Comprehensive Analysis of Bacterial Risk Factors for the Development of Guillain-Barré Syndrome after Campylobacter jejuni Enteritis

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Background. Guillain-Barré syndrome (GBS), a postinfectious autoimmune-mediated neuropathy, is a serious complication after Campylobacter jejuni enteritis.

Methods. To investigate the bacterial risk factors for developing GBS, genotypes, serotypes, and ganglioside mimics on lipo-oligosaccharide (LOS) were analyzed in C. jejuni strains from Japanese patients.

Results. Strains from patients with GBS had LOS biosynthesis locus class A more frequently (72/106; 68%) than did strains from patients with enteritis (17/103; 17%). Class A strains predominantly were serotype HS:19 and had the csfII (Thr51) genotype; the latter is responsible for biosynthesis of GM1-like and GD1a-like LOSs. Both anti-GM1 and anti-GD1a monoclonal antibodies regularly bound to other LOS classes. Mass-spectrometric analysis showed that a class A strain carried GD1a-like LOS as well as GM1-like LOS. Logistic regression analysis showed that serotype HS:19 and the class A locus were predictive of the development of GBS.

Conclusions. The high frequency of the class A locus in GBS-associated strains, which was recently reported in Europe, provides the first GBS-related C. jejuni characteristic that is common to strains from Asia and Europe.

The gram-negative spiral bacterium Campylobacter jejuni, which is a major bacterial agent in diarrheal illnesses, has been recognized as the bacterium that most frequently triggers the postinfectious autoimmune-mediated neuropathy called Guillain-Barré syndrome (GBS) [1]. An epidemiological study showed that 1 of 3285 patients with C. jejuni enteritis developed GBS [2]. Why such a small number of patients with C. jejuni enteritis develop GBS is not clear. Penner serotyping showed that, in Japan and South Africa, GBS-associated strains were more commonly serotypes HS:19 and HS:41 than were enteritis-associated strains [3–5]. Furthermore, HS:2 and the HS:4-complex were the dominant serotypes of strains from patients with Fisher syndrome (FS) [5], a GBS variant presenting the triad of ophthalmoplegia, ataxia, and areflexia [6]. The clustering of strains into particular serotypes is a strong indication that the clonality of C. jejuni strains is specifically related to the development of GBS and FS. The actual serodeterminants, however, are still unknown [7]; therefore, use of Penner serotyping schema alone to clarify the critical factors for the development of neurological syndromes would be difficult. It is noteworthy that the clustering of GBS-associated and FS-associated strains into specific serotypes has not been
whereas only α-2,3-sialyltransferase activity is needed for the biosynthesis of the GM1 and GD1a epitopes (figure 1). These findings recently led to our discovery that cstII polymorphism is important for the development of GBS and FS after C. jejuni enteritis [29]. cstII (Thr51) is closely associated with GBS and anti-GM1 and anti-GD1a autoantibodies, and cstII (Asn51) is closely associated with FS and anti-GQ1b autoantibodies.

Some of the identified bacterial risk factors for the development of GBS are closely related to each other, especially ganglioside mimics and serotype [19], cstII gene content [19, 29], and LOS locus class [15]. Therefore, it is necessary to analyze the risk factors comprehensively in a larger number of clinical isolates. We first examined whether the clustering of GBS-associated and FS-associated strains into a specific LOS locus class would also occur with a large number of Japanese strains; we then analyzed LOS locus classes comprehensively in connection with Penner serotype, cstII polymorphism, and ganglioside-like LOSs, to identify risk factors for the development of GBS.

**MATERIALS AND METHODS**

**Strains.** From December 1990 to February 2004, 138 C. jejuni strains were isolated from patients with GBS (n = 106) or FS (n = 32), and these strains were used in the present study. Most of the strains were included in our previous study [5]. Two strains, OH4384 and OH4382, were obtained from patients with GBS who were siblings [17, 30], and the others were obtained from patients with GBS who were evenly distributed geographically [5]. Diagnosis of GBS or FS was based on published clinical criteria [31, 32]. A total of 103 strains were isolated from patients throughout Japan who had uncomplicated enteritis, and these strains served as controls. Penner serotypes were determined using the passive hemagglutination technique with a *Campylobacter* antisera "Seiken" Set (Denka Seiken) [5].

**LOS locus classification and cstII polymorphism.** We used a method similar to that of Godschalk et al. [15] to classify the LOS locus (A–F). The presence of each class-specific gene was investigated by polymerase chain reaction (PCR) (table 1). The primer pair used for orf19d amplification was the same as that used in the study by Godschalk et al. [15], whereas the other primer pairs were newly designed for the present study. Class G was not examined, because it is considered to be very rare. Strains were judged to be class A when orf19d (cstII) was present and orf51b (cgta1Ib) was absent. Similarly, strains were judged to be class F when orf19d/f was present and orf17d was absent. A single bacterial colony was suspended in 300 μL of sterile distilled water and boiled for 10 min. After centrifugation at 10,000 g for 1 min, the supernatant was used as the template in the PCR amplification. Amplification reactions were performed with a total volume of 20 μL, which contained 8 pmol of each primer, 0.4 μL of DNA lysate, 0.5 U of Taq DNA
were monoclonal antibodies (mAbs; GB2 [anti-GM1], GB1
on a single agar plate, and the cells were treated as de­
described elsewhere [35], with minor modification [34]. The
ganglioside epitopes (GM1, GD1a, and GQ1b) on the C.
LOS was determined using an ELISA [34]. The reagents used
from the strains as described elsewhere [33]. The presence of
polymerase (TaKaRa Ex Taq; Takara Bio), 4 nmol of dNTPs,
30 cycles of amplification (table 1). Variation at codon 51 of
cstII was investigated by direct sequencing of the PCR fragment
was investigated by direct sequencing of the PCR fragment

Ganglioside-like LOS. Crude LOS fractions were prepared
from the strains as described elsewhere [33]. The presence of
ganglioside epitopes (GM1, GD1a, and GQ1b) on the C. jejuni
LOS was determined using an ELISA [34]. The reagents used
were monoclonal antibodies (mAbs; GB2 [anti-GM1], GB1
[anti-GD1a], and FS3 [anti-GQ1b/GT1a]) [14, 34].

Analysis of O-deacylated LOS. C. jejuni was grown over­
night on a single agar plate, and the cells were treated as de­
scribed elsewhere [35], with minor modification [34]. The
O-deacylated LOS sample was analyzed by capillary elec­
phoresis–electrospray ionization mass spectrometry (CE-ESI­MS) [36].

Sequencing of LOS biosynthesis genes. Isolation of genomic
DNA from C. jejuni strain CF90-26 was performed with a DNeasy
Tissue kit (Qiagen). A 6.1-kb PCR product bearing genes en­
coding the LOS outer core glycosyltransferases was amplified with
an Advantage 2 PCR kit (Clontech Laboratories) and the primers
CJ-99 (5'-ATTAAAAAAGACCTTGGGAATAC-3') and CJ-147
(5'-AAGGTGTGCTAAGATAAACAAGAC-3'). The 6.1-kb PCR

Table 1. Polymerase chain reactions for the
lipopoligosaccharide gene loci of Campylobacter
jejuni strains.

<table>
<thead>
<tr>
<th>Gene Symbol</th>
<th>Primer Sequence</th>
<th>Product Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>cstII</td>
<td>5'-ATTAAAAAAGACCTTGGGAATAC-3'</td>
<td>6.1 kb</td>
</tr>
<tr>
<td>cgtA</td>
<td>5'-AAGGTGTGCTAAGATAAACAAGAC-3'</td>
<td>6.1 kb</td>
</tr>
<tr>
<td>cgtB</td>
<td>(Asn51)</td>
<td>(Thr51 or Asn51)</td>
</tr>
<tr>
<td>cglA</td>
<td>(Thr51 or Asn51)</td>
<td>(Thr51 or Asn51)</td>
</tr>
<tr>
<td>cgtB</td>
<td>(Thr51 or Asn51)</td>
<td>(Thr51 or Asn51)</td>
</tr>
<tr>
<td>cglB</td>
<td>(Thr51 or Asn51)</td>
<td>(Thr51 or Asn51)</td>
</tr>
</tbody>
</table>
locus was predominant in the GBS-associated strains, and its locus classes were rarer in GBS-associated strains than in enteritis-associated strains. These findings agree with those of frequency was significantly higher in GBS-associated strains when the titer was \( \geq 500 \).

We previously sequenced this locus in multiple C. jejuni strains [27]. DNA sequencing was performed with a BigDye Terminator mix (Applied Biosystems). Products were analyzed in an ABI 3100 Genetic Analyzer (Applied Biosystems).

**Antiganglioside autoantibodies.** Serum samples obtained during acute phases of GBS and FS were available from 126 patients (95 patients with GBS and 31 patients with FS). IgG autoantibodies to GM1, GD1a, and GG1b were measured by ELISA [37]. Serum was considered to be positive for antibody when the titer was \( \geq 500 \).

**Statistical analysis.** Frequency differences between groups were compared using Fisher's exact test. Differences in medians were examined using the Mann-Whitney \( U \) test, and Scheffé's test was used in the case of multiple comparisons. The association between the LOS locus class and either GBS or FS was first investigated by univariate analysis, without adjustment for confounding variables. A multiple logistic regression model was then used to determine the relative weighting of each variable. Statistical calculations were made with SPSS (version 12.0); SPSS). A difference was considered to be statistically significant when \( P<.05 \).

**RESULTS**

**LOS locus classification.** Preliminary analysis of control strains of each LOS locus class confirmed that PCR-based LOS locus classification works well (data not shown). The class A locus was predominant in the GBS-associated strains, and its frequency was significantly higher in GBS-associated strains than in enteritis-associated strains (table 2). The other LOS locus classes were rarer in GBS-associated strains than in enteritis-associated strains. These findings agree with those of Godschalk et al. [15]. In contrast, FS-associated strains most frequently had the class B locus, but, compared with the enteritis-associated strains, the difference did not reach statistical significance, because it also was the most common class found in enteritis-associated strains. In the study by Godschalk et al. [15], all 4 FS-associated strains had the class B locus, whereas, in the present study, a significant number of FS-associated strains had the class A locus. In 12 strains (2 GBS associated, 2 FS associated, and 8 enteritis-associated), there was no amplification of any class-specific genes. Two enteritis-associated strains were grouped as having overlapping class A and C or B and C loci.

Sialyltransferase-encoding genes (cstII or cstIII) are present in class A, B, and C loci [27], and this enables strains with these LOS locus classes to be characterized as a single group. Our data showed that 96% of GBS-associated strains had sialytransferase-carrying LOS locus class (A, B, or C), and this percentage was significantly higher than that of enteritis-associated strains (70%) (table 2). FS-associated strains also regularly had these LOS locus classes (88%).

**Serotype.** Table 3 shows the associations between the LOS locus class and the Penner serotype in GBS-associated, FS-associated, and enteritis-associated strains. LOS locus classes were closely—but not absolutely—associated with the Penner serotype, because strains with each LOS locus class were grouped into several serotypes, as was reported by Parker et al. [26]. Most class A strains were serotype HS:19, whereas the serotypes of class B strains varied. Conversely, most of the HS:19 strains had the class A locus, whereas most of the HS:2 and HS:4 complex strains had the class B or A locus.

**cstII polymorphism.** Class A and B loci are reported to carry the cstII gene [27]. Therefore, the association between cstII polymorphism and the class A or B locus was examined. Most of the class A strains had the cstII (Thr51) genotype (78/
Notably, several unclassified strains also had ganglioside-mimic LOS (figure 2), and this is indicative of an unknown ganglioside-like LOS and antiganglioside autoantibodies.

On the whole, reactivity to anti-GM1 mAb was increased in class A and C strains, and that of anti-GD1a mAb was increased only in class A strains (figure 2); this is indicative of a difference in sialyltransferase substrate specificity between classes A (cstII) and C (cstIII) [25]. Some class B strains had high reactivity to anti-GM1 and anti-GD1a mAbs, but the median optical density was low. Reactivity to anti-GQlb/GTla mAb was high in class A strains and in some class A strains, but it was not high in strains with loci of other classes.

We defined ganglioside epitopes as being present on LOSs when the OD of mAb in the ELISA was $\geq 0.2$. There was an obvious difference in ganglioside epitopes between strains with the class A, B, or C locus and strains with the class D, E, or F locus, with epitopes being frequent in the former group and absent in the latter group. For example, the GM1 epitope was judged to be present in 80% of class A strains, 26% of class B strains, and 64% of class C strains but in none of the strains with the class D, E, or F locus. Furthermore, class A strains regularly expressed both the GM1 and has the GD1a epitope, whereas class C strains expressed only the GM1 epitope; the GD1a epitope was detected in 76% of class A strains but in only 3% of class C strains. The GQlb/GTla epitope was present in 37% and 50% of class A or B strains, respectively; no strain with the class C, D, E, or F locus had this epitope. Notably, several unclassified strains also had ganglioside-mimic LOS (figure 2), and this is indicative of an unknown sialyltransferase gene being present at an unclassified locus.

Patients with class A or C strains often were positive for IgG autoantibodies against GM1 (72% and 75%, respectively). Interestingly, the frequency of anti-GD1a IgG autoantibodies was higher in patients with class A strains (51%) than in patients with class C strains (33%). These data agree with the finding that anti-GD1a mAb bound to class A LOS but not to class C LOS. In contrast, patients with class B strains more commonly had anti-GQlb IgG autoantibodies (44%) than anti-GM1 IgG autoantibodies (25%) or anti-GD1a IgG autoantibodies (25%). Anti-GQlb IgG autoantibodies were rarely detected in patients with class A (14%) or class C (0%) strains. These data agree with the finding that anti-GQlb/GTla mAb regularly bound to class B LOS.

**LOS structure and glycosyltransferase genes of strain CF90-26.** Because the above data suggested the importance of the GM1 and GD1a epitopes on class A strains, we investigated in detail the LOS structure and gene sequences of the cstII, cgtA, and cgtB glycosyltransferase genes. Elsewhere, we showed that C. jejuni strain CF90-26 (a serotype HS:19 class A strain from a patient with GBS who had high anti-GM1 IgG autoantibody titers), which was used in the present study, has a GM1-like structure, on the basis of nuclear magnetic resonance analysis [16], and has the GD1a epitope, on the basis of thin-layer chromatography with immunostaining [38]. CE-ESI-MS analysis of an O-deacylated LOS sample from C. jejuni strain CF90-26 yielded various masses, and the predominant species was [M-4H]$^4-$ (3645 Da). The differences in observed masses (table 4) were due to lipid A variation, as well as to the presence or absence of a terminal sialic acid (in addition to the sialic acid that is present on the inner galactosyl residue). CE-ESI-MS analysis showed that the absence of the terminal sialic acid resulted in a GM1 mimic, and its presence in a GD1a mimic (figure 3) provided evidence that CF90-26 has both GM1-like and GD1a-like LOSs. The LOS biosynthesis gene sequence in strain CF90-26 (GenBank accession number AY661458) was

### Table 3. Associations between lipo-oligosaccharide (LOS) locus class and Penner serogroup in *Campylobacter jejuni* strains.

<table>
<thead>
<tr>
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<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>101</td>
<td>0</td>
<td>7 (7)</td>
<td>15 (15)</td>
<td>0</td>
<td>73 (72)</td>
<td>1 (1)</td>
<td>6 (6)</td>
</tr>
<tr>
<td>B</td>
<td>66</td>
<td>1 (2)</td>
<td>21 (32)</td>
<td>21 (32)</td>
<td>6 (9)</td>
<td>6 (9)</td>
<td>0</td>
<td>17 (26)</td>
</tr>
<tr>
<td>C</td>
<td>33</td>
<td>14 (42)</td>
<td>7 (21)</td>
<td>0</td>
<td>5 (15)</td>
<td>0</td>
<td>0</td>
<td>8 (24)</td>
</tr>
<tr>
<td>D</td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>3 (100)</td>
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<td>E</td>
<td>18</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>8 (44)</td>
<td>10 (56)</td>
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<tr>
<td>F</td>
<td>6</td>
<td>0</td>
<td>1 (17)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>5 (83)</td>
</tr>
<tr>
<td>A/C</td>
<td>1</td>
<td>0</td>
<td>1 (100)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>B/C</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1 (100)</td>
<td>6 (50)</td>
</tr>
<tr>
<td>Unclassified</td>
<td>12</td>
<td>2 (17)</td>
<td>2 (17)</td>
<td>0</td>
<td>0</td>
<td>2 (17)</td>
<td>0</td>
<td>6 (60)</td>
</tr>
</tbody>
</table>

**NOTE.** Data are no. (%) of strains, unless otherwise indicated.

- One strain was serotyped as the O/Y serogroup.
- One strain was serotyped as the A/G serogroup.
We confirmed the finding of Godschalk et al. [15] that GBS is evidence of the first GBS-related C. jejuni associated with the class A locus of C. jejuni (OR, 5.6 [95% CI, 2.1-15.1]; P == .001).

Risk factors for development of GBS. Because univariate analysis showed that class A strains were associated with GBS, we compared the features of GBS-associated and enteritis-associated class A strains. Differences remained significant between GBS-associated and enteritis-associated strains in the frequency of the HS:19 serotype, the frequency of cstII (Thr51), and LOS binding of anti-GM1 and anti-GD1a IgG autoantibodies (table 5). All HS:19 strains with the class A locus had the cstII (Thr51) genotype, except for the 2 GBS-associated strains (OH4382 and OH4384) that were obtained from siblings with GBS and external ophthalmoplegia [30]; these 2 strains were known to carry GD3-like or GT1a-like LOSs [17], as well as the GM1 epitope [39], all of which are present with the cstII (Asn51) genotype. Multiple logistic regression modeling was used to adjust the comparisons between GBS-associated and enteritis-associated strains for the class A locus, the HS:19 serotype, the cstII (Thr51) genotype, and GM1-like and GD1a-like LOSs. In that analysis, the difference remained significant for the HS:19 serotype (odds ratio [OR], 16.5 [95% confidence interval [CI], 4.0-68.8]; P < .001) and the class A locus (OR, 5.6 [95% CI, 2.1-15.1]; P = .001).

**DISCUSSION**

We confirmed the finding of Godschalk et al. [15] that GBS is associated with the class A locus of C. jejuni and provided evidence of the first GBS-related C. jejuni characteristic that is common to strains from Asia and Europe. Moreover, we found that strains with the class A locus regularly express both the GM1 and the GD1a epitope on their LOSs; this unique LOS profile among C. jejuni strains results in an increased risk of producing anti-GM1 and anti-GD1a IgG autoantibodies and, therefore, developing GBS. Expression of the GM1 and GD1a epitopes in class A strains was enhanced in strains that were also serotype HS:19, and this expression was possibly dependent on the predominance of the cstII (Thr51) genotype in HS:19 strains. Of course, microbial properties alone do not sufficiently explain why an autoimmune response is triggered in only a minority of individuals with C. jejuni enteritis. Host susceptibility must be much more important. Previous attempts to find common host immunogenetic factors in patients with C. jejuni GBS, however, have had negative or conflicting results [40-44].

The class A locus is 11.5 kb and has 13 genes. A and B class loci have the same gene profile, except that the class B locus has orf5II (cgtAII), which may be the result of duplication of orf5I (cgtAI) [27]. This raises the question as to why GBS-associated strains primarily have the class A locus. Our findings suggest that nucleotide sequence variation within genes is the answer. In fact, strains with the same LOS biosynthesis

**Table 4.** Lipid A variants and variable terminal sialic acids of an O-deacylated sample from Campylobacter jejuni strain CF90-26.

The table is available in its entirety in the online edition of the *Journal of Infectious Diseases.*
Table 5. Comparison of Guillain-Barré syndrome-associated and enteritis-associated Campylobacter jejuni strains with the class A lipo-oligosaccharide (LOS) locus.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Guillain-Barré syndrome-associated strains (n = 72)</th>
<th>Enteritis-associated strains (n = 17)</th>
<th>2-tailed P*</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Serotype HS:19</td>
<td>66 (92)</td>
<td>6 (35)</td>
<td>&lt;.001</td>
<td>20.2 (5.5–73.9)</td>
</tr>
<tr>
<td>cstII polymorphism</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thr51</td>
<td>66 (92)</td>
<td>10 (58)</td>
<td>.002</td>
<td>7.7 (2.1–27.6)</td>
</tr>
<tr>
<td>Asn51</td>
<td>8 (10)</td>
<td>7 (41)</td>
<td>.002</td>
<td>1.3 (0.036–0.47)</td>
</tr>
<tr>
<td>Median OD ± SD of mAb to LOSb</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GM1-like LOS</td>
<td>2.402 ± 0.897</td>
<td>1.106 ± 1.107</td>
<td>.002</td>
<td></td>
</tr>
<tr>
<td>GD1a-like LOS</td>
<td>1.976 ± 0.830</td>
<td>0.588 ± 1.215</td>
<td>.03</td>
<td></td>
</tr>
<tr>
<td>GQ1b/GT1a-like LOS</td>
<td>0.086 ± 0.431</td>
<td>0.126 ± 0.500</td>
<td>.11</td>
<td></td>
</tr>
</tbody>
</table>

**NOTE.** Data are no. (%) of strains, unless otherwise indicated. CI, confidence interval; mAb, monoclonal antibody; OR, odds ratio.

* Fisher’s exact test or Mann-Whitney U test.

b ODs were measured by an ELISA with mAbs GB2 (GM1), GB1 (GD1a), and FS3 (GQ1b/GT1a).
the makeup of glycosyltransferase genes, is responsible for determining the type of ganglioside mimic that is formed on LOSs.

In the present study, we found that most of the FS-associated strains had the class A or B locus, which supports the finding of van Belkum et al. [48] that cstII was present in all 8 strains with GQ1b-like LOS that they tested. Godschalk et al. [15] found that all 4 of the FS-associated strains that they tested had the class B locus, whereas a significant number of FS-associated strains that we tested in the present study had the class A locus. Furthermore, the differences between the class A and the class B locus were not important in our FS-associated strains, whereas the cstII (Asn51) genotype was critical. cstII (Asn51) has both α-2,3- and α-2,8-sialyltransferase activities [27], which are essential for transferring the disialyl moiety to the outer core of LOS, thereby mimicking GQ1b and GT1α gangliosides. Our findings suggest that the ganglioside-like LOS synthesis gene contents of cstII, cgtA, and cgtB, which are common to the class A and B loci, are important for triggering an autoimmune response and that cstII polymorphism is the determinant of autoantibody reactivity and neurological presentations in GBS and FS.

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References


