REVIEW ARTICLE

Activation of innate host defense mechanisms by *Borrelia*

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ABSTRACT. *Borrelia* is the causative agent of Lyme disease, a widespread disease with important health consequences. Immune-mediated mechanisms are believed to play a major role in both host defense and in late complications of Lyme disease. Recognition of *Borrelia* and the initial activation of the innate immune system are important for host defense, as well as modulation of adaptive responses. Several classes of pattern recognition receptors (PRRs) have been suggested to be involved in the recognition of *Borrelia*: Toll-like receptors (TLRs), NOD-like receptors (NLRs) and C-type lectin receptors (CLRs). TLR2 has been found to be the most important receptor of the TLRs. The intracellular receptor NOD2, a member of the NLRs, might also play an important role in recognition. Mannose receptor is also involved in *Borrelia* recognition, but little is known about other CLRs such as dectin-1. After PRRs have recognized *Borrelia*, a signaling cascade is induced that leads to transcription of NF-κB, resulting in the production of pro-inflammatory cytokines. Understanding these pathways provides not only a better insight into the pathogenesis, but also provides potential, novel, therapeutic targets during active disease or post-infection complications.

Keywords: Lyme disease, *Borrelia*, innate host defense

Lyme disease is caused by a spirochete of the *Borrelia* genus, *Borrelia burgdorferi* sensu lato (herein referred to as *Borrelia*), which can be further classified into three human pathogenic species: *Borrelia burgdorferi sensu stricto* (*s.s.*), *Borrelia afzelii*, and *Borrelia garinii*. In the United States, only *B. burgdorferi* can be found, while *B. afzelii* and *B. garinii* cause most cases of Lyme disease in Europe and Asia [1]. Lyme disease is the most frequent arthropod-borne disease in the Northern hemisphere [2, 3]. In the United States, where Lyme disease is a notifiable disease, the US Centers for Diseases Control and Prevention have reported a steady increase of cases, with 19,931 cases reported in 2006. The incidence in the different states varies significantly: from almost no cases in Montana to 73.6 per 100,000 inhabitants in Connecticut [4]. In Europe, the highest frequency occurs in Central Europe and Scandinavia, especially in forested areas, with an incidence of 111 per 100,000 inhabitants in Germany [3].

The clinical manifestations of Lyme disease can be divided into three stages: early infection, disseminated infection and persistent infection [5, 6]. In the first stage, a localized infection of the skin, so-called erythema migrans (EM), can be seen in approximately 70 to 80% of patients [2, 7, 8]. If the pathogen disseminates through the blood and lymphatics, it can localize in places such as the heart, eyes, joints, and peripheral or central nervous system (CNS). This can lead to the second stage of the disease, the so-called early disseminated Lyme disease, which is arrived at after several weeks to a few months post-infection [1]. Lyme arthritis develops in approximately 50% of patients with untreated EM, this being the most frequent symptom of disseminated disease in the US. It is characterized by recurrent, intermittent attacks of inflammation, usually in the large joints and most often the knee [9]. In addition to arthritis, CNS involvement called neuroborreliosis can develop at this stage, with manifestations such as aseptic meningitis, radiculoneuritis, cranial neuritis and meningoradiculitis (also called Bannwarth syndrome) [10, 11]. The third stage, persistent infection or late stage Lyme disease, can develop months to years after the initial tick bite. It can be characterized by acrodermatitis chronica atrophicans (ACA), which is frequently accompanied by sensory peripheral polyneuropathy, and is almost exclusively caused by *B. afzelii* [12]. Persistent infection can also include neuroborreliosis and chronic arthritis [9, 13]. Some of these symptoms occur despite long-term antibiotic treatment. There are two hypotheses for the chronic arthritis: one hypothesizes that the complication is due to persistent infection, the other that an infection-induced autoimmune process is involved [1]. There is variation
in the clinical presentation in Europe and the US, which is partly due to the relationship between the Borrelia species and the type of clinical manifestation. For example, B. burgdorferi sensu stricto is commonly associated with arthritis, while B. afzelii causes mainly skin manifestations, and B. garinii often gives rise to neuroborreliosis [14]. Many aspects of the pathophysiology of Lyme disease remain unexplained, and the nature of the immune response to the pathogen is only partly understood. One important aspect of spirochetal-host interaction is represented by the spirochetal recognition of the host. How spirochetes are recognized by the innate immune system and how they cause inflammation remains incompletely understood. Because the activation of the innate immune system is also responsible for the further modulation of the secondary adaptive immune responses, the recognition of Borrelia and the initial triggering of innate immunity are important for understanding both host defense and immune-mediated, late complications. In this review, we shall present a summary of what is known about the recognition of Borrelia species by the innate immune system, and discuss which aspects need further investigation.

THE PATHOGEN AND ITS VECTOR

Borrelia is a thin (0.2-0.5 μm), elongated (20 μm), helically-coiled, Gram-negative bacterium that belongs to the phylum Spirochaetes [15]. It has a protoplasmic cylinder surrounded by a fluid outer membrane and a peptidoglycan layer. The outer cell membrane contains many lipoproteins, including the outer surface proteins (Osp) A through F [16]. In the periplasmic space, situated between the outer cell membrane and the peptidoglycan layer, seven to eleven flagella are attached to and wound around the protoplasmic cylinder. These flagella are responsible for the shape and motility of the pathogen [17]. A flagellum consists of a helical filament made of 41-kDa flagellin, a basal body and a hook that is attached to the protoplasmic cylinder [18].

The genome of B. burgdorferi sensu stricto (strain B31) has been sequenced and seems quite small, with approximately 1.5 megabases. It consists of an unusual, small, linear chromosome of 950 kilobases and 21 plasmids, of which 12 are linear (lp) and nine circular (cp) [19, 20]. Borrelia distinguishes itself from other spirochetes by the fact that 40% of its genetic material, including genes encoding for certain outer-membrane proteins, is encoded by these plasmids [19]. Some of the plasmids can be lost during in vitro cultivation, indicating that they are not all stable and may not be essential [21]. Other plasmids are necessary, since they encode for proteins that are essential for the survival of Borrelia, such as the Osp and other lipoproteins, which will be discussed extensively later.

Borrelia is transmitted by ticks of the Ixodes complex, with I. ricinus and I. persulcatus being the primary vectors in Europe and Asia. In general, I. scapularis (or I. dammini) is considered, next to I. pacificus, to be the most important vector in North America [22, 23]. However, some groups argue that I. scapularis is a vector to humans, although this tick is infected naturally with B. burgdorferi and is an efficient experimental vector [22]. At any stage (larval, nymphal, adult) of their two-year lifespan, ticks can be infected with Borrelia. The percentage of infected ticks varies from 9% to 55% [24, 25]. Once infected, ticks transmit Borrelia by injection of Borrelia-containing saliva into the skin upon feeding [22]. This is achieved primarily by nymphs since they are small and consequently less noticed, which is important since transmission of Borrelia to a mammalian host only takes place when the tick is attached for longer than 48 hours [26]. Ticks feed on a large range of animals, and although many do not act as a reservoir, they are important for the survival of the tick since they supply nutrients. In Europe, rodents such as the Apodemus mice and voles, shrews, hares and several birds are significant reservoirs [27, 28]. In the US, mostly rodents and deer are involved as reservoirs [1].

MECHANISMS THROUGH WHICH BORRELIA PROMOTES TRANSMISSION AND DISSEMINATION

Outer surface proteins OspA, OspB and OspC

Borrelia utilizes different mechanisms to establish adequate transmission (figure 1). Outer surface proteins (Osp) play an important role. To be able to survive inside the tick, Borrelia expresses outer surface proteins OspA and OspB. They help Borrelia to attach to the tick receptor for OspA (TROSPA) [29-31]. In this way, Borrelia can stay in the tick midgut as long as the tick is unfed. Upon the tick feeding on a mammal, Borrelia travels to the salivary glands. At this time, OspA is downregulated and OspC is upregulated. Regulation of this expression is mediated by temperature and pH [32]. OspC binds a tick salivary protein, Salp15, that contributes to transmission in mammals by its immunosuppressive properties, one of which is the inhibition of antibody-mediated killing and inhibition of CD4+ T-cell activation [21, 33]. Evidence that OspC is of key importance in transmission, was provided by OspC-deficient Borrelia that were unable to colonize ticks [34] and establish infection in mice [35]. Furthermore, OspC might be important for dissemination, since disseminated disease is associated with only certain OspC variants of B. burgdorferi strains [36].

Adhesins

After Borrelia has reached the dermis, it expresses binding proteins on the surface (adhesins) to facilitate its dissemination [37]. Adhesion to the extracellular matrix is one way to accomplish this, and in particular, decorin-binding adhesins (DbpA and DbpB) seem to play an important role by binding to decorin, a collagen-associated proteoglycan [38, 39] (figure 1). Decorin is usually linked to glycosaminoglycans (GAGs) and both seem to be needed for optimal binding [40]. The binding protein BBK32 is also important for binding to the extracellular matrix since it binds to fibronectin, an extracellular matrix protein.
Expression of BBK32 is dependent not only on the type of Borrelia strain, but also on the culture conditions in vitro. Another mechanism through which Borrelia promotes dissemination is by penetrating the matrix and the endothelial monolayers. This is mediated by binding of Borrelia to plasminogen, leading to plasmin formation and the induction of proteolytic activity [43-45]. Matrix metalloprotease-1 (MMP-1) and MMP-9, whose expression and release is induced by Borrelia, also enhance the penetration of tissue barriers (in vitro) [46, 47].

Spirochetes do not only use adhesins for binding to the extracellular matrix, but for binding to cells as well. This is done by binding to non-decorin GAGs, which are produced by a wide variety of cells [48, 49]. The binding capacity is dependent on the cell type and the spirochete strain [50]. One example is the Borrelia glycosaminoglycan protein (Bgp) that binds to heparin sulfate present on the surface of endothelial cells [49]. The p66 outer-surface protein also binds to endothelial cells (and macrophages) by binding the integrin αIIβ3 that is present on their cell surface [51, 52]. Integrins are heterodimeric receptors, and are the most important metazoan receptors involved in adhesion of cells to the extracellular matrix and other cells [53]. In addition to binding endothelial cells, p66 also binds platelets through the integrin αIIβ3 [54]. Consequently, p66 seems to be very important for colonization of the blood vessel wall (figure 1).

**RECOGNITION OF BORRELIA BY THE INNATE IMMUNE RESPONSE**

The task of the innate immune system is to control the infection until the more specific adaptive response is developed. The innate immune system defends the host from infection in a non-specific way, without eliciting immunological memory. It involves the epithelium, the complement system, phagocytic cells (neutrophils and macrophages), NK cells and several cytokines that coordinate the actions of the above-mentioned cells.

**Complement-mediated killing of Borrelia**

The complement system plays a crucial role in the first line of defense against micro-organisms, by either direct lysis of the pathogen, or recruitment of leukocytes to the site of infection. Approximately thirty plasma and cellular proteins are known to be involved in the complement system that is divided in the classical and alternative
pathway. The main step in the alternative complement activation is the cleavage of C3 into C3a and C3b by C3-convertases. C3b will cover the outer surface of pathogens followed by opsonization and formation of the membrane-attack complexes [55]. To protect the host from damage by C3b deposition, vertebrates express proteins on their cell membranes that convert C3b into an inactive protein. These proteins belong to the family of complement regulatory proteins or regulators of complement activator (RCA). Factor H and factor H-like protein 1 are prominent members of this family. Micro-organisms often use similar proteins that down-regulate complement activation to avoid killing by the host complement system. The pathogenicity of Borrelia species is determined by their ability to interfere with the complement system leading to serum resistance [56].

Pathogen-associated molecular patterns and their pattern recognition receptors

Pathogen-associated molecular patterns (PAMPs) play a very important role in the activation of the innate immune system. PAMPs are conserved structures or components from micro-organisms that cannot be found in host cells. They are shared by groups of micro-organisms and show little variation among a given class. Their expression can be essential for the survival of the micro-organism [57]. This last characteristic prevents extensive changes in structure and gives the innate immune system a chance to recognize the micro-organism. Examples of PAMPs include hypomethylated DNA with CpG motifs, peptidoglycans, lipopeptides, flagellins and double-stranded RNA [58]. Gram-negative bacteria cause a major inflammatory response through the stimulatory properties of lipopolysaccharide (LPS) [59, 60]. Borrelia does not contain LPS in the structure of its cell wall, but it does express many membrane-associated lipoproteins. Several of these have been shown to stimulate the innate immune response, such as OspA and OspB [61-63].

The innate immune response is initiated when PAMPs are recognized by pattern recognition receptors (PRRs), which are expressed by cells of the innate immune system. Each PRR has broad specificities for the various conserved and non-variant structures of several micro-organisms [64]. Three types of PRRs on immune cells exist: secreted PRRs such as the LPS-binding protein (LBP), cell surface PRRs such as Toll-like receptors (TLRs), and PRRs that are only found intracellularly, such as nucleotide-binding oligomerization domain proteins (NOD) [65, 66]. TLRs are the best-characterized PRR class so far. In the case of Borrelia, several types of PRRs have been suggested to be involved in its initial recognition: TLRs, NOD1 and NOD2, and C-type lectin receptors such as the mannose receptor (MR) and dectin-1 (figure 2).

TLRs

Toll-like receptors have been found to play an important role in the innate immunity and inflammation of the host, in response to several different microbial components. They are expressed by mucosal epithelial cells, as well as professional phagocytes. TLRs are type 1 integral membrane glycoproteins, which are characterized by a single, trans-membrane domain and an intra-cytoplasmic domain, also called the TOLL/interleukin-1 receptor homology domain (TIR domain). An important characteristic that distinguishes TLRs from interleukin-1 receptors is the extracellular domain consisting of 19 to 25 leucine-rich repeats (LRR) (figure 2). Although the LRR domains of the several family members of TLRs share homology, different TLRs are able to recognize structurally unrelated proteins [58, 67]. Eleven mammalian TLRs have been reported: TLR1 through TLR11; the ligand for TLR10 has not yet been determined [58], and TLR11 is a truncated molecule in humans [68]. The localization of the various TLRs differs: TLR3, TLR7, TLR8 and TLR9 are only found in intracellular compartments, whereas TLR1, TLR2, TLR4, TLR5 and TLR6 are expressed mainly on the surface of the cell membrane, and can be recruited into the phagosomes [58, 69-71].

TLR2

The expression of TLR2 is restricted to antigen-presenting cells, epithelial and endothelial cells [72]. TLR2 has a very broad range of ligands: ranging from peptidoglycan from Gram-positive bacteria, to bacterial lipoproteins and mycobacterial cell-wall lipoarabinomannan [58]. This broad range of ligands might be explained by the fact that TLR2 can form a functionally active heterodimer receptor with other TLRs such as TLR6 or TLR1 [73-75], but also with other PRRs such as dectin-1 or CD36 [76, 77]. TLR1 and TLR6 discriminate between bacterial lipoproteins that are triacylated or diacylated at the amino-terminal cysteine residue [78]. It was recently demonstrated that TLR2 requires TLR6 to transduce efficiently signals in TLR2-transfected endothelial cells and macrophages [73, 74, 79]. The role of TLR2 in the pathogenesis of Lyme disease has been studied extensively and has proved to be important. Wooten and colleagues demonstrated that macrophages from TLR2-deficient mice were unable to induce an immune response after stimulation with the Borrelia lipoprotein OspA [62]. Another study showed that neutrophils of patients with Lyme disease have an upregulation of TLR2 mRNA and protein in combination with an elevated production of IL-6 and IL-1β after recognition of Borrelia [80]. Peripheral blood monocytes (PBMCs) of patients with a Arg753Gln mutation in TLR2 show impaired cytokine induction after stimulation with Borrelia lysates [81]. However, it remains unclear whether intact Borrelia spirochetes induce this cytokine response through TLR2 alone, or whether other TLRs might cooperate with TLR2. For example, in a study with TLR2 knock-out mice, macrophages do respond to lysates of whole spirochetes, indicating that there is also a TLR2-independent mechanism [62].

Whether TLR2 is important only for host defense against Borrelia, or whether it also induces deleterious inflammatory reactions in the pathogenesis of Lyme disease remains unclear. In a study using TLR2 knock-out mice, a 100-fold increase in the load of spirochetes was seen in tissues, including ankle joints, ears and hearts of TLR2 knock-out mice compared to wild-type mice, who
developed a relative milder, inflammatory carditis [79]. The number of spirochetes in tissues after four weeks of infection was comparable between the knock-out mice and their wild-type littermates, which suggests that TLR2 probably plays an important role in the innate immune response against *Borrelia*. This observation was able to be confirmed in humans by Schröder et al. [81]. This group found that a heterozygous mutation in TLR2 (Arg753Gln), may protect against the development of late stage Lyme disease, since smaller amounts of inflammatory cytokines such as TNF-α and IFN-γ were produced.

Most lipoproteins contain a Pam3Cys-modified cysteine that harbors the stimulatory effect [63, 82-84]. Lipoproteins which contain Pam3Cys are known to be expressed on *B. burgdorferi* during tick feeding and inflammation in mammals, and OspA is a well known example of such a lipoprotein [85, 86]. The response elicited by lipoproteins is very similar to that of LPS, and this is probably due to the similarities between TLR2 and TLR4 signaling pathways [87, 88].

**TLR4**

TLR4 is expressed by cells of the immune system, mostly by macrophages and dendritic cells [64]. The main ligand for TLR4 is lipopolysaccharide (LPS) from Gram-negative bacteria [89]. *Borrelia* spirochetes do not express LPS on their outer surface [90]. Not surprisingly,
a role for TLR4 in Lyme disease has not been demonstrated. Nonetheless, an elevated expression of TLR4 was seen in primary microglia after uptake of *B. burgdorferi*, and upregulation of TLR4 was found on dendritic cells and macrophages of healthy volunteers that were stimulated with synthetic lipopeptides corresponding to OspC of *B. burgdorferi*, although TLR1 and TLR2 were upregulated as well [91, 92].

**CD14**

CD14 is a co-receptor of both TLR2 and TLR4 that is able to recognize a variety of microbial compounds, thereby enhancing the activity of TLR4 [87, 88]. Wooten and colleagues were the first to report that the lipoproteins of *Borrelia* (OspA and OspC) could activate cells via pathways mediated by CD14 [88]. CD14 knock-out mice were found to have a more severe inflammatory response after infection with *Borrelia*, and the numbers of spirochetes in tissue were higher compared to their wild-type littermates [87]. Human neutrophil and human umbilical vein endothelial cell (HUVECs) sensitivity was decreased twenty-fold after blocking CD14 molecules. However, these cell types were still activated when CD14 molecules were absent or blocked, indicating that CD14 is able to facilitate signaling, but is not the ligand-specific receptor. In patients with acute Lyme disease, CD14 was found to be upregulated in serum, indicating that this protein may play a role in the pathogenesis [93].

**TLR5**

Bacteria derive motility from flagella and TLR5 recognizes flagellin, the main component of flagella. Flagellin is a potent, pro-inflammatory inducer which acts by inducing degradation of IkB [94], and thereby the induction of the NFkB-pathway, which will be discussed later. It was hypothesized that TLR5 does not play a major role in the recognition of *Borrelia* species, since the flagella of the spirochetes are located between the outer and inner membrane. However, in other spirochetes, for example *TREPONEMA pallidium*, it was shown that TLR5 can recognize flagellin because of transient gaps in the membrane of the spirochete [95]. Whether these gaps are present in *Borrelia* spirochetes has not yet been demonstrated, and the role of TLR5 in the recognition of *Borrelia* is an important area of investigation for the future.

**TLR9**

TLR9 recognizes unmethylated CpG motifs in bacterial DNA. This is preceded by internalization of CpG DNA into late endosomal or lysosomal compartments [96]. CpG DNA is a component of sonicated *B. burgdorferi*, and has been shown to activate murine cells through TLR9 [97]. In addition, *B. burgdorferi* was shown to release DNA in culture, which could provide ligands for induction of signaling pathways via TLR9 [98]. However, a definite role for TLR9 in the recognition of *Borrelia* has not yet been reported. Shin and colleagues were unable to find differences in cytokine induction after stimulation of cells of TLR9-deficient mice [98]. Furthermore, when astrocytes and microglia were stimulated with *Borrelia* spirochetes, upregulation of TLR9 mRNA expression was not seen, suggesting that TLR9 does not play a major role in the pathogenesis of Lyme neuroborreliosis [91].

**TLR3, TLR7 and TLR8**

TLR3, TLR7 and TLR8 are probably not involved in the innate recognition of *Borrelia*. These TLRs have ligands for fragments of viruses, such as double-stranded RNA (TLR3), and single-stranded RNA (TLR7 and TLR8), and also other small antiviral compounds are recognized by these TLRs [66]. Nonetheless, cooperation between several TLRs has been seen before, and the activation of non-involved TLRs by other activated TLRs as well [62, 74, 91, 99, 100].

**NOD-like receptors**

Another class of PRR receptors are the NOD-like receptors, also called nucleotide-binding domain and leucine-rich repeat-containing molecules (NLRs). NLRs sense the presence of intracellular muropeptides derived from bacterial peptidoglycans. Several members of this family have been shown to induce signaling pathways by acting as PRRs [101]. NOD1 and NOD2 are mainly expressed by epithelial cells and antigen-presenting cells (APCs) such as macrophages and dendritic cells [100]. Cell walls of Gram-positive and Gram-negative bacteria contain peptidoglycans that are responsible for providing shape and mechanical rigidity. Peptides derived from peptidoglycans, such as muramyl dipeptide (MDP) and γ-D-glutamyl-meso-diaminopimelic acid (iE-DAP) are found to be the NOD1 and NOD2 ligands respectively [102-107]. Several groups have reported a role for NOD1 in the recognition and induction of signaling pathways of inflammation in a variety of Gram-negative bacteria such as *Chlamydia* and *E. coli* [108, 109]. *B. burgdorferi* was reported to upregulate NOD-proteins on astrocytes after exposure to several TLR-ligands [110]. Sterka and colleagues found that NOD2, and not NOD1, was highly upregulated on primary murine microglia after stimulation with *B. burgdorferi* [111]. This may suggest that NOD-proteins are involved in the induction of inflammation. Indeed, in preliminary studies we have shown that NOD2 is involved in the release of several different inflammatory cytokines induced by *Borrelia*, such as IL-6. Persons with a non-functional NOD2 express lower cytokine levels after stimulation with *Borrelia* spirochetes (unpublished data). However, the exact role of NOD2 in the pathogenesis of Lyme disease remains unknown.

**C-type lectin receptors**

C-type lectin receptors (CLR) comprise a family of proteins that contain one or more structurally-related, C-type lectin-like domains. In vertebrates, 17 subgroups have been identified, which can be further divided in soluble lectins and cell-associated (transmembrane) C-type lectins, such as dectin-1 and mannose receptor. Many transmembrane CLRs are expressed by antigen-presenting cells. They function as PRRs by recognizing polysaccharide PAMPs of micro-organisms [112].
Mannose receptor

Mannose is found in glycoproteins on the surface of many micro-organisms. It is recognized by the mannose receptor family, a subgroup of the C-type lectin superfamily, consisting of the M-type phospholipase A2 receptor, DEC-205/gp200-MR-6, Endo180/αPARAP, and macrophage mannose receptor [113]. The mannose receptor (MR) is a transmembrane protein that is involved in the recognition of several micro-organisms including Candida albicans, Pneumocystis carinii, Leishmania donovani, Mycobacterium tuberculosis, and Klebsiella pneumoniae via distinct domains [114-119]. The MR is expressed on several cells of the innate immune system, such as tissue macrophages, dendritic cells and endothelial cells [120]. Ezekowitz and colleagues demonstrated that the MR plays a role in the endocytosis and phagocytosis of bound ligands of Candida albicans by macrophages [114]. Similar results were seen for several different strains of Mycobacterium tuberculosis [118].

The MR possibly plays a role in the host defense against Borrelia infection by facilitating the phagocytosis of the bacteria by monocytes and macrophages. Borrelia spirochetes in the dermis and epidermis can be processed by Langerhans cells and dendritic cells. The MR on dendritic cells is highly upregulated after activation by spirochetes, and B. burgdorferi can be recognized and bound by it [120]. It was also reported that the MR is able to induce the release of IL-1β, IL-6 and IL-12 after triggering by other micro-organisms [121, 122]. Whether the MR is also able to induce the secretion of cytokines after triggering with Borrelia remains to be investigated.

Dectin-1

Dectin-1 is the best-known member of the natural killer (NK)-cell-receptor-like C-type lectin family, and is the only PRR that is able to transduce its own intracellular signals without the help of TLRs [123], through pathways involving CARD9 on one hand, and Raf-1 on the other [124, 125]. The main ligands for dectin-1 are β-(1,3)-glucans. So far, there has been no evidence to support a role for dectin-1 in the recognition of Borrelia. In addition, chemical analysis of Borrelia did not reveal any potential ligands for dectin-1 in its cell wall [126].

Signaling pathways induced by recognition of Borrelia

Recognition of Borrelia by the PRRs, induces a cascade of signals that ultimately activates the cell. In the TLR signaling pathway, TLR2 and TLR4 dimerize after binding the ligand, which allows the intracellular domain to form a TIR-TIR interface with the TIR domain of the MyD88 adaptor molecule (MAL, also known as TIRAP), and, in turn, with the myeloid differentiation factor-88 (MyD88). The amino-terminal death domain of MyD88 then induces phosphorylation of IL-1R-associated kinase 4 (IRAK4) and IRAK1, allowing formation of a complex with tumor-necrosis-factor-receptor-associated factor 6 (TRAF6), a ubiquitin ligase. TRAF6 induces activation of TGF-beta-activated kinase (TAK1). Finally, these events activate the nuclear transcription factor (NF-κB) by degrading the IKK complex (inhibitor of NF-κB kinase complex). NFκB is thereby able to translocate to the nucleus and induce transcription of inflammatory genes [58, 67] (Figure 2).

The role of MyD88-dependent signals in cell activation by Borrelia has recently been shown. In MyD88-deficient mice, the number of spirochetes in tissues was considerably higher than in wild-type mice [127]. Furthermore, MyD88 seems to be necessary for efficient clearance of Borrelia [128]. However, MyD88-independent pathways are induced by Borrelia as well. MyD88-deficient mice were shown to have arthritis similar to wild-type mice [128] or even more severe [127]. This suggests that there are other pathways involved in inflammation other than through TLRs alone.

Once intracellular signals are induced by Borrelia, there is a central role for p38 mitogen-activated protein (MAP) kinase activity in the generation of the pro-inflammatory response. The p38 MAP kinase phosphorylates mitogen- and stress-activated protein kinase 1 (MSK1), which in turn phosphorylates NF-κB, resulting in transcription of pro-inflammatory and host defense genes [129].

Leukocyte effector mechanisms against Borrelia infection

Production of cytokines and chemokines

Borrelia has potent stimulatory activities, one of the most important being cytokine induction. The expression of the pro-inflammatory cytokines IL-6, IL-1β, IL-12, TNF-α and IFN-γ is increased in vitro when different cells such as PBMCs and mast cells are stimulated with Borrelia [130-138]. This response is elicited by the outer surface lipoproteins that induce translocation of NF-κB through PRR signaling [63, 84, 132, 139]. Borrelia is able to induce, not only the production of pro-inflammatory cytokines, but also anti-inflammatory cytokines such as IL-10 [140]. In addition, chemokines (e.g. IL-8) and adhesion molecules (such as E-selectin, VCAM-1 and ICAM-1 by OspA) are expressed in response to Borrelia [63, 141, 142]. Together, these molecules direct the recruitment of macrophages and neutrophils, which can eliminate the spirochetes by producing oxygen radicals such as nitric oxide [82, 83]. Finally, the innate immune system plays a role in inducing the adaptive immune system; co-stimulatory molecules on antigen-presenting cells being upregulated through PRR signaling [66]. Furthermore, proliferation of B-cells and production of immunoglobulin are induced by Borrelia [143]. The several different mechanisms through which TLRs signal might provide an explanation for the variation in inflammation duration and severity of Lyme disease [66].

Escape mechanisms of Borrelia from host response

Although the innate immune system tries to prevent Borrelia from harming the host, the spirochete has its own mechanisms to avoid the host defense system [60].
(figure 1). We mentioned earlier that Borrelia benefits from Salp15, because it suppresses the host immune response. Besides Salp15, the I. scapularis tick saliva also contains I. scapularis salivary anti-complement (Isac), which inhibits the complement system by suppressing the C3-C5 convertase enzyme [144]. Borrelia can also inactivate the host complement system by binding host complement regulatory proteins Factor H and Factor-H-like protein with complement regulator-acquiring surface proteins (CRASPs) and OspE-related proteins (Erps). Through this mechanism C3b is inactivated, and consequently the complement cascade at the surface of the spirochete is inhibited [145-149]. Subtypes of Borrelia have a different susceptibility to complement: B. afzelii is complement-resistant, B. garinii is complement-sensitive, while B. burgdorferi s.s. is immediately sensitive. Both the classical pathway and the alternative pathway are activated by all Borrelia species [145, 150].

Another mechanism employed by Borrelia to escape the immune response is to use antigenic variation. The variable, major protein-like sequence gene locus (vlsE) on plasmid 28-1 undergoes extensive variation, which is stimulated by tick feeding [151-153]. vlsE Gene expression is induced when the mammalian host is infected [154, 155]. Evidence for the importance of vlsE is provided by the fact that loss of the plasmid 28-1 results in reduced infectivity [156]. Besides vlsE, also OspA, OspB and OspC are subject to antigenic variation [157]. A different immune escape mechanism induced by Borrelia consists of using lateral gene transfer. Bacterio- phages play an important role in this by transmission of the 32-kb circular plasmids between the different Borrelia species [158]. Also, transfer of OspC genes has been reported [159, 160]. Furthermore, the fact that Borrelia does not need iron for growth in vitro might help in escaping the host defense mechanism of iron deprivation [161]. The pathogen is dependent on its host for nutrition though, since the genome encodes for very few proteins with biosynthetic activity [20]. However, Borrelia can avoid this dependence by changing its morphology by forming cysts that are serum-independent [59]. Lastly, elimination by phagocytic cells seems possible for certain strains of Borrelia [162]. As with many aspects of Borrelia infection pathogenesis, the mechanism by which this is achieved remains to be discovered.

CONCLUSION

Pattern recognition receptors play an important role in the recognition of Borrelia. Amongst the Toll-like receptors, TLR2 is the most important receptor for the recognition of the spirochete. The intracellular receptor NOD2 also seems to play an important role in recognition, while little is known about the role of C-type lectins in the recognition of Borrelia, with the exception of the macrophage mannose receptor, which can mediate Borrelia recognition. The precise role played by PRRs in host defense against Borrelia, as well as their potential effect on the immune-driven, late complications, are likely to represent a fruitful area of research in the coming years, and with the potential of providing novel, therapeutic targets against Lyme disease.

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Host defense against *Borrelia*


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