Role of Lipoteichoic Acid in the Phagocyte Response to Group B Streptococcus

Philipp Henneke, Siegfried Morath, Satoshi Uematsu, Stefan Weichert, Markus Pfitzenmaier, Osamu Takeuchi, Andrea Müller, Claire Poyart, Shizuo Akira, Reinhard Berner, Giuseppe Teti, Armin Geyer, Thomas Hartung, Patrick Trieu-Cuot, Dennis L. Kasper and Douglas T. Golenbock

*J. Immunol.* 2005;174:6449-6455

http://www.jimmunol.org/cgi/content/full/174/10/6449

References

This article cites 47 articles, 29 of which can be accessed free at:
http://www.jimmunol.org/cgi/content/full/174/10/6449#BIBL

18 online articles that cite this article can be accessed at:
http://www.jimmunol.org/cgi/content/full/174/10/6449#otherarticles

Subscriptions

Information about subscribing to *The Journal of Immunology* is online at http://www.jimmunol.org/subscriptions/

Permissions

Submit copyright permission requests at http://www.aai.org/ji/copyright.html

Email Alerts

Receive free email alerts when new articles cite this article. Sign up at http://www.jimmunol.org/subscriptions/etoc.shtml
Role of Lipoteichoic Acid in the Phagocyte Response to Group B Streptococcus

Philipp Henneke, Siegfried Morath, Satoshi Uematsu, Stefan Weichert, Markus Pfützenmaier, Osamu Takeuchi, Andrea Müller, Claire Poyart, Shizuo Akira, Reinhard Berner, Giuseppe Teti, Armin Geyer, Thomas Hartung, Patrick Trieu-Cuot, Dennis L. Kasper, and Douglas T. Golenbock

Group B Streptococcus (GBS) cell walls potently activate phagocytes by a largely TLR2-independent mechanism. In contrast, the cell wall component lipoteichoic acid (LTA) from diverse Gram-positive bacterial species has been shown to engage TLR2. In this study we examined the role of LTA from GBS in phagocyte activation and the requirements for TLR-LTA interaction. Using cells from knockout mice and genetic complementation in epithelial cells we found that highly pure LTA from both GBS and Staphylococcus aureus interact with TLR2 and TLR6, but not TLR1, in contrast to previous reports. Furthermore, NF-κB activation by LTA required the integrity of two putative PI3K binding domains within TLR2 and was inhibited by wortmannin, indicating an essential role for PI3K in cellular activation by LTA. However, LTA from GBS proved to be a relatively weak stimulus of phagocytes containing ~20% of the activity observed with LTA from Staphylococcus aureus. Structural analysis by nuclear magnetic resonance spectrometry revealed important differences between LTA from GBS and S. aureus, specifically differences in glycosyl linkage, in the glycolipid anchor and a lack of N-acetylgalcosamine substituents of the glycerophosphate backbone. Furthermore, GBS expressing LTA devoid of N-alanine residues, that are essential within immune activation by LTA, exhibited similar inflammatory potency as GBS with alanylated LTA. In conclusion, LTA from GBS is a TLR2/TLR6 ligand that might contribute to secreted GBS activity, but does not contribute significantly to GBS cell wall mediated macrophage activation. The Journal of Immunology, 2005, 174: 6449 – 6455.

Copyright © 2005 by The American Association of Immunologists, Inc.
bacterial envelope. However, its contribution to the interaction between bacteria and cells of the mammalian immune system within invasive infections remains less well understood. As an example, we previously demonstrated that cell wall preparations from GBS activate immune cells in the absence of both TLR2 and CD14. These preparations were likely to be rich in LTA, thus raising questions about the cognate receptor of LTA from GBS and the contribution of LTA to phagocyte activation by GBS (3, 4, 12).

To answer the question about the significance of PGN and LTA in GBS infection, we defined several issues: 1) whether LTA from GBS differs from LTA from S. aureus with respect to chemical structure and phagocyte activation; 2) whether LTA engages TLR2 and TLR1 on phagocytes, as has been suggested previously (10, 11); 3) whether the presence of alanine in LTA affects the inflammatory potency of GBS cell walls; and finally 4) whether LTA synergizes with PGN.

Materials and Methods
Reagents
Reagents were obtained from Sigma-Aldrich unless stated otherwise. PBS, DMEM, G418, and trypsin/versene mixture were from Cambrex. Low endotoxin FBS was from HyClone Laboratories. LPS derived from Escherichia coli strain O111:B4 was purchased from Sigma-Aldrich and twice re-extracted by phenol chloroform as described (19). Clone 55, a monoclonal LTA Ab that recognizes the glycerophosphate epitope, was from Hycult Biotechnology.

Primary cell culture and cell lines
Human PBMC were isolated by gradient centrifugation of heparinized blood from healthy donors on Histopaque 1077 (Sigma-Aldrich), resuspended in RPMI 1640 medium containing 10% FBS. Cells were seeded at a density of $10^6$ cells/ml stimulated and analyzed for TNF formation as described (3).

Bacterial strains and cell wall preparations
Bacterial type III strains COH1, NEM 316, and the isogenic NEM 316 mutant deficient in $\alpha$-alanine-$\alpha$-alanyl carrier protein ligase NEM1636 have been previously described (13, 14). All strains were grown on blood agar plates at a density of $2 \times 10^9$ cells/ml stimulated and analyzed for TNF formation as described (3).

Preparation of LTA
GBS LTA engages TLR2. LTA from GBS activated an NF-$\kappa$B reporter construct in HEK293 cells, transfected with human TLR2, but not in cells transfected with the empty expression vector (Fig. 1A). NF-$\kappa$B activation was abrogated when tyrosine residues at positions 616 or 761 were substituted by alanine. These tyrosine residues are parts of putative binding domains (YxxM and YxxW) for the PI3K subunit p85 (22). LTA from GBS required the domains around Tyr761 and Tyr616, as essential signaling domains of TLR2 (Fig. 1A). A similar dependency on the respective TLR2 tyrosine residues was observed with Pam$_{3}$CSK$_{4}$, a TLR 2 ligating lipopeptide from E. coli (data not shown). Of note, the proximal Ty616 is located right downstream of the transmembrane TLR2 domain and outside the signaling TOLL/IL-1R domain. In contrast to purified TLR2 ligands, mutation of either tyrosine-containing motif resulted in an intermediate phenotype in response to whole heat inactivated S. aureus. However, mutation of both motifs abolished activation altogether (Fig. 1B). Finally, we found that wortmannin, a PI3K inhibitor, inhibited the LTA-induced activation of the ELAM.luc reporter in HEK TLR2 cells (>60% inhibition of 20 $\mu$g/ml LTA by 100 nM wortmannin as compared with vehicle control). Hence we conclude that PI3K significantly contributes to the response to LTA via TLR2.

TLR6, not TLR1, is required as a TLR2 coreceptor for responses to LTA
Like the well studied macrophage-activating lipopeptide of 2 kDa (MALP-2), LTA comprises a diacylated moiety (16). In contrast, the predominant lipoprotein from E. coli (Pam$_{3}$CysK$_{4}$) is triacylated. In both MALP-2 and Pam$_{3}$CysK$_{4}$, the fatty acids are believed to constitute the activation domains of these lipoproteins. MALP-2 has been reported to activate a heterodimer consisting of TLR2 and TLR6, Pam$_{3}$CysK$_{4}$ and a triacylated lipoprotein from Borrelia burgdorferi (Ospa) activate TLR1 in concert with TLR2 (17, 23, 24). Furthermore, converting Pam$_{3}$CysK$_{4}$ into a diacylated
protein converts the TLR1/2 ligand into a TLR2/6 ligand (17). In apparent contrast to the effects of these ligands, the diacylated LTA has recently been reported to engage TLR1 plus TLR2 for cellular activation (10, 11). Hence, we addressed this question by testing the induced responses in cells from genetically modified mice that lack TLR1, TLR2, or TLR6. Both LTA from GBS and LTA from *S. aureus* similarly required cellular expression of TLR2 and TLR6 to mount an inflammatory response (Fig. 2, B and C). In contrast, macrophages deficient in TLR1 responded normally to LTA, whereas the response to Pam3CysK4 was markedly impaired in cells from these mice (Fig. 2A). These results imply that LTA is recognized by a receptor complex consisting of TLR2 and TLR6.

**LTA from *S. aureus* exceeds LTA from GBS in activation of inflammatory cytokines**

LTA that was extracted from GBS serotype III strain COH1 stimulated PBMC from normal human volunteers to secretion of IL-8 and TNF. However, GBS-LTA was 5-fold less potent, as assessed by the approximate shift in the midrange of the dose-response curve, than LTA extracted by the same method from *S. aureus* (Fig. 3). With respect to the release of inflammatory cytokines from PBMC LTA was consistently 1000-fold less potent than another TLR2 ligand, lipopeptide from *Mycoplasma fermentas* (MALP-2, data not shown).

**The structure of GBS LTA**

Because LTA from GBS and LTA from *S. aureus* differed substantially with respect to the extend of phagocyte activation but not the composition of the cognate receptor, we wondered whether both LTA were structurally different. To address this question we performed NMR analysis of LTA from GBS (type III, strain COH1) and *S. aureus* LTA. Several structural differences between GBS LTA and *S. aureus* LTA could be characterized by this approach (Fig. 4): 1) The average polyglycerophosphate backbone of GBS LTA

---

**FIGURE 1.** LTA from GBS engages TLR2. Tyr<sup>616</sup> and Tyr<sup>761</sup> of TLR2 are essential for LTA-induced activation of NF-κB. A. HEK293 were transfected with an ELAM-luciferase reporter and either empty vector, human TLR2<sup>FLAG</sup>, TLR2-Y616A<sup>FLAG</sup>, TLR2-Y761A<sup>FLAG</sup>, or TLR2-Y616A<sup>FLAG</sup>. After 24 h, transfected cells were incubated with LTA from GBS and human recombinant TNF (nanogram per milliliter) over 5 h and luciferase activity was determined in the cell lysates by luminometry. Depicted are fold activation as compared with unstimulated controls. B. HEK293 were transfected as outlined in A and stimulated with heat-inactivated *S. aureus* in concentrations corresponding to CFU per milliliters shown. Depicted is the activation of an ELAM-luciferase reporter normalized to TNF control as means ± SD of triplicate wells from one representative out of three experiments.

**FIGURE 2.** TLR2 and TLR6, but not TLR1, are essential for macrophage activation by LTA. Peritoneal macrophages from TLR1<sup>−/−</sup> mice (□) and C57BL/6 wild-type mice (■) (A), TLR2<sup>−/−</sup> mice (□) and C57B/6J wild-type mice (■) (B), or TLR6<sup>−/−</sup> mice (□) and C57B/6J wild-type mice (■) (C) were incubated as indicated with 10 μg/ml LTA from GBS (LTA<sub>GBS</sub>), 10 μg/ml LTA from *S. aureus* (LTA<sub>S</sub>), 100 ng/ml Pam3CysK4, 30 ng/ml MALP-2, or 100 ng/ml LPS over 18 h, and TNF-α concentrations were determined in the supernatants. Depicted are the mean ± SD of triplicate wells from one representative experiment of three.

---

**FIGURE 3.** LTA from *S. aureus* exceeds LTA from GBS in activation of inflammatory cytokines. LTA that was extracted from GBS serotype III strain COH1 stimulated PBMC from normal human volunteers to secretion of IL-8 and TNF. However, GBS-LTA was >5-fold less potent, as assessed by the approximate shift in the midrange of the dose-response curve, than LTA extracted by the same method from *S. aureus* (Fig. 3). With respect to the release of inflammatory cytokines from PBMC LTA was consistently ~1000-fold less potent than another TLR2 ligand, lipopeptide from *Mycoplasma fermentas* (MALP-2, data not shown).
was relatively short with an average of \( n = 19 \) glycerophosphate repeats; 2) In GBS LTA a kojibiose linked the polyglycerophosphate chain to the membrane anchor resulting in a Glc-\( \alpha\)-1,2Glc-\( \alpha\)-1–3-diacylglycerol, whereas gentiobiose was found at this position in \( S.\ aureus \) LTA with a different glycolipid linkage leading to a Glc-\( \beta\)-1–6Glc-\( \beta\)-1–3-diacylglycerol structure; 3) In GBS LTA the polyglycerophosphate backbone was substituted only with \( \beta\)-alanine whereas in \( S.\ aureus \) and many other Streptococcus species \( \beta\)-alanine and N-acetyl-glucosamine can be found. Nevertheless, the percentage of \( \beta\)-alanine substituents was higher in \( S.\ aureus \) LTA (70%) than in GBS LTA (46%); 4) The average chain length of the fatty acids was 14 carbons in GBS LTA.

**Alanylated LTA is not essential for GBS-induced inflammatory activation of phagocytes**

To establish the role of LTA to GBS-induced inflammatory activation of phagocytes, we used a GBS targeted deletion mutant of the dlt operon (Dlt\( \Delta \)) that completely lacks \( \beta\)-alanine esters of the polyglycerophosphate backbone (13). First, we analyzed the LTA content of GBS cells by Western blot using an LTA-specific glycerophosphate Ab. The Dlt\( \Delta \) mutant NEM1636 that exhibited normal growth in tissue culture medium (DMEM) contained approximately twice as much LTA as the wild-type parental control GBS (strain NEM 316, Fig. 5A). This slight increase in cell wall associated LTA in the Dlt\( \Delta \) mutant might indicate that deprivation of \( \beta\)-alanyl esters of LTA stimulate LTA biosynthesis by an as yet unknown mechanism.

Careful titration experiments in PBMC and RAW cells did not reveal any difference in the inflammatory activity (formation of TNF and IL-8) of wild type (NEM 316) and Dlt\( \Delta \) mutant (NEM1636) strains despite a considerably higher \( \beta\)-alanine content in NEM 316 (20 vs 0% in Dlt\( \Delta \), Fig. 5B and C) (13). Accordingly, because \( \beta\)-alanine esters are critical for LTA activity (16), LTA appears not to contribute essentially to the inflammatory activity of GBS cell wall.

**LTA and PGN do not synergize**

Because GBS cell walls are a very potent inflammatory stimulus to macrophages (nanogram per milliliter quantities are sufficient to induce substantial cytokine production), and GBS LTA proved to be only moderately effective in inducing inflammatory signals, we wondered, whether LTA synergized with other cell wall components such as PGN to elicit a more powerful inflammatory response. In light of the close structural relationship of PGN from different species of Gram-positive bacteria, we used that of \( S.\ aureus \) and combined it with LTA from GBS in both human PBMC and transfected HEK293 cells. LTA and PGN did not synergistically activate immune cells or epithelial cells overexpressing TLR2 (HEK/TLR2) disproving our hypothesis (Fig. 6A). However, a combination of LPS and TLR2 ligands results in a strong synergistic response, demonstrating that synergistic responses to bacterial products can occur (data not shown). Further, LTA synergized with muramyl dipeptides (MDP), disaccharide cleavage products of PGN, to result in increased IL-8 production.

**FIGURE 3.** LTA from \( S.\ aureus \) exceeds LTA from GBS in activation of inflammatory cytokines. Human PBMC were incubated with butanol extracted LTA from GBS (solid line) or LTA from \( S.\ aureus \) (dashed line) over 18 h, and IL-8 concentrations were determined in the supernatants. Depicted are the mean ± SD of triplicate wells from one representative experiment of three.

**FIGURE 4.** The structure of GBS LTA as determined by NMR spectroscopic analysis. A, LTA from GBS (serotype III, strain COH1) was structurally resolved by NMR. B, The published structure of \( S.\ aureus \) LTA (16). The structural differences of the membrane anchor between the two LTA species are highlighted in gray and the different substitution of the glycerophosphate backbone in each LTA is given as a percentage.
NOD2, the intracellular receptor for MDP. To synergize with each other but synergize with TLR4 and with vast bacterial counts in the neonatal lung (10⁹–10¹¹ CFU/g of lung tissue) in a primate model of neonatal GBS infection GBS accumulates to concentrations chosen (Fig. 6A). Hence, TLR2 ligands appear not to synergize with each other but synergize with TLR4 and with NOD2, the intracellular receptor for MDP.

Discussion
In a primate model of neonatal GBS infection GBS accumulates to vast bacterial counts in the neonatal lung (10⁹–10¹¹ CFU/g of lung tissue) surrounded by an intense inflammatory infiltrate. This suggests that phagocytes interacting with bacterial cell walls initiate an inflammatory response without sufficiently eliminating the bacteria in newborn species (25). In vitro, GBS cells are powerful inflammatory stimuli for phagocytes from neonates and adults (3, 4, 26). In contrast, the expression of adhesion molecules and the intracellular killing of GBS both appear to be impaired in newborn infants (27, 28). Of note, a similar imbalance of antibacterial and inflammatory responses to GBS can be observed in diabetic mice and overcome by the addition of insulin (29). Thus, a preponderance of proinflammation is likely to accord for the particular susceptibility of both newborn infants and diabetic patients to invasive GBS disease. Accordingly, the identification of GBS substructures that trigger a potentially detrimental systemic inflammation is of apparent interest.

Among several structural bacterial components LTA appeared to be a most attractive candidate toxin of GBS. LTA of S. aureus (16) and Streptococcus pneumoniae (30) had recently been shown to potently induce cytokines in phagocytes, thus clarifying a long standing controversy on the inflammatory potency of LTA, including synthetic preparations (31, 32). Because both functional and structural data on highly pure GBS LTA were missing we embarked on both biological and chemical analysis of this molecule.

TLR2, the principal signal transducer for LTA, is believed to function only in concert with other TLRs because homodimerization of the cytoplasmic domain of TLR2 does not induce inflammatory cytokines in macrophages, whereas similar dimerization of TLR4 is believed to do so (33). We found TLR6, but not TLR1, to be an essential component of the receptor for LTA from both GBS and S. aureus. This observation clearly supports the notion that diacylated ligands interact with the TLR2/6 heteromer (34).

Current differences in our data to recent reports on TLR1 as part of the LTA receptor are unclear (10, 11). Differences related to the species, mouse macrophages in our study vs human cells in previous studies, cannot be ruled out at this stage. Further, because previous reports were based entirely on data generated with TLR1 Abs or heterologous expression of TLR1 in the context of endogenous TLR1 and TLR6 (HEK cells), interference with formation of the entire TLR1/2/6 complex might have affected the specificity of these approaches (10, 11).

A disruption of this multimer by a TLR1 blocking Ab might further explain the reported complete abrogation of an LTA response in PBMC, which seemed surprising in view of the established intermediate phenotype of TLR1 deficiency in mice (17). In addition to TLR1 we identified PI3K as a critical TLR2 signaling partner for LTA induced activation of NF-κB. Purified TLR2 ligands appear to be exquisitely dependent on both putative PI3K binding domains of TLR2 whereas both motifs are capable of partially compensating for each other in response to S. aureus cells (22). This indicates the engagement of further receptor or adapter molecules by these organisms.

Whereas GBS LTA and S. aureus LTA engaged a similar receptor heteromer we observed considerable interspecies variation in inflammatory potency of equally prepared LTA. To unravel the
molecular basis of the impaired potency, albeit similar receptor engagement of GBS and *S. aureus* LTA, we chemically analyzed GBS LTA. NMR analysis revealed GBS cells to contain type I LTA: In type I LTA a polyglycophosphate is attached to the C-6 of the nonreducing glucosyl of the glycolipid anchor (6, 35). GBS shares the basic configuration of LTA with other streptococci, staphylococci, and bacilli (6, 35). However, beyond these similarities, we found interesting and as yet unknown features of the GBS LTA structure. The average length of the hydrophilic LTA chain was 19 glycophosphate units and is clearly exceeded by the length of *S. aureus* LTA (*n* = 45–50) (16). Furthermore, the structure of the glycolipid Glc-α-1,2Glc-α-1–3-diacylglycerol was different from those revealed in *S. aureus* and *S. pneumoniae* but similar to those in *Enterococcus, Leuconostoc,* and *Lactococcus* spp. (36). In addition, in GBS LTA the polyglycophosphate backbone was substituted with ω-alanine only whereas in *S. aureus* and many other species ω-alanine substituents are alternating with N-acetyl-glucosamine. The individual contributions of gentiobiose, N-acetyl-glucosamine and the length of the polyglycophosphate backbone to the substantial functional differences between GBS and *S. aureus* LTA remain to be elucidated.

Although partially substituted with N-acetyl-glucosamine, *S. aureus* LTA contains a higher percentage of ω-alanine substituents (70%) than LTA GBS (46%) (13, 16). These differences in ω-alanyl ester content might be relevant for the inflammatory properties of the molecule. Structural analysis of native and synthetic LTA from *S. aureus* revealed, that next to the lipid anchor itself, alanine substituents are required for proper inflammatory activity of the molecule (16, 31, 37). Replacing ω-alanine substituents with l-alanine reduces the activity of the molecule at least 10-fold, indicating stereoselectivity (31). Both with respect to conservation of ω-alanine residues and inflammatory potency, the butanol extraction procedure of LTA that was used in this study is far superior to the conventional phenol extraction (16). Moreover, LTA from *S. aureus* and *Lactobacillus rhamnosus* are better inducers of NO in macrophages than LTA from *Bacillus subtilis* that exhibits a low percentage of alanylated LTA (38, 39).

We used the apparent dependency of LTA ω-alanylation on cytokine induction to further explore the contribution of LTA to the inflammatory activity of GBS cell wall. In GBS, the incorporation of ω-alanine residues in LTA biosynthesis requires the *dlt* operon that encodes the four proteins DltA, DltB, DltC, and DltD. DltA is a cytoplasmic ω-alanine-ω-alanyl carrier protein ligase that catalyzes the ω-alanylation of the ω-alanyl carrier protein DltC (40). We found cell wall material from DltA− GBS that have been previously shown to completely lack alanylated LTA, to exhibit similar inflammatory activity as the isogenic parental strain (20% alanylated LTA) (13). Further, whereas purified LTA from GBS was considerably weaker with respect to inflammatory phagocyte activation as compared with LTA from *S. aureus*, whole GBS and *S. aureus* cells were similarly potent stimuli (data not shown). These observations add some insight to in vivo studies that used DltA− Gram-positive bacteria in mouse sepsis models. DltA− GBS display a severely decreased virulence in mouse and rat infection models. This loss in virulence correlates to an increased susceptibility to killing by phagocytes (14). Deletion of ω-alanine increases the net anionic charge of the bacterial cell wall and therefore alters binding of cationic peptides. Our data suggest that in contrast to the important contribution of alanylated LTA to bacterial survival in the host, additional and as yet unidentified GBS components are the dominant inflammatory stimuli of the cell wall. However, because expression of TLR2 is critical for the course of disease in a neonatal GBS sepsis model, secreted LTA might contribute to phagocyte activation in vivo (5).

In this study, we found LTA from GBS to be an ~100-fold weaker inflammatory stimulus for mouse macrophages as compared with cells from the same strain (comparison on a dry weight basis, P. Henneke and D. T. Golenbock, unpublished observations). Corresponding to this observation and in line with several reports we hypothesized that a synergism between PGN and LTA accounts for the “endotoxic” properties of Gram-positive bacteria both in vivo and in vitro (38, 41–43). LTA and PGN apparently share the cognate receptor TLR2, although considerable concern has been raised about an as yet to be identified contaminant carrying the TLR2 activity of PGN preparations. However, LTA and PGN preparations appear to differ with respect to engagement of the coreceptor because PGN appears to activate immune cells independently of TLR6 and TLR1 (44). Bearing this in mind, one could envision that both ligands engage different and independent domains of TLR2, hence resulting in synergism. In fact, a synergistic effect for PGN and LTA has been described (38, 45). To our surprise we did not observe any synergism between PGN and the highly pure LTA in vitro, whereas we and others found TLR4 ligands to synergize with TLR2 ligands (46, 47) Further, LTA synergized with MDP, disaccharide cleavage products of PGN, presumably via its intracellular receptor NOD2. These results are not entirely consistent with previously published reports. However, as has been reported elsewhere, commercial preparations of LTA that were used in previous studies were notoriously contaminated with LPS (37, 48). This contamination might have accounted for a synergism between TLR2 and TLR4 rather than between various TLR2 heteromers.

In conclusion, highly pure LTA extracted from GBS is an inflammatory TLR2/6 ligand with substantial structural and functional differences to LTA from *S. aureus*. LTA from GBS requires tyrosine phosphorylation of TLR2 for inflammatory activation. LTA synergizes with MDP but not with PGN in vitro. However, whereas synergism between LTA and MDP might contribute to secreted activity of GBS, it is unlikely to explain the strong inflammatory activity of GBS cell wall because TLR2 is nonessential for GBS activation by macrophages (3, 4, 12) and, because GBS expressing LTA without alanine substitutions that are crucial to LTA activity, elicit full inflammatory activity.

**Disclosures**

The authors have no financial conflict of interest.

**References**


