Brief report

Molecular epidemiology and antimicrobial susceptibility of *Campylobacter coli* clinical isolates

Ana Ruiz-Castillo, María José Torres-Sánchez, Javier Aznar-Martín

**A R T I C L E   I N F O**

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**A B S T R A C T**

**Introduction:** *Campylobacter* spp. is a major cause of acute bacterial diarrhea in humans worldwide, and *C. coli* is responsible for 10% of the cases.

**Materials and methods:** A study was made of the antimicrobial susceptibility using the E-test®, and the clonal relationship using PCR-RFLP, of the *flaA* gene, as well as PFGE techniques on 43 *C. coli* clinical isolates.

**Results:** Only 49% and 2% of the isolates were susceptible to erythromycin and ciprofloxacin, respectively. Imipenem and clindamycin, with 100% and 84% of the strains, respectively, being susceptible, were the most active antimicrobials. The PCR-RFLP of *flaA* gene technique grouped fourteen isolates into six clusters, while the PFGE technique grouped eleven isolates into five clusters.

**Conclusion:** Ciprofloxacin and erythromycin are not suitable for the treatment of *C. coli* infections. Clin-damycin could be considered as a therapeutic alternative in cases of enteritis, while imipenem is the best alternative for extra-intestinal infections. Both PFGE and PCR-RFLP can be useful to detect clones.

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**Introduction**

*Campylobacter* spp. is a major cause of acute bacterial diarrhea in humans worldwide, especially in developed countries. *Campylobacter jejuni* is responsible for a majority of cases (about 90% of cases) and is associated to *C. coli*. The most important sources of human infection are the handling and consumption of contaminated meat from domesticated animals, but other potential sources are described. A large proportion of cases are considered as sporadic disease, although outbreaks of campylobacteriosis have been identified.

The antimicrobials resistance rates among *Campylobacter* spp. have increased overtime, and numerous studies have been performed to understand the mechanisms of antibiotic resistance, its implication in the fitness of the bacteria as well as the epidemiology of this antimicrobial resistance. Several genotyping methods have been developed to identify as well as to study the epidemiology of *Campylobacter* spp., which include among others pulsed-field gel electrophoresis (PFGE) and *flaA* gene typing. The aim of this study is to determine the susceptibility of *C. coli* clinical isolates to several antimicrobials. Additionally, two molecular methods, PCR-RFLP of *flaA* gene and pulsed-field gel electrophoresis (PFGE), were used to establish the clonal relationship of the isolates.

**Materials and methods**

**Strains**

From January 2011 to July 2012, 406 *Campylobacter* spp. (346 *C. jejuni* and 60 *C. coli*) isolates were obtained from 13,966 human fecal samples, submitted to the clinical microbiology laboratory of the University Hospital Virgen del Rocío in Seville, Spain. The strains were isolated from fecal samples streaked onto modified Skirrow medium agar after 48 h of micro-aerobically incubation at 42°C. Identification of *C. coli* included Gram staining, oxidase and catalase activities, the hippurate test and an additional method, the matrix assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF).

**Antimicrobial susceptibility testing**

Among the 60 *C. coli* isolates, 10 were duplicated isolates and 7 could not be recovered. The susceptibility testing to erythromycin, ciprofloxacin, tetracycline, tobramycin, amoxicillin–clavulanic, clindamycin and imipenem of the 43 *C. coli* isolates was studied by the E-test® (Biomerieux) method. The MIC breakpoints for erythromycin, ciprofloxacin, tetracycline, tobramycin and amoxicillin–clavulanic established by the FSM (French Society for Microbiology) were used, and for imipenem and clindamycin those of the non-related species EUCAST breakpoints and the epidemiological of EUCAST breakpoints respectively were used for clinical categorization of the isolates.

Statistical analysis with Yates test, Chi² and Fisher’s Exact Probability Test was performed as needed.

**Molecular genotyping**

Forty-three isolates were analyzed by Restriction fragment length polymorphism of the *flaA* gene (PCR-RFLP *flaA*) with Ddel enzyme as previously described, and by PFGE using the standardized PulseNet protocol, with the *Salmonella* Braenderup H9812 strain restricted with XbaI as a size standard. In both techniques, profiles were analyzed and compared using FQuest® (Biorad) program, and clones were defined as isolates with indistinguishable banding patterns.

**Results**

A male predominance (60% of cases) of two age groups was found among the patients with *C. coli* infections: children aged 1–5 years (38%) and adults over 40 years old (21%). 83.8% of hospitalized patients belonged to the latter group, and 10% of cases 10% is associated to *C. coli*. A higher rate of resistance in *C. coli* is responsible for a majority of cases (about 90% of cases) in humans worldwide, especially in developed countries.

**Discussion**

Our results are similar to those described by Olson et al., who found a 20% higher incidence of *C. coli* infection in the male population, and in children aged 1–4 years and over 40 years. In developing countries, where exposure to the bacteria is very high, there is a peak in childhood which then decays strongly due to the protective antibodies. However, in developed countries, as in this study, with less exposure to the organism two peaks are found, one at childhood and the second in middle-aged adult as we have found.

Erythromycin is considered the antimicrobial of choice for *Campylobacter* infections treatment, but a high level of macrolides resistance in *C. coli* have been described, and we have found a 51% of non-susceptible *C. coli* human isolates. Additionally, several studies have warned of the increasing incidence of the resistance rate to this antimicrobial in various parts of the world, with especially high rates in Spain. In our study, ciprofloxacin, with 98% of resistant strains, is a highly ineffective treatment against infections.

Although antimicrobial treatment is not needed in most cases of *C. coli* gastrointestinal infections; in young children, the elderly, pregnant women, immunocompromised patients, and in serious, prolonged or extraintestinal infections, it requires antimicrobial treatment. In these cases, alternative antibiotics should be used in the treatment of infections due to resistant strains.

According to our results, clindamycin (84% of susceptible strains) could be considered as a therapeutic alternative in cases of enteritis although in other studies in both clinical and animal strains variable rates of resistance are found. The best alternative for extraintestinal infections *C. coli* is imipenem, which is active against all the clinical isolates, as previously suggested by other authors.

In the case of aminoglycosides, tobramycin could also be a good alternative for extraintestinal infections, but its use should be guided by the results of susceptibility testing since we found a 33%
of non-susceptible strains. Although in most countries the resistance to aminoglycosides is scarce, in others like China resistance rates of 20% have been found.6,9

Furthermore, we have shown a very high percentage of multiresistant strains among the erythromycin non-susceptible strains, which will increase the challenge of the treatment of these infections, with imipenem being the only alternative therapeutic in severe clinical situations.

Both PFGE and PCR-RFLP of the flaA gene allow clonal differentiation of the strains studied. The PFGE technique generates an adequate number of bands which gives greater power of discrimination. We obtained a high percentage of unique strains: 74% and 69% by PFGE and PCR-RFLP flaA gene respectively. This genetic heterogeneity is also found in numerous studies of human, animal and environmental isolates.15,16

In those cases where an outbreak is suspected both genotypic techniques can be useful to detect clones and could help to understand the epidemiology of these infections.

Conflict of interest

The authors declare no conflict of interest.

Table 1

Antimicrobial susceptibility of the 43 strains of Campylobacter coli.

<table>
<thead>
<tr>
<th>Antimicrobial</th>
<th>( \text{CM}_{50} )</th>
<th>( \text{CM}_{90} )</th>
<th>Susceptible (%)</th>
<th>Non-susceptible (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Erythromycin</td>
<td>1</td>
<td>&gt;256</td>
<td>21 (48.8)</td>
<td>22 (51.2)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>&gt;32</td>
<td>&gt;32</td>
<td>1 (2.3)</td>
<td>42 (97.7)</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>1 (2.3)</td>
<td>42 (97.7)</td>
</tr>
<tr>
<td>Tobramycin</td>
<td>1.5</td>
<td>8</td>
<td>29 (67.4)</td>
<td>14 (32.6)</td>
</tr>
<tr>
<td>Amoxicillin–clavulanic</td>
<td>4</td>
<td>&gt;256</td>
<td>23 (53.5)</td>
<td>20 (46.5)</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>0.5</td>
<td>6</td>
<td>36 (83.7)</td>
<td>7 (16.3)</td>
</tr>
<tr>
<td>Imipenem</td>
<td>0.25</td>
<td>0.38</td>
<td>43 (100)</td>
<td>0 (0)</td>
</tr>
</tbody>
</table>

Table 2

Antimicrobial resistance among erythromycin susceptible and non-susceptible Campylobacter coli strains.

<table>
<thead>
<tr>
<th>Antimicrobial</th>
<th>Erythromycin-susceptible strains (n=21)</th>
<th>Erythromycin-non-susceptible strains (n=22)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Non-susceptible (%)</td>
<td>Non-susceptible (%)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>21 (100)</td>
<td>21 (95.5)</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>15 (71.4)</td>
<td>19 (86.4)</td>
</tr>
<tr>
<td>Tobramycin</td>
<td>4 (19.1)</td>
<td>10 (45.5)</td>
</tr>
<tr>
<td>Amoxicillin–clavulanic</td>
<td>7 (33.3)</td>
<td>13 (59.1)</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>0 (0)</td>
<td>7 (31.81)</td>
</tr>
<tr>
<td>Imipenem</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Multidrug-resistance</td>
<td>8 (38.1)</td>
<td>19 (86.4)</td>
</tr>
</tbody>
</table>

\( p = 0.005. \) \( p = 0.003. \)

References


