

Translational Mini-Review Series on Toll-like Receptors: Networks regulated by Toll-like receptors mediate innate and adaptive immunity

ARTICLES PUBLISHED IN THIS TRANSLATIONAL MINI-REVIEW SERIES ON TOLL-LIKE RECEPTORS

Toll-like receptor ligands as novel pharmaceuticals for allergic disorders. Clin Exp Immunol 2007; 147: doi:10.1111/j.1365-2249.2006.03296.x

Recent advances in understanding the role of Toll-like receptors in anti-viral immunity. Clin Exp Immunol 2007; 147: doi:10.1111/j.1365-2249.2006.03301.x

L. C. Parker, L. R. Prince and I. Sabroe
*Academic Unit of Respiratory Medicine, School of
Medicine and Biological Sciences, University of
Sheffield, UK*

Summary

The Toll-like receptor (TLR) family provide key components of mammalian immunity and are part of the earliest surveillance mechanisms responding to infection. Their activation triggers the innate immune response, and is crucial to the successful induction of Th1/Th2-phenotyped adaptive immunity. Innate immunity was long considered to be non-specific and somewhat simple compared to adaptive immunity, mediated via the engulfment and lysis of microbial pathogens by phagocytic cells such as macrophages and neutrophils, and involving no complex protein–protein interactions. The emergence of the TLR field has contributed to a revision of our understanding, and innate immunity is now viewed as a highly complex process, in line with adaptive immunity. This review will give a brief overview of our current knowledge of TLR biology, and will focus on TLRs as key components in complex networks that activate, integrate and select the appropriate innate and adaptive immune responses in the face of immunological danger.

Keywords: inflammation, innate immunity, TLR

Accepted for publication 1 August 2006

Correspondence: Professor Ian Sabroe, Academic Unit of Respiratory Medicine, School of Medicine and Biological Sciences, University of Sheffield, M Floor, Royal Hallamshire Hospital, Sheffield S10 2JF, UK.

E-mail: i.sabroe@sheffield.ac.uk

An evolutionary history of Toll-like receptors (TLRs)

TLRs are products of an evolutionary process that began prior to the separation of plants and animals, and are identified by a highly conserved intracellular Toll–interleukin (IL)-1 receptor (TIR) motif [1]. In plants, homologues of these proteins are represented by plant disease resistance genes encoding TIR-bearing proteins, although their precise mechanisms of action are still unknown [2]. In insects, notably *Drosophila*, the founding member of the TLR family, Toll, was shown in 1996 to be responsible for anti-fungal responses in the adult fly [3]. This discovery led the way to identification of a mammalian TLR [4], and a crucial link to immune function was elucidated using naturally occurring mouse strains that respond poorly to endotoxin, with meticulous genetic analysis revealing mutations in the gene encoding TLR4 [5–7]. Mammalian TLRs are now known to comprise a family of a minimum of 10 proteins [8] (an eleventh functional receptor has been identified in mice but not man [9]).

TLR activation

A diverse range of endogenous (host-derived) and exogenous (pathogen-derived) putative TLR ligands have now been identified (reviewed in [10,11]). Ligand recognition is thought to be determined by leucine-rich repeat (LRR) motifs within the TLR extracellular domains [12,13]. There has been a relative lack of experimental evidence confirming direct binding or physical association of TLRs and their ligands; however, recent work has identified the structure of the TLR3 ectodomain [12,13], and located the TLR3 ligand binding site using mutational analysis [14]. Some TLRs probably recognize their ligands in a complex association of other TLRs or co-molecules forming large activation clusters at the membrane [15,16], which may account for the delay in showing direct ligand binding. Of note, some caution is necessary when investigating TLR responses due to the capacity for small amounts of contaminants within the individual preparations to cause spurious responses (reviewed in [10,17]).

TLRs frequently expressed on the cell surface (1, 2, 4, 5, 6 and 10) recognize predominantly, but not exclusively, bacterial products. TLR2 acts as a heterodimer in concert with either TLR1 or TLR6, to mediate responses to moieties including lipoproteins and lipoteichoic acids (LTA) from Gram-positive bacteria [18] and rare lipopolysaccharide (LPS) species [19], and lipoarabinomannan from mycobacteria [20]. TLR10 was the orphan member of the family, but recent work has demonstrated its ability to form homodimers and also heterodimers with TLR1 and TLR2, although specific ligands for these combinations have yet to be identified [21]. TLR4 acts essentially as a homodimer (although there is some evidence for heterodimerization with TLR1 [22] and TLR5 [23]), and it also recognizes an extensive range of agonists. The involvement of accessory proteins at the cell membrane may help to confer ligand specificity and responses (such as CD14, MD2 and CD11b/CD18 [24]). TLR4 is crucial for effective responses to the Gram-negative bacterial component LPS [5–7], but also recognizes viral proteins [25,26]. In contrast, only a single agonist group has been identified so far for TLR5 comprising the flagellins, an essential protein component of bacterial flagella found in both Gram-positive and Gram-negative bacteria [27,28].

TLRs expressed primarily intracellularly (3, 7, 8 and 9) specialize in viral detection or the recognition of nucleic acids. TLR3 recognizes double-stranded RNA [29], while TLR7 and/or 8 mediate responses to single-stranded RNA, also derived from viruses [30,31]. TLR7 and 8 also respond to potent immunomodulatory nucleoside or nucleoside-like drugs, such as loxoribine and the imidazoquinolines [30,32], and appear to be responsible for the potent actions of the imidazoquinolines in the treatment of skin tumours [33]. TLR9 recognizes unmethylated CG dinucleotides (CpG motifs), mediating responses to bacterial DNA and some viruses [34,35]. It should be noted that receptor localization is not definitive and can also depend on cell type; for example, dendritic cells and airway smooth muscle cells express TLR3 intracellularly, while fibroblasts and epithelial cells have the potential to express TLR3 both on the cell surface and within the cell [36–39]. Furthermore, in phagocytic cells there is evidence that cell surface receptors can be recruited to the phagosome upon ligand-driven activation [40–42].

There is increasing evidence that 'endogenous' ligands may also activate TLRs; these include products derived from host cells, for example mRNA [43] (recognized by TLR3), and anti-microbial molecules such as defensins [44] and reactive oxygen species (TLR2) [45]. In addition, products derived from damaged or dying cells can act as agonists, and proposed members of this category of TLR4-activators include heat shock protein B8 [46], fibrinogen [47], surfactant protein A [48] and the tissue matrix breakdown products fibronectin extra domain A [49] and hyaluronic acid oligosaccharides [50]. Finally, high mobility group box 1 (HMGB1) protein can act as a ligand for TLR2 and TLR4 [51].

TLR signalling

TLR signalling events have been the subject of intense investigation and are reviewed extensively elsewhere [52–54]. The tailoring of individual responses to pathogens is mediated partly through a family of adapter molecules comprising MyD88, Mal (MyD88 adapter-like)/TIRAP (TIR-domain-containing adapter protein), TRIF (Toll-receptor-associated activator of interferon) and TRAM (TRIF-related adapter molecule). A further adapter, SARM (sterile α and armadillo motifs) [55], is a member of the same family but does not yet have a clearly identified signalling role. The prototypic pathway is the MyD88-dependent pathway. MyD88 is utilized by all the TLRs, except TLR3, and requires the bridging adapter Mal/TIRAP for TLR2 and TLR4 signalling. Upon activation MyD88 recruits IRAK-4, allowing association and phosphorylation of IRAK-1, which in turn recruits TRAF6. TRAF6 activates the TAK-1/TAB1/2/3 complex, resulting in downstream cascades that lead ultimately to activation of nuclear factor (NF)- κ B [56], and also initiation of distinct parallel signalling pathways leading to mitogen-activated protein (MAP) kinase [57–59] and phosphoinositide 3-kinase (PI3K) [60,61] activation. These separate pathways all regulate the transcription, mRNA stability and translation of a myriad of proinflammatory cytokine genes (see TLRs and leucocytes). In addition, TLR7 and TLR9 signalling via MyD88 can induce the type I interferons (IFNs) in a cascade also involving TRAF3 [62,63] and IFN regulatory factor (IRF)-7, which translocates to the nucleus and induces the IFN- α and IFN- β promoters [64,65]. Critical roles for other IRF family members have also been identified. IRF-5 co-localizes and associates with MyD88 and TRAF-6 and is required for inflammatory cytokine, but not IFN- α/β , production upon stimulation with TLR3, 4, 5, 7/8 and 9 ligands [66]. IRF-4 is a negative regulator of the signalling pathway, competing with IRF-5 for association with MyD88 [67]. IRF-3 is involved in the MyD88-independent pathway, which utilizes the TRIF adapter [68,69]. TRIF is recruited selectively by TLR3 and TLR4, although TLR4 requires a fourth adapter molecule, TRAM, to link it to TRIF [70]. This pathway again utilizes TRAF3, which interacts with TBK-1 and IKK ϵ to mediate activation of IRF-3 and finally induction of the IFN- β promoter and several other target genes, for example CXCL10 [71,72]. TRIF also directly interacts with TRAF6, leading to NF- κ B and MAP kinase activation, and with receptor-interacting protein (RIP) 1, a kinase thought to play a critical role in NF- κ B activation [73].

Control of innate immunity by TLRs

TLRs and leucocytes

TLRs are often considered to be the starting point of immunity, continuously sampling the extracellular environment,

informing the cell to respond to infection, and facilitating these cellular responses via signalling pathways culminating in new gene transcription. One of the earliest phagocytes to respond to infection is the tissue macrophage, which originates as monocytes in the peripheral blood system. Monocytes (and other blood mononuclear cells) are highly responsive to TLR agonists, expressing a substantial complement of the TLR repertoire [74–76]. Indeed, TLR stimulation activates a myriad of genes in human monocytes, leading to the release of cytokines, chemokines and growth factors that may exert potent autocrine and paracrine inflammatory responses [77–79]. Cytokines such as tumour necrosis factor (TNF)- α , interleukin (IL)-1 β and IL-6 are often held to be principal exemplars of the panel of proinflammatory mediators produced in response to TLR stimuli; however, chemokine genes actually show the strongest gene induction [77,80]. This has important implications for the inflammatory phenotype produced during microbial insults, specifically the recruitment and infiltration of other cell types to the site of infection. CCL2, CCL3 and CCL4 are the principal CC chemokine family members produced [77], and are chemotactic mainly for monocytes and T cells, but also basophils, dendritic and natural killer (NK) cells [81]. CXCL8 and CXCL2/3 are the main CXC family members released in response to TLR activation [77], and are chemotactic primarily for neutrophils augmenting their degranulation, adhesion and microbicidal activity [82]; however, they can also influence T cell, basophil, eosinophil, NK cell and endothelial cell chemotaxis [81]. Importantly, tissue macrophages can profoundly alter their phenotype as they differentiate in tissues. For example, alveolar macrophages show poor TLR9 responses compared to macrophages from other tissues [83]. While alveolar macrophages are important in the induction of inflammation in response to inhaled LPS [84], intestinal macrophages are non-responsive to LPS from early life – indeed, even before they are ever exposed to LPS [85]. Much work therefore remains to be conducted in developing a complete understanding of the initiation and control of inflammation by macrophages from specific tissues.

As well as cell recruitment, cell–cell communication is a vital part of innate immunity. It is now clear that granulocytes require co-operation from monocytic cells in order to perform their full range of TLR-mediated functions. While LPS is an effective direct activator of neutrophils [86–88], neutrophil survival in response to LPS is dependent upon survival signals released from small numbers of monocytes that commonly contaminate neutrophil cell preparations [89,90]. A similar role for monocytes in mediating LPS-induced eosinophil survival has also been described [91]. Recruitment of neutrophils into the lung after inhaled LPS challenge [84], or recruitment of eosinophils into the pleural space after local LPS administration, requires resident macrophages and, for eosinophil recruitment, lymphocytes [92,93], further corroborating the importance of innate

immune cell communication in the context of TLR signalling and pathogen responsiveness.

TLRs and tissue cells

Although the expression of TLRs is thought typically to be a feature of immune cells, tissue cells can also respond to inflammatory stimuli via TLRs. An increasing number of tissue cell types have been shown to express TLRs, which may contribute to protection against infection; these include epithelial cells at potential sites of entry, including the skin [94,95], respiratory [78,96,97], intestinal [98] and genitourinary [99] tracts, all of which act as a protective barrier against invading pathogens. If pathogens gain entry to the host successfully, endothelial cells [39,100–102] and smooth muscle cells [39,103,104] can also play a role in their detection via TLRs.

The role of TLRs on tissue cells is highly complex, with effective inflammatory responses to some TLRs occurring directly, while others are dependent upon co-operative interactions between leucocytes and tissue cells. For example, studies from our group have shown that airway smooth muscle cells (ASMCs) express restricted members of the TLR family, which can be modulated by proinflammatory stimuli [39,104]. TLR3 activation of ASMCs leads directly to the release of chemokines and cytokines, resulting in a markedly proinflammatory phenotype [39]. One of the major chemokines released is CXCL10, a Th1-associated chemokine with the potential to recruit T cells to the lung [105] and mast cells to airway smooth muscle bundles [106,107], a specific feature of asthmatic airways [108]. ASMCs also express TLR4 mRNA, but in our hands they exhibit no or minimal responses to LPS [104], although an effective lack of an LPS response in these cells is not a universal finding [109]. If ASMCs are cultured with even low numbers of mononuclear cells, LPS is able to cause marked cytokine production from the tissue cells, an indirect response that is abrogated substantially by IL-1 receptor antagonist (IL-1ra) [39,104], and dominates any response observed to LPS in the absence of leucocytes. Similarly, ASMC are negative for TLR7/8 expression and responses to TLR7/8 agonists are, not surprisingly, also dependent upon the presence of mononuclear cells [39]. Thus, complex networks are formed in which patterns of TLR expression and co-localization of tissue cells and leucocytes are critical for both cell–cell communication and the development of effective immunity. The role of TLRs in anti-viral immunity is explored in a further paper in this mini-series.

TLRs link innate and adaptive immunity

Again, the subject of a separate paper in this mini-series, TLRs play a crucial role in linking innate and adaptive immunity through actions on T cells [110–112] and particularly via actions on dendritic cells (DCs) (reviewed in

[113–115]). DCs start out as immature cells with high endocytic activity and low T cell activation potential, and function to detect, capture and phagocytose pathogens, leading to TLR activation. Upon signal transduction through TLRs, DCs undergo a complex differentiation programme termed collectively DC maturation, characterized by up-regulation of cell surface MHC molecules containing pathogen-derived peptide fragments and co-receptors (CD40, CD80 and CD86) that enhance the ability of DCs to activate T cells [116].

Stimulation of many cell types with TLR agonists, bacteria and viruses results in type 1 interferon (IFN- α/β) production [117–119], now thought to be part of the first line of defence against infection and a central modulator of adaptive immunity [120]. The classical pathway of IFN production via TLRs is described above (see TLR signalling). Although thought to function mainly in an anti-viral capacity, IFNs have diverse functions in the development of adaptive immunity, including proliferation of memory T cells, inhibition of T cell apoptosis, enhanced IFN- γ secretion, B cell isotype switching and differentiation into plasma cells and NK cell activation [114].

TLR networks: enhancing inflammation and disease

Excessive proinflammatory cytokine production coupled with enhanced cell activation can lead to inflammatory diseases affecting a broad range of tissues and organs. Accordingly, amplification of immune responses by TLRs, while crucial in bringing together multiple aspects of the immune system, may also contribute to disease.

Asthma is one of many obvious examples of such, where it is clear that TLRs play a role in controlling bacterial and/or viral respiratory infections, which are important modulators of allergic airway inflammation [121,122]. There are numerous opportunities for multiple TLR agonists to interact directly and/or indirectly (via leucocytes) with respiratory tissue cells. Inhaled endotoxin is present routinely and can play a fundamental role in the development and progression of asthma [123,124] through differential actions on TLR4, determined by specific cell-dependent mechanisms. For example, it was demonstrated recently that inhaled endotoxin-induced bronchoconstriction is dependent upon resident lung cells, most probably epithelial cells, while recruited haematopoietic cells mediate cytokine secretion into the alveolar space in response to the same insult [125]. As well as forming a barrier against infection, epithelial cells are dynamic producers of anti-microbial peptides in response to infection [126–128] and to growth factors released when the physical barrier is penetrated [129], with subsequent tissue damage also resulting in activation of innate immunity and TLR signalling. The release of chemokines and adhesion molecules from these resident tissue cells also controls neutrophil infiltration and activation, resulting in the further release of mediators of tissue

injury and repair processes and supporting the anti-microbial potential of neutrophils themselves, but also of the resident cells such as epithelia and keratinocytes [130]. Recruited haematopoietic cells and alveolar macrophages have also been shown to play a crucial role in initiating LPS-induced neutrophil recruitment to the lung [84], while other work identifies monocytes as key players in alveolar neutrophil recruitment, with direct co-operation between monocytes and neutrophils contributing to acute lung inflammation [131]. Monocytes can also act indirectly to amplify epithelial cell production of anti-microbial peptides in response to LPS through an IL-1-mediated pathway [132,133]. Finally, monocytes directly activate endothelial cells and smooth muscle cells to support further adhesion and recruitment of leucocytes, potentially creating a self-perpetuating cycle of inflammation [104,134].

Viruses such as respiratory syncytial virus (RSV) and influenza A cause a myriad of respiratory diseases, including exacerbation of asthma, through preferential infection of host airway epithelial cells. Viral infections enhance responses to LPS and other TLR agonists by triggering additional TLR signalling pathways through presentation of agonists for TLR3, TLR4, TLR7, TLR8 and TLR9. For example, a downstream effect of viral infection is sensitization of the airway cells to subsequent exposure to viral and bacterial products; this occurs via up-regulation of TLR3 and TLR4, respectively, leading to increased signalling activity and proinflammatory cytokine production [78,135–137]. Interestingly, this can be a selective effect, as RSV infection does not enhance airway epithelial cell responses to ligands acting on the viral receptors TLR7/8 or TLR9 [135]; in contrast, the synthetic viral mimic poly(I:C), which activates TLR3, augments expression of TLR1 and TLR2, receptors that mediate bacterial responses [78]. Accordingly, the profound immune and inflammatory response triggered during diseases such as asthma will be dependent upon the complicated patterns of TLR cross-talk that occur between each individual cell type, and co-operative responses of a range of tissue cells and professional immune cells to TLR activation.

Concluding remarks

As our depth of knowledge about TLRs continues to expand, it is becoming ever more clear that an inflammatory model whereby a single microbial ligand targets a lone receptor is insufficient to describe the vast diversity of the host's response to attack. A more useful approach may be to think of inflammatory networks with microbes activating multiple receptors, resulting in the initiation of numerous signalling pathways to integrate and evaluate the threat and determine the appropriate activation status of the host cells and the ultimate inflammatory response (Fig. 1). This approach highlights the complexity of disease pathophysiology and the difficulties faced when trying to delineate

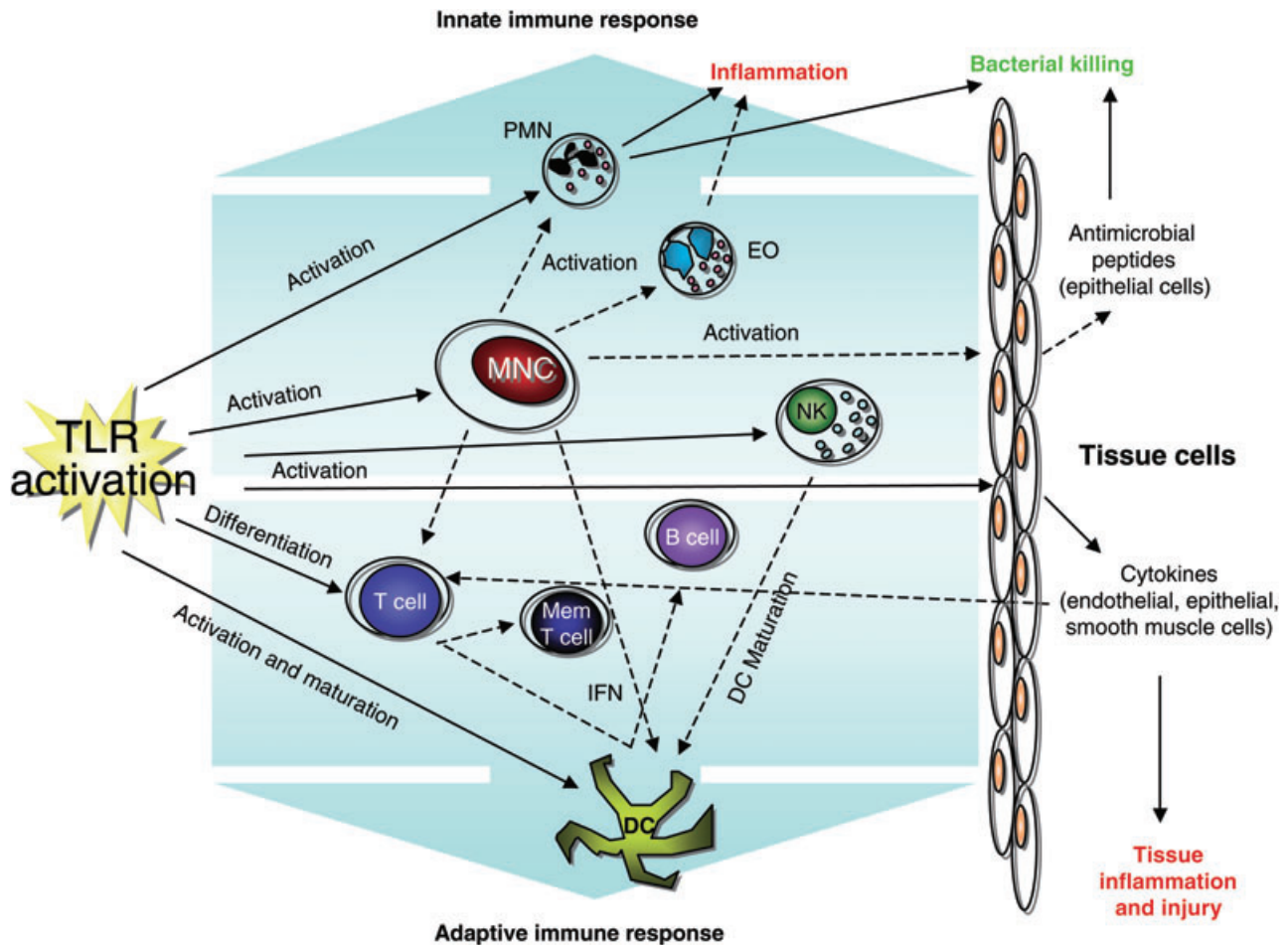


Fig. 1. Immune pathways activated by Toll-like receptor (TLR) signalling. TLR signalling activates a number of apical pathways that result in the stimulation of both the innate and adaptive immune responses. Mononuclear cells (MNC) in particular serve to amplify TLR activation by the production of cytokines and growth factors. These mediators facilitate communication between different cell types, co-ordinating the recruitment and activation of the immune response network as a whole. Solid arrows illustrate effects of direct TLR activation, dashed arrows represent paracrine actions resulting from TLR activation of an intermediary cell. MNC; mononuclear cells, PMN; polymorphonuclear cells, EO; eosinophils, NK; natural killer cells, DC; dendritic cells, Mem T cell; memory T cell, IFN; interferon.

single causes or factors, with a given disease dependent upon the network of cells and TLRs that are activated. Thus, to facilitate our ability to intervene when inflammatory responses to disease are inadequate, or indeed excessive, models of inflammatory cell networks must continue to be developed to determine the most appropriate and effective response to disease.

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