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Contributions of *Neisseria meningitidis* LPS and non-LPS to proinflammatory cytokine response

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Abstract: To determine the relative contribution of lipopolysaccharide (LPS) and non-LPS components of *Neisseria meningitidis* to the pathogenesis of meningococcal sepsis, this study quantitatively compared cytokine induction by isolated LPS, wild-type serogroup B meningococci (strain H44/76), and LPS-deficient mutant meningococci (strain H44/76[pLAK33]). Stimulation of human peripheral-blood mononuclear cells with wild-type and LPS-deficient meningococci showed that non-LPS components of meningococci are responsible for a substantial part of tumor necrosis factor (TNF)-α and interleukin (IL)-1β production and virtually all interferon (IFN)-γ production. Based on tricine sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis of LPS in proteinase K-treated lysates of *N. meningitidis* H44/76, a quantitative comparison was made between the cytokine-inducing capacity of isolated and purified LPS and LPS-containing meningococci. At concentrations of >10⁷ bacteria/mL, intact bacteria were more potent cytokine inducers than equivalent amounts of isolated LPS, and cytokine induction by non-LPS components was additive to that by LPS. Experiments with mice showed that non-LPS components of meningococci were able to induce cytokine production and mortality. The principal conclusion is that non-LPS parts of *N. meningitidis* may play a role in the pathogenesis of meningococcal sepsis by inducing substantial TNF-α, IL-1β, and IFN-γ production. *J. Leukoc. Biol.* 70: 283–288; 2001.

Key Words: LPS-deficient meningococci · meningococcal sepsis · outer membrane · 2-keto-3-deoxyoctanate · TSDS-PAGE

INTRODUCTION

It is generally accepted that the induction of cytokine synthesis and the subsequent pathophysiological events during Gram-negative septic shock are primarily elicited by the lipopolysaccharide (LPS) component (endotoxin) of the bacterial outer membrane [1]. Purified LPS is able to induce a proinflammatory cytokine pattern and a clinical condition that resembles, at a first glance, the symptoms encountered in Gram-negative septic shock. The LPS-molecule is composed of a lipid-A part harboring its toxic properties, a saccharide part, and one or more molecules of 2-keto-3-deoxy-octanate (KDO) connecting the lipid-A and the saccharide part [2].

Anti-LPS strategies explored so far have failed to ameliorate the clinical course of Gram-negative sepsis [3–6], which raises the question whether LPS is the sole toxic element in Gram-negative sepsis [7].

Fulminating meningococcal sepsis is considered the prototypical human gram-negative septic shock, characterized by extremely high endotoxin and cytokine concentrations [8–11]. Thus, the causative bacterium *Neisseria meningitidis* is a suitable subject for the study of cytokine induction by gram-negative bacteria. Recently, a viable *N. meningitidis* mutant was constructed that is devoid of LPS but still contains all other outer membrane constituents [12]. This mutant has made it possible to assess the cytokine-inducing potency of the non-LPS parts of this gram-negative bacterium in a quantitative fashion.

The principal aim of the present study is to determine the contribution of LPS and non-LPS components of *N. meningitidis* to the pathogenesis of meningococcal sepsis. Therefore, we compared quantitatively the cytokine production induced by meningococcal LPS, wild-type meningococci, and LPS-deficient meningococci.

MATERIALS AND METHODS

The wild-type serogroup B *N. meningitidis* H44/76 strain was isolated from a patient with invasive meningococcal disease [13]. Meningococcal strain H44/76[pLAK33] is a viable isogenic mutant, completely devoid of LPS in its outer membrane. This mutant was constructed by insertional inactivation of the *lpxA* gene, essential for the first committed step in biosynthesis of LPS [12, 14]. The absence of LPS in this strain was confirmed by tricine sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis (TSDS-PAGE) with silver staining of LPS [15, 16], whole-cell enzyme-linked immunosorbent assay (ELISA) with LPS-specific monoclonal antibodies, and gas-chromatographic/mass-spectrometric detection of LPS-specific 3-OH fatty acids [17]. Furthermore, absence of LPS activity in the pLAK33 batch suspension was confirmed by nonreactivity in the Limulus amebocyte lysate assay. Heat-killed (1 h, 56°C) bacteria washed in phosphate-buffered saline (PBS) were used in all experi-

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molecules. The amount of bacteria in the suspensions used was measured by spectrophotometry; an optical density (OD) of 0.2 at 620 nm appeared to be equivalent to approximately $10^8$ bacteria/mL.

Outer membrane complexes (OMCs) of both meningococcal strains were prepared by sarcosyl extraction as described previously [18]. These OMCs consist primarily of PorA (class 1), PorB (class 3), and the RmpM (class 4) outer membrane proteins. The pLAK33 OMCs contain no LPS and express increased amounts of an OpA protein [19]. H44/76 OMCs contain 10–20% LPS. Protein content was determined by a bichromonic acid assay (Pierce Chemical Co., Rockford, IL) with bovine serum albumin as a standard.

The molecular mass of meningococcal strain H44/76 LPS is 4,044 Da [20]; one molecule of LPS contains two molecules of KDO (molecular mass, 238 Da). LPS was isolated by the phenol/water extraction method as described by Westphal and Jann [21]. After isolation, LPS was treated with proteinase K (Sigma-Aldrich Co.) and with D/Nase and RNase (Roche Diagnostics) for additional purification, recovered by ultracentrifugation, freeze-dried, and stored in sterile PBS. The amount of protein contamination in this purified LPS solution was determined by bichromonic acid assay. DNA and RNA contamination was determined by spectrophotometry using a Genousum RNA/DNA calculator (Pharmacacia Biotech AB, Uppsala, Sweden).

The KDO content of the purified H44/76 LPS solution and of the bacterial suspensions was measured spectrophotometrically by the method described by Weissbach and Hurwitz [22].

TSDS-PAGE followed by silver staining of LPS was used for quantification of LPS in N. meningitidis H44/76. Cell lysates of H44/76 meningococci were made by suspending $1.35 \times 10^7$ bacteria in 500 µL of SDS-buffer (7.5% glycerol, 1.25 M Tris/HCl, 1.5% SDS) and incubating this for 5 min at 100°C. Proteins in this suspension were digested by incubation with proteinase K (0.5 mg/mL) for 4 h at 50°C [23]. Serial dilutions of purified H44/76 LPS were used as a standard. After silver staining, the polyacrylamide gel was analyzed by densitometry.

Bleed for the isolation of human peripheral blood mononuclear cells (PBMCs) was drawn in 10-mL EDTA-anticoagulated tubes (Vacutainer System; Beckton Dickinson, Rutherford, NJ) from healthy volunteers. PBMCs were isolated by density gradient centrifugation on Ficoll-Hypaque (Pharmacia Biotech AB). The cells from the interphase were aspirated, washed three times in sterile PBS, and resuspended in culture medium RPMI 1640 (Dutch Chemical Co., Rockford, IL) with bovine serum albumin as a standard.

IFN-γ (0.091 mg/mL). As- suming an average molecular mass for LPS of 4,044 Da, the amount of LPS in this solution based on the KDO assay was (0.091 × 4,044)/(238 × 2) = 0.8 mg of LPS/mL.

TSDS-PAGE with silver stain of LPS was used to determine the amount of LPS in cell lysates of N. meningitidis H44/76 (Fig. 1) [16, 23, 26]. Density analysis of the silver stain of LPS in different dilutions of cell lysates of N. meningitidis H44/76 bacteria and of serial dilutions of purified LPS showed that 7 $\times 10^4$ bacteria contain approximately 1 ng of LPS.

As an alternative approach to determine the amount of LPS in the LPS-containing H44/76 strain, the amount of KDO detected in the LPS-deficient pLAK33 suspension was subtracted from that in the H44/76 suspension. Because the only difference between these isogenic strains is the presence of LPS, the difference in KDO content reflects LPS-associated KDO. In this way, it was calculated that $10 \times 10^4$ H44/76 bacteria contain approximately 1 ng of LPS, a result rather similar to that obtained by TSDS-PAGE analysis.

Quantitative comparison of cytokine induction

The dose-response relationship of meningococcal LPS, wild-type N. meningitidis H44/76, and LPS-deficient N. meningitid-
TNF-α (ng/mL) | IL-1β (ng/mL) | IFN-γ (ng/mL)
---|---|---
ng LPS or 7 x 10⁶ bact./mL | ng LPS or 7 x 10⁶ bact./mL | ng LPS or 7 x 10⁶ bact./mL

The relative contribution of non-LPS structures to the total induction of TNF-α and IL-1β induction by N. meningitidis was assessed in a series of combination experiments. In these experiments, meningococci were supplemented with approximately the same amount of LPS as present in the wild-type strain. Figure 3 shows the results of this experiment for IL-1β after 24 h of incubation. It can be seen that IL-1β production induced by LPS-deficient bacteria was approximately half of that induced by LPS-containing bacteria, whereas after addition of LPS, the IL-1β induction by LPS-deficient bacteria was restored to the level of LPS-containing bacteria. Results for TNF-α and for experiments (n=5) with 4 h of incubation showed a similar pattern (data not shown). This additive effect of LPS to the non-LPS-induced cytokine synthesis suggests that both stimuli may use different pathways for the induction of TNF-α and IL-1β.

Cytokine induction by outer membrane complexes

To determine whether the non-LPS components responsible for cytokine induction reside in the outer membrane, cytokine induction by OMCs isolated from the wild-type H44/76 meningococci and the LPS-deficient pLAK 33 meningococci was assessed. Figure 4 shows the results for IL-1β after 24 h of incubation. It appeared that the wild-type H44/76 OMCs were potent inducers of cytokine synthesis, whereas the cytokine-inducing capacity of pLAK33 OMCs was 1,000- to 10,000-fold less than that of H44/76 OMCs. Results for TNF-α and for
experiments \((n=5)\) with 4 h of incubation showed a similar pattern (data not shown). Taken together these results indicate that the outer membrane components present in OMCs like PorA, PorB, RmpM, or OpA make a minimal contribution to cytokine induction.

**Cytokine induction and lethality in mice**

In mice we assessed whether the observed cytokine induction by non-LPS components of meningococci coincides with the capacity to provoke disease. Results in Table 1 indicate that LPS-deficient meningococci were able to induce cytokine production in murine peritoneal macrophages in vitro. Table 2 demonstrates that LPS-deficient meningococci were able to induce lethality in galactosamine-sensitized mice in vivo. The dose needed for LPS-deficient meningococci to induce mortality was approximately 100-fold higher than for LPS-containing meningococci.

**DISCUSSION**

The principal finding of the present study is that LPS is not the sole cytokine-inducing element of *N. meningitidis*. Using a meningococcal mutant completely devoid of LPS, it was shown that non-LPS components of this bacterium were responsible for a substantial part of the TNF-\(\alpha\) and IL-1\(\beta\) production, that non-LPS components induced IFN-\(\gamma\), and that non-LPS parts could provoke disease. Based on TSDS-PAGE analysis of LPS in proteinase K-treated cell lysates of *N. meningitidis* H44/76, a quantitative comparison between the cytokine-inducing capacity of LPS and that of LPS-containing bacteria became possible. It was shown that concentrations of \(>10^7/\text{mL}\) of bacteria were more potent inducers of cytokine synthesis than equivalent amounts of isolated LPS and that cytokine induction by non-LPS components was additive to that by LPS. Furthermore, it was demonstrated that the non-LPS components responsible for the cytokine induction do not reside in sarcosyl-extracted outer membrane complexes.

Non-LPS components of bacteria can induce cytokine production \([7]\), as has been shown by experiments with gram-positive bacteria \([27–31]\) and with various isolated elements of these bacteria like peptidoglycan \([32–34]\), lipopeptides \([28]\), lipoproteins \([28]\), lipoteichoic acid \([35]\), and capsular polysaccharides \([36]\). However, so far studies trying to assess quantitatively the contribution of these non-LPS structures to cytokine induction by gram-negative bacteria were hampered by the inevitable copresence of LPS, outflanking the cytokine induction by non-LPS structures. To circumvent this problem we used a meningococcal mutant that is entirely deficient of LPS. With this strain we demonstrated that approximately half the amount of TNF-\(\alpha\) and IL-1\(\beta\) induced by meningococci in human PMBCs or murine peritoneal macrophages was elicited by non-LPS structures. Similarly, LPS-deficient meningococci could cause lethal disease in galactosamine-pretreated mice, albeit the dosages of LPS-deficient meningococci required to induce mortality were approximately 100-fold higher than for wild-type meningococci.

TNF-\(\alpha\), IL-1\(\beta\), and IFN-\(\gamma\) are pivotal mediators in the pathogenesis of Gram-negative septic shock. After infusion of LPS in human volunteers or primates, TNF-\(\alpha\) and IL-1\(\beta\) appear within 1 to 2 h \([37]\), but no IFN-\(\gamma\) seems to appear \([38]\). However, after the infusion of whole bacteria, IFN-\(\gamma\) is induced and can be detected in the circulatory system after 6–8 h \([38, 39]\). During meningococcal infections, IFN-\(\gamma\) is increased in plasma or cerebrospinal fluid and correlates with the severity of disease \([40, 41]\). In our in vitro study, meningococcal LPS stimulated only minimal IFN-\(\gamma\) production, whereas both LPS-containing and LPS-deficient bacteria induced significant amounts of IFN-\(\gamma\). In addition, IFN-\(\gamma\) was not produced in response to TNF-\(\alpha\) or IL-1\(\beta\), which indicates that non-LPS components of meningococci were primarily responsible for IFN-\(\gamma\) induction. Because the primary source of IFN-\(\gamma\) is the lymphocyte and marked differences occur between individuals, it is tempting to speculate that certain non-LPS components of meningococci can act as superantigens.

In this study we used the widely employed KDO assay to determine the amount of LPS in the H44/76 LPS preparation \([22, 42, 43]\). With this method \((0.8/0.92) \times 100\%\) (i.e., 85\%)

### Table 1. Production of mTNF-\(\alpha\) and mIL-1\(\alpha\) after 24 h by Murine Peritoneal Macrophages Stimulated with Wild-Type H44/76 Meningococci and LPS-Deficient H44/76[pLAK33] Meningococci

<table>
<thead>
<tr>
<th>Stimulus (dosage)</th>
<th>mTNF-(\alpha) (ng/mL)</th>
<th>mIL-1(\alpha) (ng/mL)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>N. meningitidis</em> H44/76 ((2 \times 10^9/\text{mL}))</td>
<td>1.85 ± 0.39</td>
<td>4.67 ± 1.09</td>
</tr>
<tr>
<td><em>N. meningitidis</em> H44/76[pLAK33] ((2 \times 10^9/\text{mL}))</td>
<td>0.36 ± 0.54</td>
<td>1.96 ± 0.77</td>
</tr>
</tbody>
</table>

Mean data ± s.d are presented \([n=4\text{ for } H44/76 \text{ meningococci}; n=5\text{ for } H44/76[pLAK33] \text{ meningococci}].

### Table 2. Mortality at 24 h (%) in Mice Pretreated with Galactosamine after i.v. Injection of Heat-Killed *N. meningitidis*

<table>
<thead>
<tr>
<th>Strain</th>
<th>10^7</th>
<th>10^8</th>
<th>10^9</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>N. meningitidis</em> H44/76</td>
<td>60</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td><em>N. meningitidis</em> H44/76[pLAK33]</td>
<td>0</td>
<td>0</td>
<td>60</td>
</tr>
</tbody>
</table>

Each group contained five animals.
of the LPS was detected. Limitations of this assay are conversion of a fraction of KDO during acid hydrolysis to entities inert to the thiobarbituric acid reaction and incomplete hydrolysis, both leading to an underestimation of the amount of KDO. On the other hand, contaminants in the LPS may co-rate in the assay, which leads to overestimation of the amount of LPS [44, 45]. The relatively accurate yield of KDO in the present study showed that these limitations of the KDO assay are likely to be of minor importance for determination of H44/76 LPS.

By TSDS-PAGE analysis of LPS in lysates of *N. meningitidis* H44/76, the amount of LPS in H44/76 bacteria was determined. It appears that $7 \times 10^3$ bacteria corresponded to approximately 1 ng of LPS, which fits rather well with the results obtained by KDO analysis in H44/76 and pLAK33 bacteria. This estimate is in good accordance with reported estimates of 1 ng of LPS for $10^5$ bacteria with *Escherichia coli* [1, 46–50], taking into account that the MW of meningococcal LPS is 2- to 10-fold lower than that of *E. coli* LPS. In addition, our estimate compares fairly well to clinical data of Brandtzæg et al. [51], Mariani-Kurkdjian et al. [52], and Bingen et al. [53], who detected LPS values up to 500 ng/mL and bacterial numbers up to $5 \times 10^8$ CFU/mL in cerebrospinal fluid during meningococcal meningitis.

Based on the estimate that $7 \times 10^3$ bacteria correspond to 1 ng of LPS, we could compare the cytokine-inducing potency of isolated LPS with that of meningococci containing the same amount of LPS. It was found that at concentrations below $10^7$ bacteria/mL or equivalent amounts of LPS, LPS induced more cytokine synthesis alone are of limited value, because at this degree of bacteremia, a substantial part of the proinflammatory cytokine response is elicited by non-LPS parts of the meningococcal components not retained after sarcosyl extraction, such as outer membrane proteins (PorB, RmpM, and OpA) did not induce cytokines. Thus, other meningococcal components are able to induce cytokine production. LPS-deficient OMcs are known to interact with human cell receptors [57, 58], we hypothesize to quantify their relative contribution to the pathogenesis of invasive meningococcal disease.

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