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The Relative Roles of Factor H Binding Protein, Neisserial Surface Protein A, and Lipooligosaccharide Sialylation in Regulation of the Alternative Pathway of Complement on Meningococci

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Neisseria meningitidis inhibits the alternative pathway (AP) of complement using diverse mechanisms, including expression of capsule (select serogroups), Neisserial surface protein A (NspA), factor H (fH) binding protein (fHbp), and lipooligosaccharide (LOS) sialylation. The contribution of the latter three molecules in AP regulation in encapsulated meningococci was studied using isogenic mutants. When LOS was unsialylated, deleting NspA alone from group A strain A2594 (low fHbp/high NspA) significantly increased AP-mediated C3 deposition. C3 deposition further increased ~2-fold in a ΔfHbpΔNspA double mutant, indicating cooperative fHbp function. LOS sialylation of A2594 ΔfHbpΔNspA decreased the rate of C3 deposition, revealing AP inhibition by LOS sialic acid. Maximal C3 deposition on group B strain H44/76 (high fHbp/low NspA) occurred when all three molecules were absent; again, LOS sialylation attenuated the AP in the absence of both fHbp and NspA. When H44/76 LOS was unsialylated, both fHbp and NspA independently inhibited the AP. LOS sialylation enhanced binding of fH C-terminal domains 18–20 to C3 fragments deposited on bacteria. Interaction of meningococci with nonhuman complement is relevant for animal models and vaccine evaluation studies that use nonhuman complement. Consistent with their human-specific fH binding, neither fHbp nor NspA regulated the rat AP. However, LOS sialylation inhibited the rat AP and, as with human serum, enhanced binding of rat fH to surface-bound C3. These data highlight the cooperative roles of meningococcal NspA and fHbp in regulating the human AP and broaden the molecular basis for LOS sialylation in AP regulation on meningococci in more than one animal species. The Journal of Immunology, 2012, 188: 5063–5072.

The complement system forms an important arm of innate immune defenses against invasive meningococcal disease.

The importance of complement in curbing meningococcal disease is illustrated by the observation that individuals with defects in components of the terminal or alternative pathways (AP) are at a greatly increased risk of meningococcal infection (1, 2). Activation of the complement system on meningococci results in deposition of C3 fragments on the bacterial surface, which marks them for phagocytosis. Further activation of the complement cascade may result in direct killing by insertion of the C5b-9 complex. Activation of the complement system occurs through the classical, lectin, or AP, and all these pathways ultimately converge at the level of C3 deposition (3). Activation of complement beyond the level of C3 leads to the formation of C5 convertases and subsequent membrane attack complex (C5b-9) insertion into the bacterial membrane that can result in killing of the organism. In most instances, colonization with meningococci is followed by the development of specific Abs and protective immunity against the homologous and antigenically closely related strains (4, 5). Because meningococci possess several mechanisms to subvert complement-dependent killing (6), lack of a protective immune response may lead to development of invasive infection in such individuals.

A unique feature of the AP of complement is a positive feedback or amplification loop, where C3b deposited on surfaces participates in the formation of C3 convertase (C3bBb), which in turn serves to activate more C3 molecules. Work over the past three decades has revealed several mechanisms by which Neisseria meningitidis inhibits AP activation. The polysialic capsules of group B and group C N. meningitidis limit C3 fragment deposition on the bacterial surface (7–9). Sialylation of meningococcal lipooligosaccharide (LOS) also limits C3 deposition (10, 11), although the molecular basis of this observation remains unclear. In recent years, meningococci have been shown to bind to the AP inhibitor, factor H (fH) via two membrane proteins, fH binding protein (fHbp; previously referred to as genome-derived Neisserial Ag 1870 or LP2086) (12, 13), and Neisserial surface protein A (NspA) (14). fH blocks the positive feedback loop of the AP at several steps. It serves as a cofactor for factor I-mediated cleavage of C3b to iC3b, prevents the association of factor B with C3b, and causes irreversible dissociation of factor Bb from the C3 convertase, C3bBb (reviewed in Ref 15).

A recent study examined meningococcal bacteria in a human fH transgenic Wistar rat model (16). Meningococcal strain H44/76 normally does not cause bacteremia following i.p. inoculation into
Materials and Methods

Bacterial strains

The wild-type strains used in this study were H44/76 (B:15P1.716:ST-32; Norway, 1976) (17) and A2594 (A:4:1-9:ST-5) (12). The LOS of both strains expresses the lacto-N-neotetraose substitution from Hpt. H44/76 can endogenously sialylate its LOS because it synthesizes 5′-cytidine-monophospho-N-acetylneuraminic acid (CMP-NANA), the donor molecule for sialic acid. In contrast, group A meningococci do not synthesize CMP-NANA but can sialylate lacto-N-neotetraose expressing LOS when CMP-NANA is added to growth media (described below). Relative to rat serum (NRS) was from Complement Technologies (Tyler, TX). mouse C3 and FITC-conjugated goat anti-mouse C3 (MP Biomedicals, Solon, OH) were used to detect rat C3 fragment deposition on bacteria by Western blotting and FACS, respectively. Anti-mouse IgG, anti-goat IgG, anti-rabbit IgG, and anti-sheep IgG conjugated to alkaline phosphatase were from Sigma-Aldrich (St. Louis, MO).

Recombinant human fH/Fc fusion proteins

fH domains 5–8 and 18–20 fused to the Fc fragment of murine IgG2a (called fH/Fc) have been described previously (22). These constructs contain contiguous human fH domains (5 through 8 or 18 through 20) fused in frame at their C-terminal ends to the N terminus of the Fc fragment of murine IgG2a. Briefly, Chinese hamster ovary cells were transfected with each of the fH/Fc constructs using lipofectin (Invitrogen), according to the manufacturer’s instructions. Media from transfected cells were collected after a 2-d period, and constructs were purified over a protein G-Sepharose column. Purified proteins were concentrated using Amicon Ultra 10,000 MWCO (Millipore), and fH/Fc protein concentrations were determined using the Bicinchoninic Acid assay kit (Thermo Scientific Pierce, Rockford, IL).

Western blot analysis of fHbp and NspA expression

Relative levels of fHbp and NspA expression by strains A2594 and H44/76 was assessed by Western blot analysis. Serial 2-fold dilutions of bacterial lysates in NuPAGE LDS sample buffer (4×) (Invitrogen) were electrophoresed on a 4–12% Bis-Tris gel using MES running buffer (Invitrogen) and transferred by Western blotting on to a 0.2-μm polyvinylidene difluoride (PVDF) membrane (Millipore, Bedford, MA). Proteins migrating above the 50-kDa marker were stained with Coomassie blue (Imperial Protein Stain; Thermo Scientific) and served as loading controls. The remainder of the membrane was blocked with PBS-1% dry milk for 1 h at 23°C. Proteins migrating above 20 kDa were probed for fHbp (molecular mass, ∼29 kDa) with mAb JAR 3, and proteins migrating faster than 20 kDa on the same blot were probed for NspA (molecular mass, ∼17 kDa) with mAb 14C7 (both mAbs were mouse IgG3 and were used at a concentration of 1 μg/ml PBS-0.05% Tween 20), followed by anti-mouse IgG conjugated to alkaline phosphatase. Membranes were developed with 5-bromo-4-chloro-3-indolyl phosphate/NBT-Purple Liquid Substrate System (Sigma-Aldrich).

iC3b deposition, fH and fH/Fc fusion protein binding to bacteria by Western blotting

Incubation of bacteria with serum results in complement activation and deposition of C3b on the bacteria. C3b deposited on bacteria is converted to iC3b by Dh (cofactor) and factor I (enzyme). Almost all the C3b deposited on meningococci is rapidly degraded by factor I (iC3b). The predominant fragment detected, even on meningococcal strains that lack fHbp, NspA, and LOS sialic acid (8). Thus, the amount of iC3b deposited is indicative of the total amount of C3 fragment deposition on meningococci. AP-mediated iC3b deposited on bacteria was assessed by Western blotting as described previously (8). Briefly, 103 bacteria were suspended in HBSS containing 1 mM MgCl2 and 1 mM EGTA were incubated with NHS-MgEGTA (final concentration of 10 μg/ml) for 10 or 30 min at 37°C. Bacteria were washed twice in HBSS and lysed in NuPAGE LDS sample buffer (4×) (Invitrogen) containing 10% 2-ME. Proteins were separated on NuPAGE Novex 4–12% Bis-Tris gradient gels using NuPAGE MOPS running buffer (Invitrogen). Proteins were transferred to a 0.45-μm PVDF membrane (Millipore) by Western blotting. iC3b was detected using mAb 3F11 diluted 1:4 in TBS, followed by anti-mouse IgG conjugated to alkaline phosphatase. Similarly, fH and fH/Fc fusion protein binding was also measured by Western blotting. Bacteria were incubated with purified fH or fH/Fc (10 μg/ml) for 15 min at 37°C and washed twice, and pellets were lysed in 4× NuPAGE LDS sample buffer (Invitrogen) without the addition of 2-ME. fH migrates at its native molecular mass (~150 kDa) and was detected with polyclonal goat anti-human fH, followed by anti-goat IgG alkaline phosphatase (Sigma-Aldrich). fH/Fc fusion proteins were detected using anti-mouse IgG conjugated to alkaline phosphatase.

Flow cytometry

Human and rat C3 deposition on bacteria and fH binding to bacteria were measured using flow cytometry as described previously (12, 23). Samples were prepared as described above for Western blotting. Data were collected using a FACSCalibur instrument (BD Biosciences), and data analysis was performed using the FlowJo data analysis software package (www.flowjo.com). Events on the negative control samples (histograms with fluorescence on the x-axis) were gated such that 95% of the bacteria lay to the left.
of the gate (i.e., negative control samples showed 5% of events as positive). This gate was then applied to all samples, and the percentage of positive events for each sample was recorded. Each datum point on the FACS figures represents an average of at least five separate observations.

**Statistical analysis**

Flow cytometry data were analyzed using GraphPad Prism 5 software. Comparisons across multiple groups were performed by ANOVA; p values <0.05 were considered significant.

**Results**

C3 fragment deposition on N. meningitidis that vary in fHbp, NspA, and LOS sialic acid expression

Expression levels of fHbp (24, 25) and NspA (26) vary widely across meningococcal isolates. To compare the expression levels of fHbp relative to NspA on strains H44/76 and A2594, we used anti-fHbp mAb JAR 3 and anti-NspA mAb 14C7, which both belong to the same subclass (IgG3). Serial 2-fold dilutions of bacterial lysates that were Western blotted were probed with the mAbs. As shown in Fig. 1, and as reported previously (14), A2594 expressed more NspA than H44/76, whereas H44/76 expressed more fHbp than A2594.

Deposition of human C3 fragments (C3b is initially deposited on bacteria, which is then converted to iC3b by the action of factors H and I) on isogenic mutants of group A strain A2594 (low fHbp, high NspA) and group B strain H44/76 (high fHbp, low NspA) that differed only in expression of fHbp, NspA, and LOS sialic acid was measured by flow cytometry. As shown in Fig. 2A, loss of NspA, but not fHbp alone, from unsialylated A2594 resulted in significantly higher C3 deposition compared with the wild-type strain. The mutant that expressed only fHbp bound ~2-fold less C3 when compared with the unsialylated mutant that lacked both fHbp and NspA, thus demonstrating that fHbp could augment the function of NspA in regulating the AP on this strain. When the LOS of A2594 was sialylated, C3 deposition on the ∆NspA mutant decreased significantly. However, LOS sialic acid alone (in the absence of both fHbp and NspA) did not significantly reduce the amount of C3 deposited on strain A2594 at 30 min. Representative histogram tracings are shown in Supplemental Fig. 1A. We hypothesized that LOS sialic acid could reduce the rate of C3 deposition on the ΔfHbpΔNspA mutant. As shown in Fig. 2B, LOS sialic acid significantly increased the lag-phase of AP activation. Although C3 accumulated rapidly on the unsialylated ΔfHbpΔNspA mutant (>50% of maximal C3 deposition was seen at 10 min and reached maximal levels between 10 and 20 min), the presence of LOS sialic acid significantly delayed C3 accumulation on the bacterial surface. C3 deposition was only marginally above baseline levels at 10 min, following which C3 deposition reached maximal levels between 20 and 30 min. Representative histogram tracings are shown in Supplemental Fig. 1B.

Fig. 2C shows C3 deposition on group B strain H44/76 and its isogenic mutants (see Supplemental Fig. 1C for representative histograms). Again, loss of fHbp, NspA, and LOS sialic acid resulted in the highest levels of C3 deposition. The presence of fHbp, NspA, or LOS sialic acid alone or in combination restricted C3 deposition. A noteworthy observation was that in contrast to A2594, LOS sialic acid alone on H44/76 could limit C3 deposition at 30 min. Previous work has shown that the group B capsule (independent of fHbp, NspA, and LOS sialic acid), but not the group A capsule, of *N. meningitidis* inhibits AP activation and C3 fragment deposition on bacteria (8). Thus, the combined effects of the group B capsule of H44/76 and LOS sialic acid may have served to limit C3 deposition on this mutant.

We also performed Western blotting to examine the major targets for C3 fragment deposition on these mutants and also to verify the results obtained above by a second method. Activation of the AP results in C3b deposition on bacteria. C3b binds to surfaces through the thioester in its ~106-kDa α’ chain. The α’ chain is linked to the 75-kDa β-chain by a disulfide bond. iC3b is formed by cleavage of the α’ chain into α1’ (~68 kDa) and α2’ (~40 kDa) fragments by fH and factor I. In the unreduced state, the α1’ and α2’ fragments remain united through a second disulfide bond. Electrophoresis under reducing conditions results in migration of the β-chain (present in both C3b and iC3b) at its calculated mass of ~75 kDa, whereas the 106-kDa α’ chain of C3b and the 68-kDa α1’ chain of iC3b migrate complexed with their targets; the α2’ chain of iC3b migrates independently at 40 kDa. Although the iC3b is covalently linked to its bacterial targets through an ester bond, a proportion of the α1’ chain is released from its targets spontaneously even without treatment with nucleophiles such as methylamine (27–29). Hydrolytic attack by a His residue, located 113 aa downstream of the ester-forming Glu residue (30), is responsible for the free α1’ chain seen in the blots in Fig. 2. We have shown previously that almost all the C3b is converted to iC3b even on meningococcal mutants that lack fHbp, NspA, and LOS sialic acid (8). Therefore, an anti–iC3b-specific mAb was used in the Western blotting assays to measure C3 deposition on strains A2594 and H44/76 and their mutant derivatives (Fig. 2D, 2E).

The amount of iC3b deposition paralleled the data obtained above in flow cytometry assays. The major targets for iC3b on the A2594 mutants included LOS and Opa as previously described (31) and were similar across the mutants. Of note, strain H44/76 expresses very low levels of Opa (31). An anti–iC3b-reactive band at ~130 kDa (a doublet at this location is seen in the Fig. 2E [lane containing fHbp-, NspA-, LOS sia-]) was also noted and the identity of this target has not been defined.

These results suggested that regulation of AP-mediated C3 fragment deposition on A2594 (low fHbp, high NspA; LOS not sialylated) was mediated primarily by NspA, even when capsule and lacto-N-neotetraose LOS were expressed. A role for fHbp in AP regulation on this strain was evident from the ΔfHbpΔNspA double mutant, which showed higher C3 fragment deposition compared with the ∆NspA single mutant. Growth of these strains in media that contained CMP-NANA to sialylate LOS resulted in a marked decrease in C3 deposition on the ∆NspA mutant and also slowed the rate of C3 deposition on the ΔfHbpΔNspA mutant. Although these data confirm the role for fHbp in inhibiting AP-mediated C3 deposition on H44/76 that expresses the group B
capsule, they illustrate a key role for NspA in limiting AP activation on this strain.

Thus, all three molecules (fHbp, NspA, and LOS sialic acid) contribute to restricting C3 deposition on encapsulated meningococci and highlight redundancy in complement regulatory mechanisms. The relative roles of fHbp and NspA in limiting C3 fragment deposition through the AP likely correlate with their expression levels.

LOS sialylation and surface-bound C3 fragments cooperatively enhance fH binding

Having confirmed the importance of LOS sialylation in AP inhibition on meningococci, we next investigated the molecular basis of this observation. Earlier work has shown that although sialic acid on sheep erythrocytes does not affect the affinity of factor B for C3b, surface-bound C3b enhances the affinity of fH (32). We hypothesized that in an analogous manner, meningococcal LOS sialylation would enhance human fH binding to bacteria when C3 fragments were deposited on the bacterial surface. In contrast, the ability of factor B to bind to C3b deposited on bacteria would not be affected by LOS sialylation.

We first incubated A2594 ΔfHbp ΔNspA with NHS-Mg/EGTA to allow for C3 fragment deposition and then grew one half of the bacteria in gonococcal growth media with CMP-NANA for 1 h to sialylate LOS and grew the other half in media without CMP-NANA to generate organisms that lacked LOS sialylation. Sialylation of bacteria after C3 fragment deposition ensured that similar amounts of C3 were deposited and that C3 deposition occurred at similar sites on both sialylated and unsialylated bacteria (Fig. 3A). Control reactions included bacteria incubated with heat-inactivated serum (HIS) or with buffer alone. Loss of mAb 3F11 binding (Fig. 3B) confirmed that bacteria that had been incubated

FIGURE 2. iC3b deposition on strains A2594 and H44/76 and their ΔfHbp, ΔNspA, and ΔfHbp ΔNspA mutants that either possess or lack LOS sialic acid. (A) Flow cytometry quantifying human C3 deposition on strain A2594 and its mutants. A2594 and its derivatives were grown in media supplemented with 0.02 mM CMP-NANA to sialylate LOS where indicated. Bacteria were incubated with NHS-Mg/EGTA (25% [v/v]) for 30 min at 37°C. The percentage of positive events relative to organisms incubated with HIS was determined as described in Materials and Methods. Each bar represents the mean (SEM) of at least five independent data points. The comparison across groups was performed by one-way ANOVA. ***p < 0.001 compared with all other groups, except where indicated by “ns” (not significant). (B) LOS sialylation of A2594 ΔfHbp ΔNspA reduces the rate of C3 fragment deposition. The wild-type strain (expresses fHbp and NspA but not LOS sialic acid) was used as a control. Bacteria were incubated with 25% NHS-Mg/EGTA for the time periods indicated on the x-axis. C3 deposition on bacteria was measured by flow cytometry as described in (A). Each point represents the mean (SEM) of five separate observations. The comparison across groups was carried out by two-way ANOVA. The p values shown compare ΔfHbp ΔNspA (LOS not sialylated) with its sialylated derivative. (C) Human C3 deposition on strain H44/76 and its mutants. The methods and analysis are as described in (A), (D) and (E) Western blotting analysis of iC3b deposition on A2594 and H44/76, respectively. Bacteria were incubated with NHS-Mg/EGTA (25% [v/v]) for 30 min at 37°C. Bacteria were lysed, and proteins were separated on a 4–12% Bis-Tris gel, followed by transfer to a PVDF membrane by Western blotting. iC3b and iC3b complexes with its meningococcal surface targets were detected with mAb G-3E. The 68-kDa α19 chain of iC3b in (A) migrates as a doublet (~68- and ~70-kDa bands) likely because a fraction of the α1 chain of C3b was not cleaved at the second site by factor I to release the 2-kDa C3f fragment in some lots of purified iC3b, as reported previously (8). Complexes of the α1 chain of iC3b with LOS or opacity protein (Opa) have previously been characterized (31) and are indicated. The lower section of the blot (proteins migrating faster than ~40 kDa) was stained with Coomassie blue (labeled as “load”) and served to illustrate similar loading of bacteria across lanes.
with serum and then grown in CMP-NANA-containing media incorporated sialic acid onto their LOS. Bacteria (coated with C3 fragments with or without LOS sialic acid) were then incubated with purified human fH (10 µg/ml), and bound fH was detected by flow cytometry (Fig. 3C) and Western blotting (Fig. 3D). The highest levels of fH binding were seen to sialylated bacteria on which C3 fragments were deposited. Approximately 3-fold lower levels (as measured by the percentage of positive events) of fH bound to unsialylated bacteria coated with C3 fragments; this level of fH binding was significant when compared with fH binding to bacteria without C3, LOS sialic acid, or added fH. Each bar represents the mean (SEM) of five independent observations. Comparisons across groups were made using one-way ANOVA. (D) Western blotting to demonstrate that LOS sialylation augments binding of full-length fH to meningococci coated with C3 fragments. Bacteria (A2594 ΔHbpΔNspA) were coated with C3 fragments and incubated with human fH, as in (C). Controls included bacteria that lacked C3 and/or added human fH. Bacteria were washed and lysed, and proteins were separated on a 4–12% Bis-Tris gel, followed by Western blotting. Proteins below the 50-kDa marker were stained with Coomassie blue to measure bacterial lysate loading. This experiment was repeated thrice separately with similar results. (E) LOS sialylation does not affect factor B binding to C3 fragments deposited on meningococci. Strain A2594 ΔHbpΔNspA was incubated with NHS-Mg/EGTA (20%) that contained an anti-factor I mAb to decrease conversion of C3b to iC3b and then grown in media that either contained or lacked CMP-NANA, as in (C). Organisms incubated with HIS served as a control. Bacteria were then incubated with purified factor B (fB) at concentrations of 3 or 15 µg/ml, and factor B to bacteria was measured by Western blotting.

In the next experiment, we sought to determine whether LOS sialic acid affected the interaction between factor B and bacteria-bound C3b. Strain A2594 ΔHbpΔNspA was incubated with NHS-Mg/EGTA containing an anti-factor I mAb that blocked the function of factor I to limit conversion of C3b to iC3b and then grown in media that either contained or lacked CMP-NANA, as in (C). Organisms incubated with HIS served as a control. Bacteria were then incubated with purified factor B (fB) at concentrations of 3 or 15 µg/ml, and factor B to bacteria was measured by Western blotting.

**LOS inhibits the AP of nonhuman complement**

Previous studies have shown that binding of fH to meningococcal fHbp and NspA is restricted to humans, which could contribute to the species-specificity of meningococcal infection. Group B strain
H44/76 is rapidly cleared from the bloodstream of wild-type infant rats (23). Preincubation of bacteria from this strain with human fH enhanced bacteremia and decreased rat C3 deposition (23). A recent study demonstrated that H44/76 causes bacteremia in human fH transgenic rats (16). Interestingly, meningococcal lacking expression of both fHbp and NspA (H44/76 ΔfHbpΔNspA) also caused bacteremia in human fH transgenic rats and survived in wild-type infant rat serum supplemented with human fH (16). In contrast, a fully encapsulated ΔfHbpΔNspAΔlst mutant that was unable to sialylate LOS or bind human fH via fHbp or NspA did not cause bacteremia.

In the current study, we have demonstrated a decrease in AP-dependent human C3 fragment deposition mediated by meningococcal LOS sialic acid. We next asked whether this was also restricted to humans. Rat serum was used in the following species specificity experiments because of its relevance to the results described above on the effect of human fH on bacteremia in the transgenic infant rat model of meningococcal bacteremia (16). Strains A2594 and H44/76 and their ΔfHbp and/or ΔNspA mutants that differed in sialylation of their LOS were incubated with Mg/EGTA-treated adult rat serum, and rat C3 fragment deposition on bacteria was measured by flow cytometry (Fig. 4A, 4C) and Western blotting (Fig. 4B, 4D) under reducing conditions. In both strains, LOS sialylation of each of the mutants significantly decreased C3 deposition when compared with the corresponding mutant that lacked LOS sialic acid (Fig. 4A, 4C; see Supplemental Fig. 3 for representative histograms). Consistent with the ability of meningococcal fHbp and NspA to bind only to human, but not to rat fH, the presence of either of these molecules did not affect AP-dependent rat C3 deposition on bacteria.

The polyclonal anti-mouse C3 Ab preferentially detects the ~40-kDa α2 fragment of rat C3b, which is also part of the 105-kDa α’ chain C3b. Thus, rat C3b will migrate independently as a 40-kDa band, whereas the ~105-kDa α’ chain of deposited C3b will migrate covalently complexed with its target. Fig. 4B and 4D show deposition of rat C3 fragments on the mutants of A2594 and H44/76, respectively. The only prominent band detected was the ~40-kDa α2 fragment of iC3b, which suggested that, as with human serum, most of the rat C3b deposited on meningococci was also converted to iC3b. In accordance with the flow cytometry data presented above, expression of fHbp and/or NspA did not affect deposition of rat C3 fragments on bacteria. However, absence of LOS sialic acid resulted in a uniform increase in rat C3 deposition on the wild-type strain and the three mutants of both A2594 and H44/76.

We next asked whether LOS sialic acid enhanced binding of rat fH (as supplied in 5% heat-inactivated rat serum) to rat C3 fragments “predeposited” on meningococci as described above (Fig. 3C, 3D). As expected, binding of rat fH to meningococci in the absence of C3 deposition was not detected. Similar to observa-
tions with the human complement system (Fig. 3D), LOS sialylation increased the interactions between rat fH and rat C3 fragments deposited on strain A2594 ΔfHbpΔNspA (Fig. 4E). A meningococcal band that nonspecifically reacted with polyclonal anti-mouse fH and migrated just above the rat fH band is indicated by the asterisk.

The LOS sialic acid–fH–C3 fragment interaction selectively involves the C-terminal domains of fH

A recent study by Kajander et al. (33) proposed a model where the simultaneous binding of surface-bound C3 fragments to fH SCR domain 19 and glycosaminoglycans to fH SCR domain 20 contributed to AP inhibition and rendered a surface a complement nonactivator.

To assess whether the C-terminal domains of fH selectively interact with C3 fragments deposited on meningococci and LOS sialic acid, strain A2594 ΔfHbpΔNspA coated with C3 fragments and then sialylated as described above was incubated with a construct that contained human fH domains 18–20 fused to mouse IgG Fc (18–20/Fc). We also used a second construct that contains fH SCRs 5–8 fused to mouse IgG Fc (5–8/Fc). This construct binds to both fHbp and NspA (20, 134) and further, fH domains 19–20 contain a heparin binding site (35, 36), and can interact weakly with C3b (36). Schematics of the recombinant fH/Fc fusion molecules used in this experiment and the ligands for the fH domains are shown in Fig. 5A. Consistent with the model proposed recently (35) and evidenced in Fig. 5B, the presence of bacteria-bound C3 fragments enhanced binding of fH 18–20/Fc, which further increased when LOS was also sialylated; binding of fH 5–8/Fc was not affected by LOS sialylation in the mutant strain A2594 ΔfHbpΔNspA (see Supplemental Fig. 4 for representative histograms). The synergy between LOS sialic acid and C3 fragments in enhancing binding of the fusion protein containing the three C-terminal fH domains was also confirmed by Western blotting (Fig. 5C). Taken together, these data suggest that LOS sialic acid and C3b on the meningococcal surface enhance fH binding through its C-terminal domains and may contribute to AP regulation by LOS sialylation.

Discussion

AP regulation on meningococci is a complex process that is modulated by several redundant mechanisms. The expression of groups B or C capsular polysaccharides (7–9), LOS sialic acid (10, 37), fHbp (12, 38, 39), and NspA (14, 38, 40) all contribute to decreasing C3 fragment deposition on meningococci and enhance the organisms ability to resist killing by complement. In this study, we have shown how LOS sialic acid, fHbp, and NspA interact cooperatively to mitigate deposition of C3 fragments through the AP on encapsulated meningococci that express the lacto-N-neotetraose LOS species.

The role of meningococcal fHbp in complement regulation has received considerable attention in recent years because this molecule is a key component of two group B meningococcal vaccines that are currently undergoing preclinical trials in humans (41, 42). fHbp binds to fH with affinity in the nanomolar range (13, 43, 44), and although different fHbp molecules bind to human fH with affinities that vary as much as 50-fold (44), these differences in affinity do not appear to contribute to bacterial survival in serum or blood (43, 44). Rather, the amount of fHbp expressed by a strain may correlate directly with its contribution to serum resistance (38, 44). Similarly and consistent with recently published data (14, 38), the current results show that the amount of NspA expressed may also contribute to the extent of AP regulation by a strain. The high levels of NspA expressed by A2594 (Fig. 1) plays a key role in limiting AP activation on this strain (Fig. 2). Evidence for the importance of fHbp and NspA in complement evasion is further supported by the observation that the genes that encode both proteins are upregulated when bacteria are exposed to blood (38, 45), where they encounter high levels of complement.

Redundancy of complement inhibition mechanisms may also permit some strains to cause disease in the absence of one of these variables—for example, a recent study has identified strains from patients with invasive meningococcal infection that lack fHbp.
expression (46). Furthermore, Welsch et al. (47) have provided evidence for fHbp-independent survival of select meningococcal strains in whole blood. Loss of fHbp from strains such as NZ98/254 and 4243 has minimal impact on their survival in whole human blood; in contrast, deleting fHbp from other strains, such as MCS8 and H44/76, adversely affects bacterial survival in serum as well as whole blood (44, 47).

We previously showed that binding of fH to NspA on intact meningococci by flow cytometry was best observed when either the capsule is expressed and when LOS elaborates unsialylated N-Neotetraose species from HepI. Giuntini et al. (40) showed that anti-fHbp mAbs that blocked fH binding to H44/76 were more bactericidal against H44/76 ΔNspA than against the wild-type parent strain, which underscores the role of NspA even in strains that express low levels of this protein. fH binding assays using flow cytometry likely underestimate the amount of fH bound to bacteria, perhaps because the number of fluorophores per bacterium on low fHbp expressers lies below the threshold of detection and/or because binding may in some cases be of lower affinity. Using the Western blotting assays described in this study, we have readily detected fH binding to strains such as 2996 and 4243 that are low fHbp expressers and show barely detectable binding to fH by flow cytometry (data not shown). It is noteworthy that Western blotting also reveals binding of pure fH to the A2594 ΔfHbpΔNspA double mutant (Fig. 3D). We have observed similar binding of fH to corresponding double mutants of strains H44/76, 2996, 4243, and NZ98/254 (data not shown). Recently, the ΔfHbpΔNspA double mutant of group B strain H44/76 was shown to cause bacteremia in human fH transgenic rats (16); furthermore, the addition of human fH to wild-type rat serum permitted survival of the double mutant in a bactericidal assay (16). Collectively, the data indicate the presence of additional ligand(s) for fH that are distinct from fHbp and NspA on meningococci and contribute to evasion of innate immunity.

The data presented in this article demonstrate an important role for LOS sialylation in inhibition of the AP of complement. The molecular basis for complement regulation by LOS sialic acid on Neisseriae is multifaceted and complex. In studies where all pathways of complement are intact, LOS sialylation has been shown to limit classical pathway activation (48–50). One study has suggested that LOS sialic acid may limit the binding of Abs, in this instance, the binding of specific mAbs to gonococcal porin (51). LOS sialic acid may interfere with binding of C1q on the gonococcal surface (50). LOS is one of the bacterial targets for C3 and C4 (31, 52), and it is likely that the addition of a sialic acid residue may obscure targets for these complement components either on LOS itself or on other proximate molecules (53). Sialylation of the lacto-N-neotetraose LOS species appears to modulate binding of fH to “non-LOS” structures. As examples, LOS sialylation on gonococci increases the association of fH to gonococcal porin (54), whereas LOS sialylation on meningococci increases fH binding to NspA (14). Neisserial LOS sialylation also inhibits opsonophagocytosis by polymorphonuclear leukocytes (55, 56). The importance of LOS sialylation in meningococcal pathogenesis is illustrated by the observation that most strains recovered from the bloodstream or CSF express the sialylated lacto-N-neotetraose LOS species; in contrast, carriage isolates often elaborate LOS immunotypes with more truncated glycan extensions from HepI (57).

Sialylation of host cells serves to limit activation of the AP (58–60), thereby limiting complement-mediated damage to host tissue. fH plays a key role in “self-nonself” discrimination (59, 61) and a recent study by Kajander and colleagues (33) has provided mechanistic insights for this function. They proposed a model where the C-terminal domains 19 and 20 of fH interacted with surface-associated C3 fragments and glycosaminoglycans, respectively, and facilitated regulation of the AP. In addition to Neisseria, other Gram-negative bacteria such as Haemophilus influenzae and Campylobacter jejuni express LOS molecules that can be modified by sialic acid (62, 63). Sialylated LOSs of these bacteria mimic gangliosides elaborated by their human hosts and contribute to limiting complement activation (62, 63). Whether sialic acid on other bacterial species also enhances the interaction between fH and surface-bound C3 fragments remains to be determined.

Strain H44/76 does not cause disease in wild-type infant Wistar rats. Given that fHbp and NspA do not bind to rat fH, this suggests that regulation of the AP by LOS sialic acid alone in this context is insufficient for virulence (23). Further attenuation of the AP as occurs in the human fH transgenic rat permitted virulence when LOS was sialylated, even in the absence of fHbp and NspA expression, or in the Δ1st mutant where LOS was not sialylated but human fH could interact with fHbp and NspA (16). Only when fHbp, NspA, and LOS sialic acid were all deleted did the strain become avirulent in the human fH transgenic rat (16). For reasons not fully understood, meningococcal strains vary widely in their ability to cause bacteremia in rats. As an example, strain 4243 can disseminate into the bloodstream of wild-type infant Wistar rats following i.p. inoculation (18, 64). The mechanisms of complement regulation by such strains may merit further investigation.

In conclusion, the current study has shed further light on the molecular basis of AP regulation on meningococci and provides a more detailed understanding of how these bacteria escape an important arm of innate immune defense. Elucidation of independent and redundant mechanisms of complement evasion will allow a better understanding of how escape variants may be selected under immune pressure, which may be an important consideration as newer vaccines targeting Ags such as fHbp are tested in humans.

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Supplemental Figure 1. Flow cytometry showing human C3 fragment deposition on strains A2594 and H44/76 and their ΔfHbp, ΔNspA and ΔfHbp ΔNspA mutants that either possess or lack LOS sialic acid. Supplemental Figures 1A, 1B and 1C show histogram tracings of a representative experiment from Figures 2A, 2B and 2C, respectively. The x-axis represents fluorescence on a log_{10} scale and the y-axis the number of events.
**Supplemental Figure 2.** LOS sialylation enhances human fH binding to C3 fragments deposited on meningococci, but does not affect factor B interactions with surface-bound C3b. The strain used is A2594 ΔfHbp ΔNspA. Flow cytometry histograms from a representative experiment from Figure 3C are shown. The x-axis represents fluorescence on a log$_{10}$ scale and the y-axis the number of events.
Supplemental Figure 3. LOS sialylation, but not fHbp or NspA, regulates the rat alternative pathway. The upper panel shows data with strain A2594 and its mutant derivatives and is one representative experiment from Figure 4A. Each histogram compares isogenic mutants with sialylated LOS (shaded histogram) or unsialylated LOS (solid black line). Controls (wild-type strain incubated with heat inactivated rat serum) are shown by the broken line. Similarly, the lower panel depicts a representative experiment from Figure 4C with strain H44/76 and its mutants. In all graphs, the x-axis represents fluorescence on a log_{10} scale and the y-axis the number of events.
Supplemental Figure 4. Meningococcal LOS sialylation selectively enhances the interaction of the C-terminal domains of human fH with C3 fragments on the bacterial surface. Experiments were performed with strain A2594 ΔfHbp ΔNspA. One representative experiment from Figure 5B is shown. Binding of fH 5-8/Fc is shown in the histogram graphs on the left side and binding of fH 18-20/Fc in the graphs on the right side. The control graph (bacteria plus anti-mouse IgG FITC) was similar to the grey shaded histograms and has been omitted for simplicity. The x-axis represents fluorescence on a log$_{10}$ scale and the y-axis the number of events.