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**Bartonella quintana** Lipopolysaccharide Is a Natural Antagonist of Toll-Like Receptor 4

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**Bartonella quintana** is a gram-negative microorganism that causes trench fever and chronic bacteremia. *B. quintana* lipopolysaccharide (LPS) was unable to induce the production of proinflammatory cytokines in human monocytes. Interestingly, *B. quintana* LPS is a potent antagonist of Toll-like receptor 4 (TLR4), as it inhibited both mRNA transcription and the release of tumor necrosis factor alpha, interleukin 1β (IL-1β), and IL-6 by *Escherichia coli* LPS in human monocytes, at ratios ranging from 1,000:1 to 10:1 (*B. quintana* LPS to *E. coli* LPS). Likewise, *B. quintana* LPS blocked the interaction of *E. coli* LPS with TLR4 in transfected cell lines. The extent of the inhibitory effect of *B. quintana* LPS was demonstrated in microarray studies, which showed downregulation of practically all genes induced by LPS in monocytes. Because of the role of TLR4 in inflammation, *B. quintana* LPS may prove useful as a potent anti-TLR4 agent with therapeutic potential in both infections and autoimmune inflammation.

**Bartonella quintana** is a gram-negative pathogen initially described during World War I as the agent of trench fever, a disease associated with recurrent fever and headaches. In the past few decades, *B. quintana* infection has been identified in homeless people (4). While most individuals with *B. quintana* infection recover, some 5 to 10% eventually develop chronic bacteremia (4) and subsequent complications, such as chronic endocarditis in the absence of preexisting heart valve lesions (20). New manifestations of *B. quintana* infections, such as bacillary angiomatosis, bacillary peliosis hepatitis, and chronic lymphadenopathy, have also been described (2). These manifestations have been attributed to proliferative and antiapoptotic effects of *Bartonella* spp. (6).

A characteristic of *B. quintana* bacteremia is the absence of symptoms of high fever and signs of septic shock, disseminated intravascular coagulation, or organ failure. Lipopolysaccharide (LPS, or endotoxin) is a main component of the outer membranes of gram-negative microorganisms, and the LPSs from gram-negative enteric bacteria (such as *Escherichia coli* and *Salmonella enterica*) are able to induce proinflammatory cytokines, chemokines, and adhesion molecules (23) and thereby to evoke the clinical signs of sepsis. The lipid A moiety of LPS interacts with a membrane receptor complex containing Toll-like receptor 4 (TLR4), MD-2, and CD14 (17, 19, 23). Because of strong proinflammatory effects of most species of LPS, the apparent absence of sepsis syndrome in patients with *B. quintana* bacteremia is a puzzling aspect of the infection. As an explanation, overproduction of the anti-inflammatory cytokine interleukin-10 (IL-10) and an attenuated inflammatory cytokine profile during *B. quintana* bacteremia have been proposed (5), but the molecular mechanisms have remained elusive.

Recently, the LPS of the related organism *Bartonella henselae* was purified and characterized as a penta-acylated deep-rough LPS with low endotoxic activity (17, 27). In the present study, we investigated the biologic activities of *B. quintana* LPS in terms of induction of proinflammatory cytokines and interaction with TLRs and other species of LPS.

**MATERIALS AND METHODS**

Reagents and microorganisms. LPS (*E. coli* serotype O55:B5) was purchased from Sigma Chemical Co., and synthetic Pam3CSK4 was purchased from EMC Microcollections (Tübingen, Germany). The *B. quintana* Oklahoma strain was kindly provided by D. Raoult (Marseille, France) and grown on sheep blood agar at 37°C in a 5% CO2 atmosphere. For stimulation experiments, 5-day cultures of *B. quintana* were heat killed for 60 min at 56°C. *B. quintana* LPS was extracted either by a single-step phenol-water extraction, as previously described (13), or by a two-step extraction method (9) which eliminates contamination with proteins. *E. coli* LPS from Sigma was also double purified (9). Both purified and unpurified *E. coli* and *B. quintana* LPS (100 µg of each) were run in a 10% polyacrylamide gel and subjected to silver staining to visualize contaminating proteins.

**Signaling through human TLR2 and TLR4 in a transfected cell line.** Chinese hamster ovary (CHO) fibroblasts stably transfected with human CD14 (3E10-CD14), a combination of CD14 and TLR4 (3E10-TLR4), and TLR2 (3E10-TLR2) were a kind gift from Robin Ingalls. These cell lines express inducible membrane CD25 under the control of a region of the human E-selectin (ELAM-1) promoter containing NF-kB binding sites. Cells were maintained at 37°C in 5% CO2 in Ham’s F-12 medium (Gibco, Invitrogen, Breda, The Netherlands) supplemented with 10% fetal calf serum, 0.01% L-glutamine, 50 µg/ml gentamicin, 400 U/ml hygromycin, and 0.5 mg/ml of G418 (for 3E10-TLR2) or 0.05 mg/ml of puromycin (for 3E10-TLR4) as an additional selection antibiotic.
After 16 h, hybridization arrays were washed and incubated with streptavidin-coupled phycoerythrin (Molecular Probes, Eugene, OR). The GeneChips were then scanned using a GeneChipScanner laser scanner (Affymetrix, Santa Clara, CA) according to the manufacturer's instructions and were analyzed by using GCOS (Affymetrix, Santa Clara, CA). Normalization, model fitting, and filtering were performed by using dChip (Harvard) (12). Subsequently, pairwise and multiple comparisons were performed by dChip, applying different criteria (>2-fold change with P value of <0.05 and/or >2-fold change with P value of <0.05). High-level analyses such as cluster analysis, principal component analysis, and analysis of variance were performed by dChip on filtered genes and a gene list generated by multiple comparisons. Hierarchical cluster analysis was performed using algorithms that assemble all elements in a single tree based on computed similarity scores.

### RESULTS

**Role of TLR2 and TLR4 in recognition of B. quintana.** The first sets of experiments were designed to explore the induction of proinflammatory cytokines by whole B. quintana microorganisms and the role of TLR2 and TLR4 in this induction. Interestingly, heat-killed B. quintana did not stimulate TLR4-transfected CHO cells, while TLR4-transfected CHO cells reacted to B. quintana, indicating that the microorganism is able to signal through this receptor (Fig. 1A to D). To further assess the biological significance of these findings, we investigated the production of proinflammatory cytokines by human PBMC upon stimulation with heat-killed B. quintana. As shown in Fig. 1E, a blocking TLR4 antibody did not influence the capacity of B. quintana to stimulate the production of TNF-α, IL-1β, and IL-6 from human PBMC. This finding implies that the stimulation of cytokines by B. quintana is not induced by its LPS component and that B. quintana LPS stimulates cytokines through a TLR4-independent mechanism.

**B. quintana LPS is a TLR4 antagonist.** To investigate the two above-mentioned possibilities, we isolated B. quintana LPS in a two-step purification process which warrants the absence of protein contaminants (14). The purity of both E. coli and B. quintana LPSs after the two-step purification was determined using silver staining for proteins. Silver staining revealed the absence of any protein contaminants in both LPS samples after purification (Fig. 2A). As shown in Fig. 2B, purified B. quintana LPS did not stimulate the production of TNF-α, IL-1β, and IL-6 from human PBMC. IL-8 was also not induced by B. quintana LPS (not shown). Similar negative results were obtained when peritoneal murine macrophages were stimulated (not shown). These results demonstrate that B. quintana LPS is not able to induce cytokine production and suggest that it is devoid of direct biological activity.

It was shown previously that certain LPS structures with no direct agonistic activity can function as TLR4 antagonists. To assess whether B. quintana LPS also functions as a TLR4 antagonist, we preincubated human PBMC with various concentrations of B. quintana LPS before stimulating the cells with E. coli LPS. As shown in Fig. 3A, B. quintana LPS completely abolished E. coli LPS-induced TNF-α production when ratios of at least 10:1 were used and inhibited the induction of cytokines approximately 50% when a 1:1 ratio of B. quintana LPS to E. coli LPS was employed. In addition, when a 10:1 ratio was used, B. quintana LPS was able to completely inhibit the ex.
pression of proinflammatory cytokine TNF-α, IL-1β, and IL-6 mRNAs from E. coli LPS-challenged human PBMC (Fig. 3B). The inhibitory effect of B. quintana LPS was exerted by blocking TLR4, as further demonstrated by the blockade of E. coli LPS-induced stimulation of CHO cells transfected with TLR4 (Fig. 3C). In addition, the effects of B. quintana LPS are targeted specifically to TLR4, since the stimulation of TLR2 was not influenced by the presence or absence of B. quintana LPS in the cultures (not shown).

Microarray analysis. We performed oligonucleotide genome array (Affymetrix) analysis to evaluate the impact of B. quintana LPS on gene expression on its own and in combination with E. coli LPS. Cluster analysis revealed that samples treated with E. coli LPS clustered together, whereas samples treated with B. quintana LPS or E. coli LPS plus B. quintana LPS clustered together with the control (Fig. 4A). In spite of the strong influence of donor differences, the effect of B. quintana LPS was unambiguous, as the expression profile for B. quintana LPS alone or in combination with E. coli LPS was hardly different from that of the corresponding control. This indicated that B. quintana LPS exerted no effect on its own but totally inhibited the effect of E. coli LPS. The complete mode of inhibition indeed suggests that B. quintana LPS binds to TLR4 but does not transduce the signal, hereby acting as a competitive inhibitor of E. coli LPS. When the effects of different treatments on gene expression were compared, E. coli

FIG. 1. TLR4 is not involved in the host response to B. quintana. CHO cells transfected with CD14, CD14 and TLR4, or CD14 and TLR2 were stimulated with 1 × 10⁶ heat-killed B. quintana cells. Expression of CD25 on the cell membrane was measured by fluorescence-activated cell sorting analysis. B. quintana stimulated CD25 expression only in CHO-CD14/TLR2 cells (B and D), not in CHO-CD14 (A and D) or CHO-CD14/TLR4 (C and D) cells. (E) Human PBMC were stimulated for 24 h with 1 × 10⁷ heat-killed B. quintana microorganisms/ml in the presence of either control IgG1 (open bars) or an anti-TLR4 antibody (aTLR4) (10 μg/ml; hatched bars). Unstimulated cells are presented as solid bars.
LPS regulated 679 genes (>2-fold change and \( P < 0.05 \); both up- and downregulation) compared to the control (Fig. 4B). In contrast, \( B.\) \( quintana \) LPS alone or in combination with \( E.\) \( coli \) LPS regulated no single gene compared to the control by these criteria.

**DISCUSSION**

In the present study, we show for the first time that the gram-negative bacterium \( B.\) \( quintana \) does not trigger host defense mechanisms via TLR4-dependent pathways and, instead, that its LPS component is a powerful TLR4 antagonist. Septic shock is often preceded by gram-negative bacteremia, and the LPS component of these pathogens is known to play a crucial role in this respect. Interestingly, \( B.\) \( quintana \) was previously described to induce chronic infections (4), whereas...
FIG. 4. (A) PBMC were isolated from two individual donors (1 and 2). They were preincubated or not with *B. quintana* LPS (Inh) for 15 min and thereafter stimulated or not with *E. coli* LPS (LPS). The numbers designate the donor origins. Gene expression profiling was performed and analyzed as described in Materials and Methods. Hierarchical cluster analysis was performed on genes (vertical dendrogram) and samples (horizontal dendrogram) according to the algorithm described in Materials and Methods to visualize the gene expression patterns and relatedness of samples. Red, upregulation; blue, downregulation; white, average regulation. The magnified view in the box shows sample information in color blocks (first row, individual sample color code; second row, treatment groups, with dark green for control, light green for LPS, dark brown for inhibitor alone, and light brown for LPS plus inhibitor; third row, treatment groups, with dark and light gray for with and without *E. coli* LPS, respectively) and clustering of samples according to the gene expression profiles. (B) Samples were compared to the control, and the numbers of differentially expressed genes were determined using the criteria of a >2-fold change and a *P* value of <0.05. The number above each bar indicates the number of differentially expressed genes.
signs of an important acute response were absent in those infected with the pathogen (2, 20). In line with this, the results of our present study strongly suggest that TLR4 is not involved in the host defense against *B. quintana*, and this fact might also be responsible for the absence of hypotension and shock in *B. quintana*-infected persons. The limited role of LPS-TLR4 interaction in the induction of an immune response and shock in *B. quintana*-infected persons is due to the inability of its LPS component to stimulate cytokine production. Furthermore, its LPS component and TLR4. Moreover, while being unable to stimulate cytokines at concentrations as high as 10 μg/ml. The nature of these differences remains to be established. It should be noted, however, that other LPS species with antagonistic properties, i.e., *R. sphaeroides* or *C. violaceum* LPS, have tetra-acylated lipid A structures (25). As we previously proposed, the three-dimensional structure of lipid A is responsible for the differential interaction with TLR4, with strictly cylindrical structures being antagonists, whereas more conical shapes function as strong TLR4 agonists (18). In addition, a hexa-acylated biphosphoryl LPS is likely to represent the structure that could best trigger a proinflammatory response upon binding to TLR4 (17). Other LPS structures with antagonistic properties for human TLR4, such as a mutant LPS from *N. meningitidis* (T. Sprong, personal communication), have been shown to be agonists of murine TLR4. Initial studies suggest that this is not the case for *B. quintana* LPS (1).

The role of TLR4 in the pathogenesis of endotoxic shock has been demonstrated extensively, and recently the receptor was proposed to be a potential therapeutic target for several autoimmune diseases, including rheumatoid arthritis (3). In line with this, the results of our study underline the large potential of *B. quintana* LPS for therapeutic use in these diseases. Firstly, in experiments conducted in vitro, *B. quintana* LPS could block *E. coli* LPS-induced effects at ratios as small as 10:1. Secondly, *B. quintana* LPS specifically binds TLR4 and does not interfere with the stimulation of other receptor pathways. Finally, unlike studies using a selected number of genes, the genome array approach enables the evaluation of total transcript levels in an unbiased way. Therefore, these results clearly demonstrate that *B. quintana* LPS is a potent TLR4 antagonist and also suggest that its potential to interfere with other immunologic pathways, if any, is extremely limited. Eventually, this might be translated into a limitation in side effects in the case of therapeutic applications. This may give *B. quintana* LPS a significant advantage with respect to other biological drugs currently on the market.

In conclusion, we demonstrate in the present study that stimulation of cytokines by *B. quintana* is independent of both its LPS component and TLR4. Moreover, while being unable to stimulate cytokine production, *B. quintana* LPS is a potent TLR4 antagonist. Because TLR4 proinflammatory signals are involved in a variety of pathological inflammatory reactions, the use of the TLR4 antagonistic properties of *B. quintana* LPS may prove of potential therapeutic value.

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