaTEM-1*, dfrA15, dfr1A1, floR, strAB, and sul2 resistance genes (4).

References


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The plasmid was mobilizable by conjugation (conjugation efficiency = 1.3–9.9 because of lower gene expression (7). This plasmid has additional resistance determinants and the lack of resistance in clindamycin, and decreased susceptibility to azithromycin (Table). The lack of azithromycin (Table) susceptibility testing of the transformant demonstrated transfer of a unique set of resistance determinants (aac(3)-Ia, blà CMY-2, blà CTX-M-2, blà TEM-1, dfrA15, mphA, sul1, and tetA) and a second copy of the resistance genes floR, strAB, and sul2 identical to those located in ICEVchHai1 (8). Antimicrobial-drug susceptibility testing of the transformant demonstrated transfer of the resistance profile and additional resistance to chloramphenicol, tetracycline, and decreased susceptibility to azithromycin (Table). The lack of association between the presence of the resistance determinants floR and tetA and the lack of resistance in V. cholerae has been observed previously, possibly because of lower gene expression (9). The plasmid was mobilizable by conjugation (conjugation efficiency = 1.3–1.4 × 10^3) when E. coli J53 was used as the recipient.

IncA/C plasmids are widespread in Enterobacteriaceae and commonly confer multidrug resistance. BLASTn (http://blast.ncbi.nlm.nih.gov/Blast.cgi) comparison of the completed plasmid p2012EL-2176 sequence with the National Center for Biotechnology Information nucleotide collection showed similarities to other IncA/C-bla CMY plasmids; most similarity (total score = 3.009 × 10^4) was to pAR060302, found in an E. coli isolate from a dairy calf (10). Most IncA/C-bla CMY plasmids have 3 resistance regions: sul2 region (floR-tetA-strAB-sul2), cmy-2 insertion region, and Tn21-like region (aad-aac). Plasmid p2012EL-2176 contains the sul2 and cmy-2 insertion regions and a putative ars-drfA27-aadA16-sul1 resistance gene cassette at the Tn21 location. This plasmid has additional resistance gene insertions: a putative cassette containing a blà TEM1 and aac(3)-Ia gene upstream of the sul2 region and insertions of blà CTX-M-2, sul1, and mphA genes downstream of the ars-drfA27-aadA16-sul1 cassette (online Technical Appendix, http://wwwnc.cdc.gov/EID/article/20/11/14-0889-Techapp1.pdf).

Since discovery of isolate 2012EL-2176, sentinel surveillance has not detected increased antimicrobial-drug resistance among V. cholerae in Haiti. The ability of IncA/C plasmids to acquire novel resistance cassettes from multiple sources makes it difficult to hypothesize as to the origins of plasmid p2012EL-2176. Although this plasmid p2012EL-2176 was most closely related to a plasmid found in E. coli, it was also closely related to plasmids in Salmonella, Klebsiella, and Providencia. Enterobacteriaceae are found in the environment and/or in the host gut; therefore, the isolate could have acquired the plasmid in the environment or within the host. The latter scenario would limit the possible spread of this plasmid and explain its rarity. The original Haiti outbreak isolate has been shown to be poorly naturally transformable, accounting for the lack of acquired chromosomal genes and highly homologous genomic content among outbreak isolates (6). Therefore, the acquisition of plasmids, and their resistance genes, may represent the major source of future variability among V. cholerae involved in the Haiti outbreak.

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Table. Susceptibility, resistance genes, and plasmids associated with Haiti Vibrio cholerae outbreak isolates

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Resistance profiles [MIC mg/L]</th>
<th>Resistance genes/mutations</th>
<th>Plasmids</th>
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<tbody>
<tr>
<td>V. cholerae</td>
<td></td>
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<tr>
<td>2010EL-1786</td>
<td>STR [&gt;64], FIS [&gt;256], TMP/SXT [&gt;4], CIP ([0.5], NAL [&gt;32]</td>
<td>strAB sul2, dfrA1, floR, gyrA(S83I)parC(S85L)</td>
<td>None</td>
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<tr>
<td>V. cholerae</td>
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<tr>
<td>2012EL-2176</td>
<td>AMP [&gt;32], AMC [&gt;32], CRO [&gt;64], FOX [&gt;32], TIO [&gt;8], CHL([16], GEN [&gt;8], STR [&gt;64], FIS [&gt;256], TMP/SXT [&gt;4], TET([8], CIP([0.5], NAL [&gt;32]</td>
<td>blà CMY-2, blà CTX-M-2, blà TEM-1, floR, aac(3)-Ia, strAB, sul2, dfrA1, aac(3)-Ia, strAB, sul2,</td>
<td>IncA/C2</td>
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<tr>
<td>Escherichia coli</td>
<td></td>
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<tr>
<td>DH10B</td>
<td>AMP [&gt;32], AMC [&gt;32], CRO [&gt;64], FOX [&gt;32], TIO [&gt;8], AZM [&gt;16], CHL([32], GEN [&gt;8], STR [&gt;64], TMP/SXT [&gt;4], TET([2]</td>
<td>blà CMY-2, blà CTX-M-2, blà TEM-1, mphA, floR, aac(3)-Ia, strAB, sul2,</td>
<td>IncA/C2</td>
</tr>
<tr>
<td>p2012EL-2176</td>
<td>FIS [&gt;256], TMP/SXT [&gt;4], TET([2]</td>
<td></td>
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</tr>
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</table>

*Drugs tested were AMP, ampicillin; AMC, amoxicillin/clavulanic acid; AZM, azithromycin; CHL, chloramphenicol; CIP, ciprofloxacin; CRO, ceftriaxone; FIS, sulfisoxazole; FOX, cefoxitin; GEN, gentamicin; KAN, kanamycin; NAL, nalidixic acid; STR, streptomycin; TET, tetracycline; TIO, cefotiofur; and TMP/SXT, trimethoprim/sulfamethoxazole; S83I, serine-to-isoleucine change at amino acid position 83; S85L, serine-to-tyrosine change at amino acid position 85. Drugs that yielded intermediate results are followed by (I). Clinical Laboratory Standards Institute break points are not established for AZM. The AZM break points used in this study (>16 mg/L) were established by the National Antimicrobial Resistance Monitoring System and should not be used to predict clinical efficacy.

†E. coli DH10B is intrinsically resistant to STR.
Human Co-Infection with Avian and Seasonal Influenza Viruses, China

To the Editor: In April 2013, a case of co-infection with avian-origin influenza A(H7N9) virus and seasonal influenza A(H3N2) virus was reported in Jiangsu Province, China (1). This case raised concern over the possible occurrence of new reasortants with enhanced transmissibility among humans. Because of the nature of the dynamic reassortment following a single-source introduction to Haiti, the possibility of new reasortant strains in human patients with A(H7N9) infection is needed. We report co-infection in 2 patients in Hangzhou, the capital Zhejiang Province, China, in January 2014.

The co-infections involved influenza A(H7N9) virus and a seasonal influenza virus in the environment and in poultry (2,3), close surveillance for possible new reasortment in human patients with A(H7N9) infection is needed. We report co-infection in 2 patients in Hangzhou, the capital Zhejiang Province, China, in January 2014.

The specific primers used are listed in Table 1 (http://wwwnc.cdc.gov/EID/content/20/11/14-0897-Techapp1.pdf). The accession numbers of these viruses from these 2 patients were deposited in GenBank.

Of 60 patients with laboratory-confirmed influenza A(H7N9) infections in Hangzhou in April 2013 and in January–February 2014, testing of pharyngeal swab samples indicated that 2 patients were also positive for seasonal influenza virus. The pharyngeal swabs were tested by real-time reverse transcription PCR according to protocols provided by the Chinese National Influenza Center. Informed consent for this study was provided by each patient’s spouse.

On January 6, 2014, patient 1 (male, 58 years of age), a resident of Xiaoshan District, had a high fever (39.6°C) and a cough; at a hospital, he received a diagnosis of severe acute interstitial pneumonia. The patient had a history of chronic myelogenous leukemia; his history of exposure to live poultry was not clear. On January 13, infection with influenza A(H7N9) virus was laboratory confirmed; viral RNA from a pharyngeal swab sample collected before oseltamivir treatment was positive for the following: influenza A virus (cycle threshold $C_t = 26$), H7 ($C_t = 27$), N9 ($C_t = 26$), influenza A(H1N1)pdm09 virus H1 ($C_t = 30$), and N1 ($C_t = 30$). The 2 viruses were named A/Hangzhou/10–1/2014(H7N9) and A/Hangzhou/10–2/2014(H1N1)pdm09. The patient received oseltamivir while in the hospital but died on January 18.

On January 5, patient 2 (male, 54 years of age), also from Xiaoshan District, had fever and a cough; at a hospital, he received a diagnosis of severe acute pneumonia. He had a history of aplastic anemia and had been exposed to live poultry 1 week before symptom onset. On January 18, infection with influenza A(H7N9) virus was laboratory confirmed. Viral RNA from a pharyngeal swab sample collected before oseltamivir treatment was positive for the following: influenza A virus ($C_t = 22$), H7 ($C_t = 23$), N9 ($C_t = 22$), and influenza B virus ($C_t = 22$). The viruses were named A/Hangzhou/17–1/2014(H7N9) and B/Hangzhou/17–2/2014(H1N1)pdm09. This patient received oseltamivir but died on January 22.

The hemagglutinin (HA) and neuraminidase (NA) sequences of viruses from these 2 patients were determined by Sanger sequencing. The specific primers used are listed in online Technical Appendix Table 1 (http://wwwnc.cdc.gov/EID/article/20/11/14-0897-Techapp1.pdf). The accession numbers of these sequences and the reference sequences for phylogenetic analyses are