Campylobacter jejuni isolates in Finnish patients differ according to the origin of infection

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Abstract

Background: Campylobacter jejuni is a significant cause of bacterial enteritis worldwide. Very little is known about the pathogenicity mechanisms and virulence factors of this important enteropathogen. C. jejuni isolates from 166 Finnish patients, collected from July to December in 2006, were studied for the presence of putative virulence factors and susceptibility to antimicrobials. Isolates were tested for production of γ-glutamyltransferase (GGT) as well as the presence of genes ceuE, cgtB, ciaB, cj0486, pldA, virB11, wlaN, and the gene cluster cdtaABC. Bacterial characteristics were compared to information on foreign travel history as well as information on the course and the symptoms of disease obtained from questionnaires returned by patients.

Results: Except for one domestic isolate, antimicrobial resistance was only detected in isolates of foreign origin. Univariate analyses showed association between bloody stools and both GGT production (p = 0.025) and the presence of cgtB (p = 0.034). Multivariate analysis verified that GGT production was more prevalent in domestic isolates (p < 0.0001), while the genes cj0486 (p < 0.0001) and ceuE (p < 0.0001) were associated with C. jejuni isolates of foreign origin.

Conclusions: The results indicate that imported and domestic C. jejuni isolates differ significantly in several aspects from each other.
may show ganglioside-mimicking structures important for the triggering of Guillain-Barré syndrome, an acute peripheral polyneuropathy, after C. jejuni infection [18]. Cytotoxic distending toxin (CDT, encoded by the gene cluster cdtABC) has been present in most of the tested isolates [19] but its role in the outcome of the disease still remains uncertain. Likewise, a recent report showed γ-glutamyl transpeptidase (GGT, encoded by the gene ggt) to have a role in the persistent colonization of the avian gut [20], but its importance in the course of human campylobacteriosis is not known.

We have recently demonstrated that C. jejuni isolates of domestic origin and those highly susceptible for ciprofloxacin were associated with a more severe form of enteritis characterized by bloody stools [21]. Our aim in the present study was to reveal other bacterial factors that may affect the outcome of the C. jejuni infection in a well-characterized clinical material including both infections acquired abroad or in Finland. For that purpose, we analyzed 166 clinical isolates of C. jejuni for the presence of GGT and the presence of the genes virB11, ciaB, cgtB, wlaN, cj0486, ceuE, pldA and cdtABC.

Methods

Patients and Campylobacter isolates

A total of 166 patients with sporadic stool culture-verified C. jejuni infection (no other bacterial enteropathogens detected) were included in the present study. Their stool samples were collected from July 1 to December 31, 2006, and they had returned questionnaires including questions concerning travelling abroad within two weeks before the onset of symptoms, the clinical course of the illness and antimicrobial therapy. The patients belonged to a group of 192 persons (originally also including C. coli positive patients), some results of which have earlier been presented [21]. All the isolates were hippurate positive and were stored at -70°C before analyzed.

Susceptibility testing

The minimal inhibitory concentration (MIC) values of ciprofloxacin (Bayer, Leverkusen, Germany), doxycycline (Orion Pharma, Espoo, Finland) and erythromycin (Amdipharm Ltd, Dublin, Ireland) were determined by an agar dilution method according to the CLSI guidelines [22]. Mueller-Hinton agar (Oxoid, Basingstoke, UK) plates supplemented with defibrinated sheep blood (5%) and the control strain C. jejuni ATCC 33560 were used. The susceptibility of the isolates was interpreted according to CLSI [23]. The results of susceptibility of the isolates to ciprofloxacin have been published earlier [21].

PFGE typing

PFGE analysis was performed for 75 (all 40 domestic and all 35 travel-associated isolates collected in July, as the prevalence of cases per month was the highest during this month) isolates as described earlier [3,24]. Isolate was considered to represent a new type when PFGE KpnI profile differed by at least one band.

γ-Glutamyl transpeptidase activity

In the first phase we studied the presence or absence of ggt gene as described in our previous study [25]. All isolates positive for the gene were further analyzed for the production of GGT. Qualitative detection of GGT activity was achieved as described previously for Helicobacter pylori [26]. Briefly, approximately 10⁸ bacteria were suspended in a reagent containing 50 mM Tris (pH 8.25), 1.5 mM L-γ-glutamyl-carboxyl-3 nitro-4 anilide and 50 mM glycylglycine. The mixture was incubated for 1 h at 37°C. Cleavage of the substrate by γ-glutamyl transpeptidase turned the mixture yellow in color.

PCR detection of other putative C. jejuni virulence factors

DNA was extracted from C. jejuni isolates using the following protocols. Bacteria (10⁶ CFU) were harvested from blood agar plates (Columbia agar II containing 8% vol/vol whole horse blood), dissolved in 500 μl of ddH₂O and incubated in a boiling water bath for 10 min. Cell debris was removed by centrifugation at 18 000 g for 2 min. For some isolates DNA was extracted using either a method utilizing guanidium thiocyanate [27], DNeasy Blood & Tissue kit (Qiagen) or Wizard Genomic DNA Purification Kit (Promega, UK) according to the manufacturer’s instructions. Successful extraction of template C. jejuni DNA from each isolate was confirmed by PCR amplification of the house keeping gene glyA. The presence of the gene glyA and the putative virulence factors virB11, ciaB, cgtB, wlaN, pldA, ceuE, cj0486 as well as the cdtABC operon were determined by PCR using the primers listed in Table 1. The reaction mixture was prepared in 1× AmpliTaq Gold 360 buffer with 1.25U of AmpliTaq Gold 360 polymerase (Applied Biosystems, USA), 200 μM dNTP (Fermentas, Germany), 0.2 μM of each primer (Eurogentec, Ougrée, Belgium) and 5 μl of template DNA in a total volume of 25 μl.

The PCR reactions started with a denaturation step at 95°C for 10 min. The cycling conditions were 25 cycles of 95°C for 30 s, annealing temperatures (Table 1) for 30 s and 72°C for 60 s (120 s for cdtABC). For virB11 and glyA a touch down protocol was run with 5 cycles at 53°C, 5 cycles at 52°C and 15 cycles at 51°C. The reactions ended with an additional extension step at 72°C for 7 min. DNA extracted from C. jejuni NCTC 11168 was used as a positive control for the genes cdtABC, wlaN and CJ0486 and DNA from C. jejuni 81176 served as a positive control for all other virulence genes. A PCR reaction without added template was used as a negative control.
Table 1: Primer sequences, annealing temperatures and PCR product sizes for the putative virulence factors studied

| Gene   | Primers      | Sequence (5'-3') | Annealing temp (°C) | Product (bp) | Reference |
|--------|--------------|------------------|---------------------|--------------|-----------|
| gyIA   | Gy-Fw        | GAGTTAGAGGCCTCAATGTGAAGG | 53-51               | 1052         | [36]      |
|        | Gy-rev       | AAACCTTCGGTAATGAAGG |                     |              |           |
| virB11 | VirB-232     | TCTTGAGTTGCGCCTAACCCTTT  | 53                  | 494          | [35]      |
|        | VirB-701     | CTCGGCGTTCTGTTGTAATTACC |                   |              |           |
| ceuE   | CeuE405F     | GATAAAGTGTTGGCCTC | 60                  | 405          | *         |
|        | CeuE405R     | CCGGATTGCGGACCAAGG |                     |              |           |
| cidB   | ciaB355F     | CAGAAAGGCAATTTTGAGGC | 58                  | 355          | *         |
|        | ciaB355R     | ATATCCCTTTACGACCCAC |                     |              |           |
| pldA   | pldA-84fwd   | AAGCTTATGCCTTTTT | 45                  | 913          | [35]      |
|        | pld-981rev   | TATAAGGCTTTCTCCA |                     |              |           |
| Cj0486 | Cj0486fwd    | GATAGAGCATTAATTTGGAATGC | 58              | 1263         | [13]      |
|        | Cj0486rev    | CCTATAAAGCCATACCCAAGCC |                   |              |           |
| wlaN   | wlaN-DL 39   | TTAAGGCGAGTAATGAAAGGTTG | 60              | 434          | [17,37]   |
|        | Gj1139CF    | TGGTTGATACAAAGGTTG |                     |              |           |
| cgtB   | wlaN-DL 39   | TTAAGGCGAGTAATGAAAGGTTG | 56              | 563          | [17]      |
|        | cgBrev      | GCACATAGAGAAGGCTCAA |                     |              |           |
| cidABC | LYT-F        | CTTATGCGATCTTCTAAAAATTT | 55              | 2111         | [38]      |
|        | MII-R       | GTAAGGATGGGGTATATCATTT |                     |              |           |

*Personal communication: Rafal Gierczyński, National Institute of Public Health, Warsaw, Poland.

Statistical analyses
Statistical analyses were performed with GraphPad Prism version 4.03 (GraphPad Software, San Diego, CA, USA) and PASW Statistics 18 (SPSS for Windows, Rel. 18.0.2. 2010. SPSS Inc, Chicago, IL, USA). The χ² test and Fisher’s exact test were used for comparison of categorical variables. Multivariate analyses were performed with stepwise binary logistic regression models. All tests were two-sided, and a p-value < 0.05 was considered to be significant.

The study was approved by the Ethics Committee of the Hospital District of Helsinki and Uusimaa.

Results
Of the 166 cases of C. jejuni infection in the study 126 were acquired abroad and 40 were acquired in Finland. Resistance to erythromycin (4 isolates) and resistance to doxycycline (59 isolates) were only detected in isolates of foreign origin. All except one of the isolates of domestic origin were susceptible for ciprofloxacin whereas 83/126 (66%) of isolates of foreign origin were resistant to ciprofloxacin as published earlier [21]. Prevalence of the putative virulence markers among the isolates according to MICs to ciprofloxacin and doxycycline, respectively, is presented in Table 2. GGT-production was associated with susceptibility to ciprofloxacin and doxycycline in the univariate analysis. On the other hand, both ciprofloxacin- and doxycycline-resistant isolates were more likely than the susceptible ones to harbor the genes cj0486 and ceuE (Table 2).

Contingency tables were also used to assess whether the presence of putative virulence factors correlated with clinical data. In the univariate analysis (Table 3), GGT production and the presence of the gene cgtB were associated with bloody stools. In addition, isolates lacking the ceuE gene were associated with hospitalization, as 8/24 (33%) of the patients infected with ceuE-negative isolates were hospitalized, compared to 21/139 (15%) of those with ceuE-positive isolates (p = 0.031). GGT production was strongly associated with infections acquired in Finland as compared to infections from abroad. On the other hand, the genes cj0486 and ceuE were markedly more common among isolates of foreign origin. Of all the domestic isolates, 34/40 (85%) were positive for both cj0486 and ceuE whereas the number of foreign isolates was 60 (48%), respectively (p < 0.0001). A total of 69/126 (55%) of the imported isolates, but only 7/40 (18%) of the domestic isolates were positive for both cj0486 and ceuE (p < 0.0001). The significant findings in the univariate model were controlled with a multivariate analysis to assess whether some of the variables were independently associated with each other. GGT-production was independently associated with domestic infections, and the genes cj0486 and ceuE were independently associated with imported infections, respectively (Table 4). Although bloody diarrhea was significantly associated with both GGT-production and the presence of cgtB in the univariate analysis, this factor could not be further analyzed with a multivariate analysis as the proportion of missing data in the questionnaires regarding this specific finding was too high (28%).

PFGE analysis with KpnI digested samples revealed that among the 40 domestic isolates, a total of 32 PFGE types were identified indicating a high diversity.
Furthermore, all the 35 isolates of foreign origin analyzed had different PFGE profiles, which did not overlap with those of domestic isolates. Thus, the isolates were highly diverse and did not seem to have a common source.

**Discussion**

We recently showed that bloody stools were more common among patients infected with *C. jejuni* isolates of domestic origin and those highly susceptible for ciprofloxacin [21]. *C. jejuni* isolates of Finnish origin have even earlier been shown to differ significantly from those of foreign origin as being almost exclusively susceptible for ciprofloxacin [28,29]. In the present study, we further analyzed possible differences between *C. jejuni* isolates acquired in Finland and those from abroad and screened for the presence of certain putative virulence markers. Significant differences were detected as GGT production was independently associated with infection of domestic origin and the isolates of foreign origin significantly more often harbored the genes *cj0486* and *ceuE*, findings also verified with a multivariate analysis.

GGT is an enzyme present in both bacteria and eukaryotes. It has a role in glutathione and glutamine metabolism in *C. jejuni* [30]. The presence of *ggt* has been shown to vary among *C. jejuni* isolates [20,31] and we

### Table 2 Contingency table results for antimicrobial susceptibility and putative virulence markers among 166 *C. jejuni* isolates

| MIC values | GGT-production | virB11 | ciaB | cgtB | wlaN | cj0486 | ceuE | pldA | cdtABC |
|------------|----------------|--------|------|------|------|--------|------|------|--------|
| Ciprofloxacin MIC ≤ 1 (82/166) * | 20/82 (p = 0.001) § | 1/82 | 81/82 | 16/82 | 17/82 | 31/82 | 62/82 | 52/82 | 69/82 |
| Ciprofloxacin MIC ≥ 4 (84/166) † | 5/84 | 3/84 | 83/84 | 15/84 | 22/84 | 50/84 (p = 0.0051) ¶ | 80/84 (p = 0.0003) ¶ | 49/84 | 62/84 |
| Doxycycline MIC ≤ 2 (102/166) * | 22/102 (p = 0.0032) § | 1/102 | 101/102 | 22/102 | 20/102 | 40/102 | 82/102 | 59/102 | 82/102 |
| Doxycycline MIC ≥ 4 (64/166) † | 3/64 | 3/64 | 63/64 | 9/64 | 19/64 | 41/64 (p = 0.0018) ¶ | 60/64 (p < 0.0001) ¶ | 42/64 | 49/64 |

Table 3 Characteristics of 166 patients and putative virulence factors present in the respective *C. jejuni* isolates

| Clinical characteristics | GGT-production | virB11 | ciaB | cgtB | wlaN | cj0486 | CeuE | pldA | cdtABC |
|--------------------------|----------------|--------|------|------|------|--------|------|------|--------|
| Female sex (99/166) | 17/99 | 3/99 | 98/99 | 19/99 | 23/99 | 52/99 | 85/99 | 62/99 | 78/99 |
| Underlying disease (38/162) | 9/38 | 3/38 | 37/38 | 10/38 | 9/38 | 18/38 | 32/38 | 23/38 | 31/38 |
| Domestic infection (40/166) * | 16/40 (p < 0.0001) | 1/40 | 40 | 9/40 | 8/40 | 7/40 | 26/40 | 25/40 | 34/40 |
| Infection from abroad (126/166) | 9/126 | 3/126 | 124/126 | 22/126 | 31/126 | 74/126 (p < 0.0001) ¶ | 116/126 (p < 0.0001) ¶ | 76/126 | 97/126 |
| Vomiting (41/156) | 8/41 | 1/41 | 40/41 | 8/41 | 9/41 | 17/41 | 34/41 | 25/41 | 32/41 |
| Fever (136/156) | 20/136 | 4/136 | 134/136 | 27/136 | 30/136 | 66/136 | 115/136 | 82/136 | 104/136 |
| Bloody stools (21/119) | 6/21 (p = 0.025) | 1/21 | 21 | 8/21 (p = 0.034) | 3/21 | 9/21 | 17/21 | 16/21 | 18/21 |
| Long-lasting (≥ 10 d) diarrhea (42/161) | 6/42 | 1/42 | 42 | 12/42 (p = 0.051) | 7/42 | 18/42 | 35/42 | 24/42 | 31/42 |
| Hospitalization (29/163) | 3/29 | 1/29 | 29 | 7/29 | 8/29 | 15/29 | 21/29 (p = 0.031) ¶ | 19/29 | 23/29 |

*interpreted as susceptible, †interpreted as resistant, §interpreted as resistant or intermediate (5 isolates with MIC 4 mg/L), ¶associated with susceptible isolates, #associated with resistant isolates, ‡associated with resistant or intermediate isolates
Table 4 Multivariate analysis showing independent association between origin of infection and certain C. jejuni markers

| Virulence marker | OR  | 95% Confidence interval | p-value |
|------------------|-----|------------------------|---------|
| GGT*             | 8.67| 3.43-21.91             | < 0.0001|
| cj0486†          | 6.71| 2.75-16.39             | < 0.0001|
|ceuE             | 6.71| 2.67-16.95             | < 0.0001|

*associated with domestic infection, †associated with imported infection

recently demonstrated that ggt was common among human and chicken C. jejuni isolates but significantly less common among bovine isolates [25]. GGT activity in C. jejuni has been suggested to affect the persistent colonization of the avian gut [20] and in a mouse model for C. jejuni it was shown to enhance colonization [30].

In our study, GGT-production was present in 15% of the isolates and associated with bloody diarrhea in the univariate analysis, although the latter, due to a lack of data available, could not be further analyzed in a multivariate analysis. Interestingly, the domestic C. jejuni isolates were able to produce GGT significantly more often than the imported isolates, a finding also verified by the multivariate analysis. PFGE typing of all domestic isolates verified the sporadic nature of the domestically acquired infections confirming also that GGT production was not linked with a certain genotype.

The gene cj0486, encoding a putative sugar transporter and suggested to be related to invasiveness [13], as well as the gene ceuE, encoding a transport protein for uptake of the siderophore enterochelin [32] were detected in 49% and 86% of the isolates in the present study, respectively, in line with some other reports [19]. Although their presence was not associated with the outcome of the disease, interestingly they were significantly more often found among isolates of foreign than among those of domestic origin. Furthermore, the isolates lacking ceuE seemed to cause infections requiring hospital treatment, but this finding was not verified by the multivariate analysis. In addition to the typing of all domestic isolates, PFGE typing of travel-associated isolates from July indicated that almost all patients had unique genotypes and none of the studied characteristics was linked with a genotype. Travel-associated isolates originated from a total of 36 different countries.

Only few studies have been promising in trying to show correlation between putative virulence factors or the characteristics of C. jejuni and the outcome of the disease. Of the different C. jejuni markers studied in the present report, GGT production and the presence of cjgB were associated with bloody stools in the univariate analysis, but the other putative virulence factors did not correlate with any specific clinical findings. The β-1,3 galactosyltransferase gene cjgB in the LOS gene clusters A and B involved in the biosynthesis of ganglioside-like LOS [16,17] also showed a trend of being associated with longer-lasting diarrhea. C. jejuni LOS gene clusters A, B and C have even earlier been associated not only with a more severe outcome of the disease as characterized by bloody stools and longer duration of diarrhea but also with the development of post-infectious complications [33]. However, in the present study, the other β-1,3 galactosyltransferase gene wlaN, expressed in the LOS gene cluster C [34] was not associated with any clinical characteristics. The gene ciaB has been suggested to be involved in invasiveness [11,12] and thus, could be needed for the development of the disease. Indeed, all except two of the 166 isolates in our study were ciaB positive, which is in line with earlier reports [19,35]. The presence of another putative virulence factor the gene plda, encoding phospholipase A [14], was detected in the present study to a somewhat lower extent (61%) as compared to other reports (91-100%) [19,35], and did not correlate with the clinical outcome of the disease. As CDT and virB11 were concerned, our results supported those of others showing CDT activity in the great majority [19] but the presence of virB11 in only a tiny proportion [13,19] of clinical C. jejuni isolates. Thus, it seems very unlikely that these particular markers would play a role in the diversity of the outcome of the human disease.

Conclusions

In conclusion, we suggest for the first time that GGT production could be a marker associated with a more severe outcome of C. jejuni infection as characterized by bloody stools, however, additional work is needed to clarify the importance of this finding. Furthermore, to the best of our knowledge, this is the first report to describe the presence of putative virulence markers significantly and independently to differ between C. jejuni isolates of foreign and domestic origin. Whether this also reflects the different sources of C. jejuni infections locally in Finland remains to be studied.

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Authors’ contributions
BF participated in the design of the study, collected and analyzed data, performed statistical analyses and prepared the draft manuscript. PE
participated in the selection of virulence factors, performed and supervised some PCR experiments. HR performed the PFGE and conducted some PCR
experiments. SS provided expertise in statistical analyses. MLH participated in
the design of the study and supervised the performance of some experiments. HR participated in the design of the project, coordinated and supervised the study and helped to draft the manuscript. All authors
provided ideas and comments on the draft manuscript and approved the final manuscript.

Competing interests
The authors declare that they have no competing interests.

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