In 1988, Megraud et al. reported the first isolation of UPTC from human clinical infection, where these organisms were isolated from an appendix as well as from human faeces. This group of organisms is the Campylobacter found most frequently in shellfish and waters.

UPTC organisms were isolated by selective enrichment from shellfish grown in several marine inshore waters around Northern Ireland, as previously described. From these samples, 21 isolates of this taxon were obtained and their susceptibility to ciprofloxacin (5 µg), enrofloxacin (5 µg), ofloxacin (5 µg), tetracycline (30 µg) and erythromycin (5 µg) was determined by disc susceptibility testing, in accordance with NCCLS methodology. As there is no standardized disc method specifically for Campylobacter, including guidance criteria for interpretation of zone sizes, susceptibility was assigned arbitrarily in comparison with known resistant and susceptible clinical isolates of Campylobacter jejuni, Campylobacter coli and Campylobacter lari isolated from human faeces. Results demonstrated that none of the environmental campylobacters isolated from the shellfish was resistant to any of the antibiotic agents tested. Although UPTC have been described occasionally in humans, we have not identified any of these organisms as a cause of gastrointestinal disease from human faecal specimens submitted to the Northern Ireland Public Health Laboratory for the period 1980–present, nor have we been able to isolate these from the stools of healthy individuals. Similarly, we have not been able to isolate these organisms from poultry in Northern Ireland. Previously, we have reported that the niche for these organisms has been aquatic environments and wild seagulls. Consequently, as these organisms have never been isolated from human and animal sources, where antibiotics may have been used, it is unlikely that they have developed or acquired resistance mechanisms to overcome artificial antibiotic selective pressure. Conversely, where fluoroquinolones have been used in Northern Ireland and the Republic of Ireland in human and animal populations, we do experience varying degrees of fluoroquinolone resistance. This report therefore suggests that where selective antibiotic pressure is not applied, fluoroquinolone resistance is less likely to be acquired. Therefore, this report supports the concept of minimizing the employment of such antibiotics in both human and veterinary medicine to help reduce the burden of antibiotic resistance.

Acknowledgements

Anne Canney contributed to the work described in this article and in ordinary circumstances would have been a named author. Unfortunately, we were unable to contact her to obtain her consent to the submission of this article and we were therefore unable to add her name to the author list.

References


Correspondence

Sir,

Between May and September 2001, six glycopeptide (vancomycin and teicoplanin)-resistant (GRE) strains of Enterococcus faecalis were isolated from six patients admitted to hospital (Complejo Hospitalario Universitario Juan Canalejo, La Coruña) for treatment of different diseases. Microbiological identification was performed by MicroScan and confirmed by PCR, with specific primers to ddi of E. faecalis. The antibiotic resistance phenotype was determined by microdilution following NCCLS criteria, and the MICs of glycopeptides were confirmed by Etest. Clonal identity was performed by analysis of the genomic DNA of the E. faecalis isolates digested with Smal, by PFGE, as described previously. The isolates were classified epidemiologically, according to published criteria. The putative presence of vanA and vanB were analysed in the E. faecalis GRE strains. The six patients, who were either infected or colonized by the GRE strains, had been admitted to four different wards in the hospital complex (Table 1). The enterococci strains were isolated from urine.

Keywords: enterococci, hospital infections, glycopeptide resistance

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Table 1. Patients included in this study from whom the different strains of *E. faecalis* were isolated

<table>
<thead>
<tr>
<th>Patient data [no., sex/age (years)]</th>
<th>Type of infection*</th>
<th>Underlying disease</th>
<th>Specimen</th>
<th>Ward*[b]</th>
<th>Previous antibiotic treatment*[c]</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. F/53</td>
<td>UTI</td>
<td>lymphoma</td>
<td>urine</td>
<td>Haem</td>
<td>AMC, SXT</td>
</tr>
<tr>
<td>2. F/22</td>
<td>ulcer</td>
<td>leukaemia</td>
<td>exudate</td>
<td>Haem</td>
<td>PEN, AMK, FEP, VAN, MTZ</td>
</tr>
<tr>
<td>3. F/54</td>
<td>UTI</td>
<td>myeloma</td>
<td>urine</td>
<td>ICU</td>
<td>IPM, MEM, SXT, FLC, AMK, AMP, MTZ, FEP</td>
</tr>
<tr>
<td>4. F/81</td>
<td>UTI</td>
<td>myeloma</td>
<td>urine</td>
<td>Haem</td>
<td>AMP, FEP</td>
</tr>
<tr>
<td>5. M/70</td>
<td>AbA</td>
<td>renal failure</td>
<td>abscess</td>
<td>SUNI</td>
<td>IPM</td>
</tr>
<tr>
<td>6. F/77</td>
<td>UTI</td>
<td>blood infection, diabetes</td>
<td>urine</td>
<td>MUNI</td>
<td>IPM, FLC, CIP, TEC, MEM</td>
</tr>
</tbody>
</table>

*UTI, urinary tract infection; AbA, abdominal abscess.

*a Haem, haematology; ICU, intensive care unit; SUNI, surgical unit; MUNI, medical unit.

*c AMC, co-amoxiclav; AMK, amikacin; AMP, ampicillin; CIP, ciprofloxacin; FEP, cefepime; FLC, fluconazole; IPM, imipenem; MEM, meropenem; MTZ, metronidazole; PEN, penicillin; SXT, trimethoprim/sulfamethoxazole; TEC, teicoplanin; VAN, vancomycin.

(n = 4), abdominal abscess (n = 1) and ulcer exudate (n = 1). The index case was patient no. 1 (Table 1). All of the patients had severe underlying diseases and received antibiotic treatment prior to GRE isolation. The outbreak was controlled by implementation of certain measures, such as isolation of patients in single wards and strengthening of the standard precautions for the prevention of infection by contact. All surfaces in the wards were also cleaned. Healthcare personnel were reminded to wash their hands carefully before and after contact with patients and to wear disposable gloves and gowns.

According to the results of the PFGE, the GRE strains were classified as indistinguishable (data not shown).

All GRE strains were resistant to vancomycin and teicoplanin (MIC > 128 mg/L), as well as to erythromycin (MIC > 4 mg/L), ciprofloxacin (MIC > 2 mg/L) and ofloxacin (MIC > 4 mg/L), and they remained susceptible to ampicillin, piperacillin–tazobactam, imipenem, meropenem, rifampicin and tetracycline. The patients were treated with ampicillin with good resolution of clinical symptoms.

The six GRE strains of *E. faecalis* harboured the vanA gene and yielded a negative PCR result with vanB primers.

Overall, the results showed that high levels of glycopeptide resistance were associated with the presence of the vanA gene in the strains under study.

A single clone of *E. faecalis* carrying the vanA gene has recently been detected in hospitals in different areas of Spain. However, to our knowledge the present report is the first description of a nosocomial outbreak of infection in Spain caused by a GRE strain of *E. faecalis* harbouring the vanA gene and in addition several virulence factors (data not shown). Fortunately, although the presence of the vanA gene was associated with a high level of resistance to glycopeptides, the patients were treated with ampicillin and the GRE strains were eradicated and infectious clinical symptoms resolved.

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References


