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 cstII (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 class A LOSs, whereas no or either antibody 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 class A locus and serotype HS:19 seem to be linked to cstII polymorphism, resulting in promotion of both GM1-like and GD1a-like structure synthesis on LOS and, consequently, an increase in the risk of producing ganglioside autoantibodies and developing GBS.

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

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seen worldwide and, in particular, has not been seen in Western countries [8, 9].

Most patients who develop GBS after C. jejuni enteritis have IgG autoantibodies in their blood that react with gangliosides (such as GM1, GD1a, and GQ1b) [10]. Many patients with FS have anti–GQ1b IgG autoantibodies that cross-react with GT1a [11, 12]. The C. jejuni lipo-oligosaccharide (LOS) is a major candidate for the producer of such autoantibodies [13–15], because its terminal sugar regions mimic the gangliosides GM1, GD1a, and GQ1b [16–18]. The frequency of the GM1 and GD1a epitopes on the LOS of GBS-associated strains is hypothesized to be a risk factor for the development of GBS [19, 20]. Acute motor axonal neuropathy and anti-GM1 antibodies developed in rabbits after inoculation with GM1-like LOS, which indicates that GM1 mimicry of C. jejuni LOS is a cause of GBS [14].

Most studies have failed to find a specific C. jejuni genotype that was associated with GBS and FS [9, 21–24]. Gilbert et al. [25] reported that C. jejuni has 7 classes (A–G) of LOS locus that are based on the organization of the 37 distinct genes found in the LOS biosynthesis loci of 20 strains. This LOS locus typing scheme should help in the identification of the gene content that is responsible for the development of GBS and FS. Godschalk et al. [15], who used clinical isolates from The Netherlands and Belgium, recently reported that the class A locus was overrepresented in GBS-associated strains, compared with enteritis-associated strains (9/17 [53%] vs. 3/21 [14%]), whereas all FS-associated strains had the class B locus (FS-associated strains, 4/4 [100%]; enteritis-associated strains, 7/21 [33%]). The high frequency of the class A locus in GBS-associated strains has been confirmed by Parker et al. [26], who used 16 GBS-associated strains from various countries, although the frequency of this locus in GBS-associated strains could not be compared with that in enteritis-associated strains from each country. Godschalk et al. [15] suspected that the frequent expression of a GM1-like LOS in class A strains and a GQ1b-like LOS in class B strains is responsible for the development of GBS and FS, respectively. Their findings, however, do not clarify which genetic difference leads to the presence of diverse ganglioside mimics (GM1 and GQ1b) in spite of the almost identical gene profiles in class A and B loci [27] or why class C is relatively rare (2/17 [12%]) in GBS-associated strains in spite of the expression of GM1-like LOS in all 5 strains with the class C locus.

The sialyltransferase gene cstII has an Asn/Thr polymorphism at codon 51, which determines substrate specificity; cstII (Thr51) has only α-2,3-sialyltransferase activity and is termed “monofunctional” cstII, whereas cstII (Asn51) has both α-2,3- and α-2,8-sialyltransferase activities and is termed “bifunctional” cstII [27]. Both sialyltransferase activities are required for the biosynthesis of the GQ1b and GT1a epitopes on LOS, 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 orf7a/b (cstII) was present and orf51b (cgtA1b) was absent. Similarly, strains were judged to be class F when orf9a/d 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 lyase, 0.5 U of Taq DNA
polymerase (TaKaRa Ex Taq; Takara Bio), 4 nmol of dNTPs, and buffer (2 mmol/L Mg²⁺). After the first denaturation step of 5 min at 95°C, the amplification mixture was subjected to 30 cycles of amplification (Table 1). Variation at codon 51 of cstII was investigated by direct sequencing of the PCR fragment [29].

**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 overnight on a single agar plate, and the cells were treated as described elsewhere [35], with minor modification [34]. The O-deacylated LOS sample was analyzed by capillary electrophoresis–electrospray ionization mass spectrometry (CE-ESI-MS) [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 encoding the LOS outer core glycosyltransferases was amplified with an Advantage 2 PCR kit (Clontech Laboratories) and the primers CJ-99 (5'-ATTAAAAAAAGACCTTGGGAATAC-3') and CJ-147 (5'-AAGGTGTGCTAAGATAAACAAGAC-3'). The 6.1-kb PCR

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**Figure 1.** Proposed biosynthesis pathway of Campylobacter jejuni lipo-oligosaccharides (LOSs) mimicking gangliosides with a single sialic acid on the inner galactosyl residue [27, 28]. Gal, galactose; GalNAc, N-acetylgalactosamine; NeuAc, N-acetylneuraminic acid.

**Table 1.** Polymerase chain reactions for the lipo-oligosaccharide gene loci of Campylobacter jejuni strains.

The table is available in its entirety in the online edition of the Journal of Infectious Diseases.
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 GQ1b 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 weight of each variable. Statistical calculations were made with SPSS (version 12.0J; 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 sialyltransferase-carrying LOS loci classes (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 loci 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.

\section*{cstIII polymorphism.} Class A and B loci are reported to carry the \( cstiII \) gene [27]. Therefore, the association between \( cstiII \) polymorphism and the class A or B locus was examined. Most of the class A strains had the \( cstiII \) (Thr51) genotype (78/
Notably, several unclassified strains also had ganglioside-mimicking LOS (figure 2), and this is indicative of an unknown strain with the class C, D, E, or F locus had this epitope. The GDla epitope was detected in 37% and 50% of class A or B strains, respectively; no GDla epitope was detected in 76% of class A strains but in only 3% of class C strains. The GQlb/GTla epitope was present in 86% of class A, 16% of class B, and 0% of class C strains. 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-GDla 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-GMI IgG autoantibodies (25%) or anti-GDla 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]+ (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
100% identical to the corresponding region in the *C. jejuni* HS:19 type strain (GenBank accession number AFI67344), which also expresses a mixture of GM1 and GD1a mimics in its LOS outer core [17].

**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 Godsckalk 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...
Serotype HS:19 66 (92) 6 (35) <.001 20.2 (55-73.9)

Characteristic strains

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&lt;sup&gt;a&lt;/sup&gt;</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>cstI polymorphism</td>
<td>66 (92)</td>
<td>10 (58)</td>
<td>.002</td>
<td>7.7 (2.1-27.6)</td>
</tr>
<tr>
<td>Thr51</td>
<td>6 (8)</td>
<td>7 (41)</td>
<td>.002</td>
<td>0.13 (0.036-0.47)</td>
</tr>
<tr>
<td>Asn51</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Median OD ± SD of mAb to LOS&lt;sup&gt;b&lt;/sup&gt;</td>
<td>2.402 ± 0.897</td>
<td>1.106 ± 1.107</td>
<td>.002</td>
<td></td>
</tr>
<tr>
<td>GM1-like LOS</td>
<td>1.976 ± 0.830</td>
<td>0.588 ± 1.215</td>
<td>.03</td>
<td></td>
</tr>
<tr>
<td>GD1a-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.

<sup>a</sup> Fisher’s exact test or Mann-Whitney U test.

<sup>b</sup> ODs were measured by an ELISA with mAbs GB2 (GM1), GB1 (GD1a), and FS3 (GQ1b/GT1a).

Figure 3. Proposed lipo-oligosaccharide outer core structures as determined on the basis of capillary electrophoresis-electrospray ionization mass spectrometric analysis of O-deacylated lipo-oligosaccharide samples from Campylobacter jejuni strain CF90-26. Gal, galactose; GalNAc, N-acetylgalactosamine; Hep, L-glycero-D-manno-heptose; Glc, glucose; Kdo, 3-deoxy-o-manno-2-octulosonic acid; NeuAc, N-acetylneuraminic acid; PEtn, phosphoethanolamine.

Candidate enzyme functions of the class A locus have been proposed, and most of them seem to be essential for the biosynthesis of ganglioside-like LOS [28, 45-47]. This suggests that the content of a single gene of C. jejuni is insufficient for the development of GBS; the entire gene content of the class A locus is essential. Nachamkin et al. [19] reported that the 3 glycosyltransferase genes that are necessary for ganglioside-like biosynthesis—cstII/cstIII (sialyltransferase), cgtA (β-1,4-N-acetylgalactosaminyltransferase), and cgtB (β-1,3-galactosyltransferase)—[28] are more often present in GBS-associated strains than in enteritis-associated strains. These 3 genes are present in class A, B, and C loci [27], which agrees with our finding that 96% of GBS-associated strains had the class A, B, or C locus. This strongly suggests that the class A, B, or C locus is required to induce the development of GBS, although the class C locus is a much weaker risk factor than is the class A locus.

Interestingly, class A strains regularly express GM1-like and GD1a-like LOSs, whereas class C strains express GM1-like LOS only. GM1 and GD1a are candidate target antigens for the circulating autoantibody [10]. Our results suggest that multiple ganglioside mimicry is more effective for developing GBS than is single ganglioside mimicry. This disagrees with the findings of Nachamkin et al. [19] that the expression of the GD1a epitope alone is associated with GBS. The reason for this discrepancy is not known. We have shown in the present study, however, that patients from whom class A strains were isolated often had both anti-GM1 and anti-GD1a IgG autoantibodies; in addition, the inoculation of rabbits with CF90-26 LOS (which has GM1 and GD1a mimics) caused acute motor axonal neuropathy that was accompanied by anti-GM1 antibodies, not by anti-GD1a antibodies [14]. The assumption that GM1 mimicry, in addition to GD1a mimicry, is responsible for the development of GBS, therefore, is reasonable.

On the basis of chemical analysis, the coexistence of the GM1 and GD1a epitopes on the outer core of the LOS of the HS:19 serotype reference strain has been reported [17]. Elsewhere, we showed by use of mAb immunostaining that both epitopes were present in a GBS-associated HS:19 strain (CF90-26) [38], and we confirmed that finding in the present study by use of mass-spectrometric analysis. Furthermore, the nucleotide sequence of the 6.1-kb PCR product that included cstII, cgtA, and cgtB (as well as downstream and upstream sequences) was identical to the corresponding region in the C. jejuni HS:19 type strain that also expresses mixed GM1 and GD1a mimics [17]. This finding confirms that the DNA sequence, as well as...
the makeup of glycosytransferase 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 GGQ1b-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 dialyl moiety to the outer core of LOS, thereby mimicking GGQ1b and GT1a gangliosides. Our findings suggest that the ganglioside-like LOS synthesis gene contents of cstII, cgA, and cgB, 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


