Mechanisms of Quinolone Resistance in Clinical Isolates of Shigella dysenteriae

In gram-negative bacteria, gyrase and topoisomerase IV are primary and secondary targets, respectively, of the fluoroquinolones. In addition to the mutations in the genes encoding the target enzymes (1, 4), quinolone resistance may also be associated with increased efflux of the drugs (2, 5). Possible mechanisms of quinolone resistance were investigated in clinical isolates of Shigella dysenteriae obtained from the International Centre for Diarrhoeal Disease Research, Dhaka, Bangladesh (AK) and the National Institute of Cholera and Enteric Diseases, Calcutta, India (CI, DS, IPB, and IMC). The quinolone resistance-determining regions (QRDR) of gyrA and parC were amplified with the primer pairs 5'TACACCG GTCAACATTGAGG3 and 5'TATGCGATGTCTGAACTGGGCCTG3' and 5'GTATGCGATGTCTGAACTGGGCCTG3' and 5'CGAC AACCGGGATTCGGTG3', respectively. The Ser83→Leu substitution appeared sufficient to confer high-level nalidixic acid resistance (MIC > 250 μg/ml) as determined by standard methods (3) (Table 1). Four strains—DS-1, DS-2, CI-1, and CI-2—for which the norfloxacin MICs were 2 μg/ml and the ciprofloxacin MICs were between 0.5 and 1 μg/ml harbored the mutation Asp87→Gly in GyrA. None of the isolates examined had any mutations in the QRDR-encoding part of the parC gene.

Accumulation of norfloxacin was studied as described by Ghosh et al. (2) by using carbonyl cyanide m-chlorophenylhydrazone (CCCP) (100 μM) as proton motive force (PMF) uncoupler. The DS, CI, and AK series (with the exception of AK19520) showed steady-state levels of accumulation similar to that of AK19520 (Table 1)—evidence against involvement of a PMF-dependent efflux pump in resistance in these strains. Considering the DS and CI series, the mutation corresponding to Asp87→Gly therefore appeared sufficient to confer approximately 10-fold resistance to the fluoroquinolones in comparison with AK19520. On the other hand, the accumulation of norfloxacin at steady state (before addition of CCCP) was less in the IPB and IMC series in comparison with AK19520. Addition of CCCP increased the level of accumulation in these resistant strains to a level comparable to that of AK19520, suggesting a role of a PMF-dependent efflux pump in the development of resistance. Since these strains lacked gyrA or parC mutations in the QRDR, increased efflux pump activity appears likely to be sufficient to confer 20- to 80-fold resistance to the fluoroquinolones compared to AK19520. We have previously shown, using isogenic strains (2), that increased efflux of the fluoroquinolones may be a mechanism of development of fluoroquinolone resistance. The data obtained in this study with clinical isolates supports this notion. However, the possible involvement of gyrB or parE mutations in the decreased susceptibilities of the isolates to quinolones cannot be excluded.

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### TABLE 1. Quinolone susceptibility, alterations in GyrA, and norfloxacin accumulation in clinical isolates of S. dysenteriae

<table>
<thead>
<tr>
<th>Strain(s)</th>
<th>MIC (μg/ml)</th>
<th>Codon change at position:</th>
<th>Accumulation of NFLX&lt;sup&gt;a&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>NAL</td>
<td>NFLX</td>
<td>OFLX</td>
</tr>
<tr>
<td>AK19520</td>
<td>16</td>
<td>0.25</td>
<td>0.25</td>
</tr>
<tr>
<td>AK21104</td>
<td>&gt;250</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>AK27228</td>
<td>&gt;250</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>AK24467</td>
<td>&gt;250</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>AK21809</td>
<td>&gt;250</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>IPB32, IPB34, IMCI18, IMCI19</td>
<td>32</td>
<td>16</td>
<td>4</td>
</tr>
<tr>
<td>IPB38</td>
<td>16</td>
<td>16</td>
<td>4</td>
</tr>
<tr>
<td>IMC67</td>
<td>16</td>
<td>16</td>
<td>4</td>
</tr>
<tr>
<td>DS-1, DS-2</td>
<td>64</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>CI-1, CI-2</td>
<td>64</td>
<td>2</td>
<td>2</td>
</tr>
</tbody>
</table>

<sup>a</sup>NAL, nalidixic acid; NFLX, norfloxacin; OFLX, ofloxacin; CFLX, ciprofloxacin.

<sup>b</sup>The data are means of three determinations ± standard deviations, expressed in micrograms per milligram (dry weight) of cells.

<sup>c</sup>—, identical to the codon in E. coli.

<sup>d</sup>ND, not determined.

### REFERENCES


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