Macrolide-Resistant
Shigella sonnei

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Shigella sonnei UCN59, isolated during an outbreak of S. sonnei in January 2007, was resistant to azithromycin (MIC 64 mg/L). The isolate contained a plasmid-borne mph(A) gene encoding a macrolide 2′-phosphotransferase that inactivates macrolides. Emergence of the mph(A) gene in S. sonnei may limit usefulness of azithromycin for treatment of shigellosis.

Shigellosis remains a common gastrointestinal disease in developing and industrialized countries. It occurs mostly in children <5 years of age; Shigella sonnei is the most frequently isolated species (1). Ampicillin and trimethoprim-sulfamethoxazole alleviate the dysenteric syndrome of shigellosis and reduce the infectious period. However, current resistance patterns limit the use of these drugs (2). Although fluoroquinolones are an effective alternative for adults, they are not approved for shigellosis treatment in children <18 years of age because of their potential toxicity (2,3). Azithromycin, a macrolide, represents an attractive treatment option for several reasons. It has in vitro activity against most Shigella spp. isolates (4), can be given once a day, and attains high intracellular concentrations (5). Despite MICs from 2 to 8 mg/L for Shigella spp., sufficient concentrations of azithromycin in the colon may inhibit Shigella spp. growth (6). Azithromycin is recommended by the American Academy of Pediatrics for treatment of shigellosis in children, by the World Health Organization as a second-line treatment in adults, and, since June 2004, by the Agence Française de Sécurité Sanitaire des Produits de Santé (2,7; www.agmed.sante.gouv.fr/html/10/ficoids/mpr040601.pdf). In 1996, 2002, 2003, and 2007, outbreaks of shigellosis caused by S. sonnei resistant to ampicillin and trimethoprim-sulfamethoxazole occurred in children in northern Paris. The outbreaks occurred in religious schools, similar to cyclic outbreaks in US Jewish schools related to secondary transmission (8,9). We report an outbreak of shigellosis in and around Paris, France, in which azithromycin failure was related to emergence of plasmid-mediated resistance to macrolides.

The Study

On January 24, 2007, S. sonnei strain UCN59 was isolated from a 4-year-old girl admitted to Robert Debré Hospital, Paris, for bloody diarrhea and fever. The strain was resistant to ampicillin, trimethoprim, sulfonamides, and cotrimoxazole but susceptible to quinolones, third-generation cephalosporins, and doxycycline according to the disk-diffusion technique. MICs of macrolides were markedly increased for S. sonnei UCN59 compared with those for a susceptible control S. sonnei UCN62 (Table). From January to April 23, 2007, a total of 50 cases of laboratory-confirmed shigellosis were identified. Isolates included, in addition to UCN59, 31 S. sonnei that had an azithromycin MIC >64 mg/L from 31 children <15 years of age, who had each been prescribed azithromycin for diarrhea. All patients lived in the Paris area and attended 8 religious schools.

Typing by pulsed-field gel electrophoresis (PFGE) and repetitive sequence–based PCR (rep-PCR) by using the automated DiversiLab system (bioMérieux, La-Balme-les-Grottes, France) (10) was performed on the 32 azithromycin-resistant and on 11 azithromycin-susceptible (MIC <16 mg/L) sporadic or outbreak isolates obtained during 1996–2007 in the Paris area. Five different PFGE patterns were obtained by using the enzyme BlnI. All the 2007 outbreak isolates, including the 32 azithromycin-resistant isolates and 2 azithromycin-susceptible isolates, were clustered into a single profile, profile 1 (Figure 1). The presence of azithromycin-susceptible isolates with profile 1 was detected among the 1996 and 2002–2006 outbreak isolates (data not shown), showing the persistence of this clonal type over 10 years in this area of Paris. Other isolates displayed PFGE types 2 to 5. Low diversity of PFGE profiles was consistent with isolation of strains in the same area and for most of them from the same community. Four different patterns with <97% similarity were distinguished by rep-PCR (Figure 2). Again, all the 2007 azithromycin-resistant isolates were clustered; however, they could be distinguished from the 2007 azithromycin-susceptible isolates.

In contrast to PFGE findings, rep-PCR showed that isolates representative of the 1996, 2002, and 2003 outbreaks were genetically related.

The mph(A) gene, which encodes a macrolide 2′-phosphotransferase that inactivates macrolide antimicrobial drugs, was amplified from S. sonnei UCN59 DNA by PCR (11). PCR was negative for the erm(A), erm(TR), erm(B), erm(C), and erm(X) methylase genes; the ere(A), ere(B) genes encoding esterases; the mph(B) gene encoding a phosphotransferase; and the efflux genes mef(A) and msr(A). Sequence of the genes that encode ribosomal structures composing the target of macrolides, rrl, rplD, and

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**rplV** genes in *S. sonnei* UCN59, did not display any mutation in the critical bases of resistance to macrolides.

The genes conferring resistance to ampicillin and erythromycin were transferred en bloc by conjugation from *S. sonnei* UCN59 to a macrolide-susceptible mutant *Escherichia coli* AG100A at a frequency of \( \approx 10^{-3} \) per donor cell-forming unit after the mating period. A single plasmid was extracted from a transconjugant *E. coli* AG100A/pUV21. After restriction analysis, its size was estimated at \( \approx 90 \) kb. PCR experiments showed that this plasmid belonged to incompatibility group I (12). MICs of macrolides for *E. coli* AG100A/pUV21 confirmed that this plasmid conferred cross-resistance to macrolides (Table).

EcoRI-restricted fragments of plasmid pUV21 were transferred to a nylon membrane and hybridized to an *mph*(A) probe. The *mph*(A) gene was borne by an \( \approx 20\) kb EcoRI fragment, confirming that resistance to azithromycin was plasmid-mediated.

After plasmid digestion with *PstI* enzyme, a DNA fragment that conferred resistance to erythromycin was cloned in plasmid pUC18 and introduced by transformation into *E. coli* AG100A to generate *E. coli* K12 AG100A/ pUC18\(\Omega mph*(A). Sequence of the inserted DNA was determined. The fragment contained 4 open reading frames (ORFs) in the same orientation: *mph*(A), *mrx* that putatively encodes a membrane protein, *mphR*(A) that regulates the expression of *mph*(A), and an ORF of unknown function. This series of ORFs was flanked by a copy of IS26 at the 5’ end and a copy of IS6100 at the 3’ end. BLAST analysis (www.ncbi.nlm.nih.gov/blast/Blast.cgi) showed that the nucleotide sequence was nearly identical to that of fragments of plasmid pU302L from *Salmonella enterica* serotype Typhimurium (C.Y. Chen et al., unpublished data, GenBank accession no. NC_006816), of *Shigella flexneri* transposon TnSF1 (J.H. Chen and J.Y. Chen, unpublished data, GenBank accession no. AF188331), and of plasmids pRSB101 and pSRB107 (13,14).

**Conclusions**

Few data are available on azithromycin resistance in *Shigella* spp. A recent report from Bangladesh mentioned that 16% of *Shigella* isolates were resistant to azithromycin and that 62% had intermediate resistance according to the Clinical Laboratory Standards Institute breakpoints recommended for streptococci (\( \geq 1 \) mg/L, resistant; \(< 0.25 \) mg/L, susceptible) (15). However, the MIC\(_{90}\) (MIC at which 90% are susceptible) of \( 8 \) mg/L displayed by the microorganisms was within the normal range of MICs for this microorganism; no isolate had an azithromycin MIC \( > 24 \) mg/L, which suggests that none had acquired resistance to azithromycin. Surveillance for resistance to azithromycin in *Shigella* spp. requires specific breakpoints for this species (3).

The *mph*(A) gene has been detected in the sequence of transposon TnSF1 isolated from *S. flexneri* (J.H. Chen and J.Y. Chen JY, unpublished data, GenBank accession no. AF188331). The *mph*(A) gene was first reported in an *E. coli* isolate from Japan (10). Since then, the gene has been found in *Aeromonas hydrophila*, *Pseudomonas*
References


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