Antibiotic Resistance Patterns of *Vibrio mimicus* Isolated from Human and Environmental Sources in Bangladesh

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Twenty-five environmental and 19 clinical strains of *Vibrio mimicus* were tested for antibiotic susceptibility patterns. Environmental strains were resistant to streptomycin, kanamycin, and trimethoprim-sulfamethoxazole; clinical strains were susceptible. Environmental strains showed variable resistance to ampicillin (44%), but clinical strains were susceptible. All strains tested were susceptible to chloramphenicol and gentamicin.

Atypical strains of *Vibrio cholerae* which do not ferment sucrose and which are Voges-Proskauer negative have been shown to be a distinct species and are now called *Vibrio mimicus* (5, 7, 13).

*V. mimicus* isolations were recently made from aquatic environments (6) and patients (11) in Bangladesh. It has been reported that clinical isolates of *V. mimicus* are susceptible to common antibiotics, including ampicillin, carbenicillin, cephalothin, chloramphenicol, gentamicin, kanamycin, streptomycin, trimethoprim-sulfamethoxazole, and tetracycline (7, 11, 12). We are unaware of published studies that deal with the antibiotic susceptibilities of environmental strains of *V. mimicus*. In this study, environmental strains were collected from September 1984 to April 1985 from a river, lake, and pond in Dacca, Bangladesh. In addition, we collected several isolates from patients attending the Dacca hospital of the International Centre for Diarrhoeal Disease Research, Bangladesh (ICDDR,B). Identification of the isolates was done with the API 20E system (10) and conventional biochemical tests. Human and environmental isolates were characterized as *V. mimicus* with some minor biochemical differences. Production of β-galactosidase (o-nitrophenyl-β-D-galactopyranoside) and gelatinase was noted with all environmental isolates. Clinical isolates were 74 and 90% positive, respectively, for these characteristics.

After biochemical identification, all *V. mimicus* isolates were immediately tested for antibiotic susceptibility. We used the standard agar disk diffusion method (3), which is a modification of that described by Bauer et al. (4). Nearly all the environmental strains were resistant to streptomycin, kanamycin, tetracycline, and trimethoprim-sulfamethoxazole, whereas the clinical strains were susceptible to these drugs. There was a variable resistance of environmental isolates to ampicillin (44%) which was not seen with clinical isolates (0%). Both environmental and clinical isolates were uniformly susceptible to chloramphenicol and gentamicin (Table 1).

These results show a marked difference in the antibiotic resistance patterns of *V. mimicus* from human and environmental sources. Human isolates were uniformly susceptible to several commonly used antibiotics, in agreement with the observations of other investigators (8). However, the high levels of antibiotic resistance we encountered with our environmental strains were surprising. If this difference is consistently observed with *V. mimicus* strains, it could be a useful marker for differentiating human and environmental isolates. These observations may also have taxonomic implications, in that *V. mimicus* may in fact be a heterologous group of closely related organisms with various virulence capabilities. The marked differences in antibiotic susceptibility patterns between human and environmental strains may be a reflection of this intragenetic variation. Further characterization of the antibiogram patterns of environmental and human strains is necessary.

It would likewise be helpful to determine the stability of the so-called environmental and human antibiogram patterns we observed with *V. mimicus*. In vivo recombinatory events between gut flora may significantly alter the antibiotic susceptibility patterns of ingested strains. The existence of such transfer is well documented with members of the family *Enterobacteriaceae* (1, 2) and has likewise been reported with the *Vibrionaceae* (9; E. J. Threlfall, B. Rowe, and I. Huq, Letter, Lancet i:1247–1248, 1980). However, if there is a stable virulence-associated antibiotic susceptibility pattern, it is of potential diagnostic significance. These issues remain to be clarified and are under investigation in our laboratory.

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**TABLE 1. Antibiotic susceptibility pattern of environmental and clinical isolates of *V. mimicus***

<table>
<thead>
<tr>
<th>Antibiotic and amt (μg)</th>
<th>Resistant <em>V. mimicus</em> isolates (%)</th>
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</thead>
<tbody>
<tr>
<td></td>
<td><strong>Environmental</strong></td>
</tr>
<tr>
<td></td>
<td><em>(n = 25)</em></td>
</tr>
<tr>
<td>Streptomycin (10)</td>
<td>100</td>
</tr>
<tr>
<td>Kanamycin (30)</td>
<td>92</td>
</tr>
<tr>
<td>Tetracycline (30)</td>
<td>92</td>
</tr>
<tr>
<td>Trimethoprim-sulfamethoxazole (1.25/23.75)</td>
<td>92</td>
</tr>
<tr>
<td>Ampicillin (10)</td>
<td>44</td>
</tr>
<tr>
<td>Chloramphenicol (30)</td>
<td>0</td>
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<tr>
<td>Gentamicin (10)</td>
<td>0</td>
</tr>
</tbody>
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