

# Toll-like receptors and intestinal defence: molecular basis and therapeutic implications

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**Toll-like receptors (TLRs) play a principle role in distinct pathogen recognition and in the initiation of innate immune responses of the intestinal mucosa. Activated innate immunity interconnects downstream with adaptive immunity in complex feedback regulatory loops. Intestinal disease might result from inappropriate activation of the mucosal immune system driven by TLRs in response to normal luminal flora.**

A broad variety of immune cells of the intestinal mucosa express so-called pattern recognition receptors (PRRs) that specifically discriminate between 'self' and microbial 'nonself' based on the recognition of conserved pathogen-specific molecular patterns (PAMPs) (Ref. 1). Toll-like receptors (TLRs), which comprise one class of PRR, play a key role in microbial recognition, in the induction of antimicrobial genes and in the control of adaptive immune responses (Ref. 2). Immune reactions in the intestinal mucosa are complicated by the need to recognise pathogens specifically and to mount defensive responses rapidly, yet remain quiescent to harmless, commensal bacteria that normally inhabit the gut. Activation of the host defence system of the intestinal mucosa appears to be substantially regulated by TLRs in order to maintain a protective equilibrium.

## TLR definition and structure

Following the discovery of a role for Toll in *Drosophila* host defence, a human homologue of

the *Drosophila* Toll protein was cloned in 1997 (Ref. 3). A constitutively active mutant of a human Toll homologue transfected into human cell lines could induce: (1) activation of the transcription factor NF- $\kappa$ B; (2) expression of the inflammatory cytokines interleukin 1 (IL-1), IL-6 and IL-8; and (3) expression of the costimulatory molecule B7.1, which is required for the activation of naive T cells (Ref. 3). Signalling through Toll therefore appears to parallel the signalling pathway induced by the IL-1 receptor (IL-1R) in mammalian cells. In 1998, five Toll-like molecules in humans were characterised and named the 'Toll-like receptors' (Ref. 4) and, to date, a total of ten TLRs (1–10) have now been identified (reviewed in Ref. 5). The TLRs therefore constitute a class of putative human receptors with a protein architecture that is similar to the *Drosophila* Toll protein.

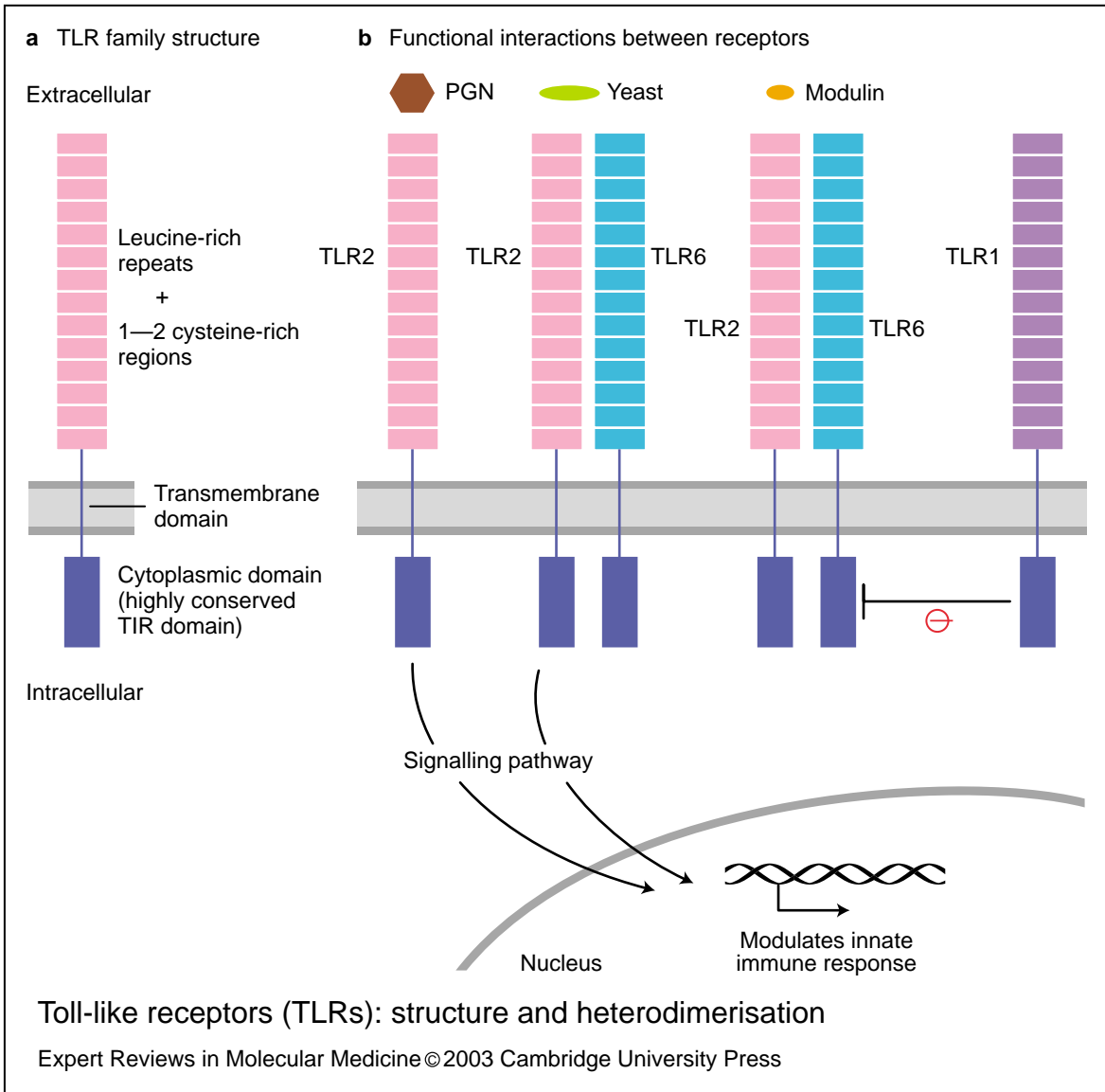
Mammalian TLRs are type I transmembrane proteins and contain several common structural features, including multiple leucine-rich repeats (LRRs) and one or two cysteine-rich regions in the large and divergent ligand-binding ectodomain,

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as well as a short transmembrane region and a highly conserved cytoplasmic domain (Ref. 5) (Fig. 1a). The intracellular domain is highly homologous among the individual TLRs and contains a Toll/IL-1R (TIR) domain similar to the

cytoplasmic domain of the IL-1R. Mutagenesis and functional studies have shown that human TLRs interact via TIR with downstream signalling partners such as the MyD88 adaptor molecule (Ref. 6), as described below.



**Figure 1. Toll-like receptors (TLRs): structure and heterodimerisation.** (a) The mammalian TLR family are type I transmembrane proteins with the following common structural features: multiple leucine-rich repeats and one or two cysteine-rich regions in the large and divergent ligand-binding ectodomain; a short transmembrane region; and a conserved cytoplasmic domain that is highly homologous among the individual TLRs and contains a Toll/IL-1R (TIR) domain similar to the cytoplasmic domain of the interleukin 1 receptor (IL-1R). (b) TLRs function in activating innate immunity by recognising conserved molecular patterns carried by microorganisms. Pattern recognition can be achieved by individual TLRs [e.g. recognition of peptidoglycan (PGN), which is a bacterial cell wall component, by TLR2], or by heterodimerised TLRs (e.g. recognition of yeast components or bacterial modulin by TLR2–TLR6). Furthermore, functional interactions between TLRs can lead to inhibition of responses, as shown here by the interference of TLR1 in the TLR2–TLR6 response (dfig001ece).

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### Diversity of TLRs and their ligands

TLRs are variably expressed in a wide variety of intestinal cell types, including intestinal epithelial cells (IECs; Refs 7, 8, 9, 10, 11), gastric pit cells (Ref. 12), foetal intestinal cells (Ref. 13) and intestinal macrophages of the lamina propria (Refs 14, 15, 16). TLRs are also expressed in Kupffer cells (Ref. 17) and hepatocytes (Refs 18, 19) of the liver.

Specific TLRs bind different 'molecular signatures' of different classes of microorganisms or individual features present on different microbes. 'Nonself' but also 'self' ligands might distinctly activate TLRs to mediate either pro- or anti-inflammatory responses in different cell types and organs. This complex ligand discrimination and specificity might be accounted for by diverse TLR dimerisation that is dynamically modulated by different PAMPs, thereby expanding the plasticity of this family of receptors to maximise innate pattern recognition (Fig. 1b). It is not yet clear whether modulatory cross-recognition of additional as-yet-unknown co-receptors also contributes either to the specificity of activated TLR complexes or to the diversity of differential immune responses in cells activated with certain TLR stimuli. In addition, endogenous TLR antagonists have not yet been identified.

### TLR1, TLR2 and TLR6

TLR2 recognises a broad spectrum of molecular patterns from Gram-positive bacteria and mycobacterial species, including peptidoglycan (PGN), bacterial lipoprotein/lipopeptides, glycosylphosphatidylinositol (GPI) anchors and lipoteichoic acid, as well as yeast and fungal cell wall components (Refs 20, 21, 22, 23, 24, 25, 26, 27). TLR2 might synergistically cooperate with TLR6 and TLR1 in the recognition of certain PAMPs in order to expand the repertoire of TLR-mediated responses (Refs 20, 28, 29) (Fig. 1b). However, cooperation is not necessarily needed for all TLR2-mediated immune responses; for instance, TLR6<sup>-/-</sup> and TLR1<sup>-/-</sup> mice respond to PGN, whereas TLR2<sup>-/-</sup> mice are unresponsive to PGN, implying that TLR1 and TLR6 are not essential for responses to PGN via TLR2 (Ref. 30). Furthermore, TLR1 appears to interact with TLR2 only in response to certain lipid configurations of lipoproteins, implying rigid specificity in the differential recognition of PAMPs by individual TLR combinations (Ref. 31). Conversely, cotransfection studies have

recently shown that TLR1 might block TLR4-induced downstream signalling effects (Ref. 32), suggesting that TLRs might also negatively regulate the activity of each other through heterodimerisations.

### TLR3

Although TLR3 is mostly expressed by mature human dendritic cells (DCs) (Ref. 33), IECs also constitutively express TLR3 (Ref. 14). Mammalian TLR3 recognises polyinosine-polycytidylic acid [poly(I:C)], which is a synthetic analogue of double-stranded RNA (dsRNA), leading to NF-κB activation and production of type I interferons (IFNs) (Refs 34, 35). However, so far, it remains to be shown whether viral dsRNA is actually a ligand of TLR3 (Ref. 36).

### TLR4

The first in vivo evidence that mammalian TLR4 primarily subserves the pattern recognition of lipopolysaccharide (LPS) was achieved by Poltorak et al. (Ref. 37), and has been confirmed by subsequent genetic and biochemical evidence (Ref. 38). Although early studies have suggested that TLR2 might also mediate responses to LPS, Hirschfeld et al. (Ref. 39) provided convincing evidence that contaminants in commercially available LPS preparations were responsible for TLR2-mediated signalling and not purified LPS itself. MD-2, an accessory protein to TLR4, is essential for the correct intracellular distribution of TLR4 (Ref. 40) in order to initiate LPS signalling (Refs 41, 42, 43). CD11, CD18, CD14 and LPS-binding protein (LBP) might also cooperatively increase TLR4-mediated cellular activation by LPS (Refs 44, 45). Of note, IECs lack constitutive expression of membrane-bound CD14 in vitro (Ref. 7), but expression might be induced under inflammatory conditions in vivo (Ref. 46).

TLR4 does not mediate responses to all LPS serotypes derived from different species (Ref. 47), and this might be dependent on conformations of the lipid A component of LPS (Ref. 48). Furthermore, bacteria can alter the acylation state of their LPS in response to environmental changes during bacterial-host adaptation (Ref. 49). For instance, *Pseudomonas aeruginosa* synthesises more highly acylated (hexa-acylated) LPS structures when found in the airway of individuals with cystic fibrosis compared with bacteria in normal airways, which synthesise penta-acylated LPS. The TLR4-MD-2 complex recognises

this adaptation and transmits pro-inflammatory signals only in response to hexa-acylated but not penta-acylated LPS (Ref. 49).

TLR2 and TLR4 are present at the apical pole of differentiated IECs *in vitro* and *in vivo* and thus are well positioned to monitor the luminal milieu of bacterial products (Ref. 50). TLR4 is present in lipid rafts at the cellular membrane, and these are enriched in glycosphingolipids and cholesterol (Ref. 51). In response to LPS stimulation, TLR4 is redistributed from its apical location to intracytoplasmic compartments near the basolateral membrane in differentiated IECs (Ref. 50). Conversely, Hornef et al. have recently demonstrated that TLR4 preferentially resides in the Golgi apparatus, co-localising with endocytosed LPS in immature murine IECs (Ref. 10).

#### TLR5

Pathogenic and commensal bacteria secrete flagellin, the structural component of bacterial flagella, and this protein has recently been identified as a ligand for TLR5 (Ref. 52). In contrast to TLR2 and TLR4 (Refs 14, 50), TLR5 on IECs appears to be preferentially expressed at the basolateral pole (Refs 9, 53). Pathogenic enteric *Salmonella* translocate flagellin across IECs, and it has been demonstrated that detection of flagellin by basolateral TLR5 activates pro-inflammatory gene expression, driving epithelial inflammatory responses to *Salmonella* (Ref. 9).

#### TLR7 and TLR8

Plasmacytoid DCs and B cells express high levels of TLR7 (Ref. 54). The antiviral imidazoquinoline resiquimod (R-848) activates immune cells via both TLR7 (Ref. 55) and TLR8 (Ref. 56), inducing potent antiviral immune responses through NF- $\kappa$ B activation, suggesting a possible redundancy among these two TLRs. Of note, murine TLR8 appears to be nonfunctional (Ref. 56). The natural ligands for TLR7 and TLR8 have not yet been identified.

#### TLR9

CpG DNA (rich in cytosine-phosphatediester-guanosine) interacts with two independent receptor molecules, DNA-dependent protein kinase (DNA-PKcs) (Ref. 57) and TLR9 (Refs 58, 59), stimulating immune responses characterised by the production of various cytokines, chemokines and antibodies in B cells, natural killer (NK) cells,

macrophages and DCs (Refs 54, 60, 61, 62, 63), as well as in IECs (Ref. 64). TLR9 is localised to intracellular endosomal compartments (Ref. 65). Cellular uptake via endocytosis and subsequent endosomal maturation is therefore essential for signalling induced by CpG DNA (Ref. 66).

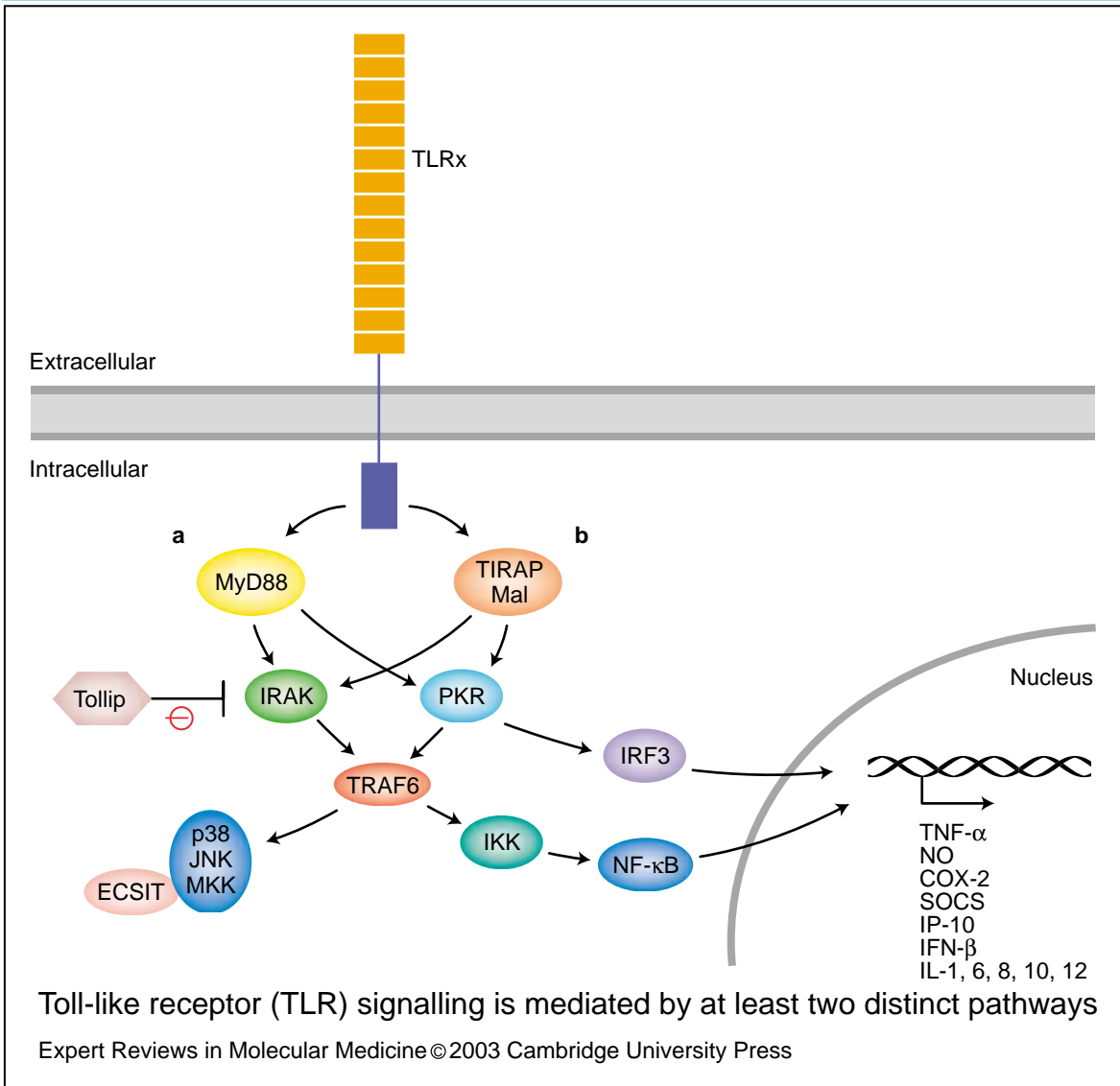
#### TLR10

TLR10 mRNA is expressed in plasmacytoid DCs and B cells (Ref. 54), and also in IECs (Ref. 67). Its ligands and function have not yet been identified.

#### TLR signalling and downstream effects MyD88-dependent and -independent pathways

TLRs might differentially activate distinct downstream signalling events via different cofactors and adaptor proteins mediating diverse immune responses. The conserved TIR cytoplasmic domain in TLRs is required for activation of the 'classical' TLR signalling pathway by providing a scaffold for recruitment of the adaptor molecule MyD88 and serine/threonine kinases of the IL-1R-associated kinase (IRAK) family (Fig. 2a). IRAK becomes autophosphorylated and another adaptor, TRAF6, then interacts with IRAK. In addition, TLRs bridge the signalling pathway via ECSIT (for 'evolutionarily conserved signalling intermediate in Toll pathways') to TRAF6 for p42/p44 mitogen-activated protein kinase (MAPK), p38 and JNK in response to specific bacterial products (Refs 68, 69). This signalling module results in the translocation of the transcription factor NF- $\kappa$ B to the nucleus, and the transcriptional activation of genes encoding cytokines and chemokines, as well as the induction of costimulatory molecules (Refs 3, 6). Toll-interacting protein (Tollip) plays an inhibitory role in TLR2/4-mediated cell activation (Ref. 29) by suppressing the activity of IRAK (Ref. 70).

MyD88-deficient mice have profound defects in the activation of antigen-specific T helper 1 (Th1) but not Th2 immune responses, suggesting distinct pathways for activation of the two effector arms of adaptive immunity (Ref. 71). LPS-induced activation of NF- $\kappa$ B and MAPK is not abolished in the absence of MyD88 (Ref. 72). MyD88-deficient cells respond to LPS by activating IFN-regulatory factor 3 (IRF3), and inducing IP-10 gene expression and DC maturation, suggesting MyD88-independent signal propagation via TLR4



**Figure 2. Toll-like receptor (TLR) signalling is mediated by at least two distinct pathways.** After recognition of a pathogen-specific molecular pattern, TLRs are capable of differentially activating distinct downstream signalling events via different cofactors and adaptor proteins mediating diverse immune responses. (a) The 'classical' MyD88-dependent TLR signalling pathway is activated via the conserved, cytoplasmic TIR domain [for 'Toll/interleukin 1 receptor (IL-1R)], which provides a scaffold for recruitment of the adaptor molecule MyD88 and serine/threonine kinases of the IL-1R-associated kinase (IRAK) family. Following IRAK autophosphorylation, the TRAF6 adaptor protein interacts and induces translocation of the transcription factor NF- $\kappa$ B to the nucleus, resulting in transcriptional activation of genes encoding cytokines and chemokines [e.g. tumour necrosis factor  $\alpha$  (TNF- $\alpha$ ), nitric oxide (NO), cyclooxygenase 2 (COX-2), SOCS (for 'suppressor of cytokine signalling'), IP-10, interferon  $\beta$  (IFN- $\beta$ ) and IL-1, 6, 8, 10, 12]. In addition, TLRs bridge the signalling pathway via ECSIT (for 'evolutionarily conserved signalling intermediate in Toll pathways') to TRAF6 for p42/p44 mitogen-activated protein kinase (MAPK) kinase (MKK), p38 and JNK in response to specific bacterial products. Toll-interacting protein (Tollip) plays an inhibitory role in TLR2/4-mediated cell activation by suppressing the activity of IRAK. (b) The MyD88-independent TLR signalling pathway is activated via the TIR-domain-containing adaptor protein (TIRAP; also designated Mal for 'MyD88-adapter-like') and results in activation of the dsRNA-binding protein kinase PKR. This protein has been proposed to be a central downstream component of both the TIRAP- and MyD88-dependent signalling pathways and could mediate potential crosstalk between them. The MyD88-independent pathway appears to utilise both IFN-regulatory factor 3 (IRF3) and NF- $\kappa$ B, and results in the expression of IFN- $\gamma$ -inducible genes including IP-10 (**dfg002ece**).



to LPS (Ref. 73). The TIR-domain-containing adaptor protein (TIRAP; also designated Mal for 'MyD88-adaptor-like') (Ref. 74) has recently been identified as controlling activation of these MyD88-independent signalling pathways downstream of TLR4 (Ref. 75) (Fig. 2b). The dsRNA-binding protein kinase PKR has been proposed to be a central downstream component of both the TIRAP/Mal- and MyD88-dependent signalling pathways and could mediate potential crosstalk (Ref. 75). Receptor-interacting protein (RIP) has also recently been identified as acting downstream of TLRs as a common checkpoint (Refs 76, 77), thus possibly allowing potential regulatory crosstalks to the Nod pathway (Ref. 78) and tumour necrosis factor receptor (TNFR) pathway (Ref. 77).

### IFN-STAT and JAK-STAT pathways

The IFN-STAT pathway might mediate differential patterns of gene expression in response to activation of certain TLRs. The TLR4 ligand LPS, but not any of the TLR2 ligands, induces TIRAP-dependent IFN- $\beta$  mRNA expression, leading to phosphorylation of signal transducer and activator of transcription 1 (STAT1) (Ref. 79). Furthermore, IFN- $\gamma$  upregulates expression of the crucial TLR4 co-receptor MD-2 through Janus kinase (JAK)-STAT in IECs, thus conferring mucosal responsiveness in inflammatory conditions of the intestine (Ref. 80). By contrast, the TLR9 agonist, CpG DNA, triggers synthesis of SOCS (for 'suppressor of cytokine signalling') proteins that act as negative regulators of the JAK-STAT pathway (Ref. 81).

### Downstream effects

Activation of individual TLRs induces gene transcription of distinct cytokines in different cell types (Ref. 60), including IL-1, IL-6, IL-8, IL-10, IL-12 and TNF- $\alpha$  (Refs 82, 83, 84). TLR-regulated transcription of cytokine genes is coordinated by complex nucleosome remodelling, apparently independently from NF- $\kappa$ B (Ref. 85). This suggests that other, as-yet-unknown, TLR-inducible factors stimulate remodelling, perhaps leading to NF- $\kappa$ B-mediated transcription of specific cytokine genes such as IL-12. Furthermore, following stimulation with TLR2 ligands, chromatin remodelling also occurs at the TLR2 promoter region itself, possibly allowing the access of transcription factors to initiate the transcription of TLRs (Ref. 86). These observations suggest that TLR-regulated

transcription is regulated by at least two independent pathways: one that activates certain transcription factors and one that leads to chromatin remodelling that allows access of the transcription factors to certain promoter regions. However, the signalling mediator that forms and controls the remodelling complex has yet to be identified.

Cytokines produced in response to pathogen-induced TLR activation might essentially drive adaptive immune responses. For instance, IL-12 secretion by DCs and phagocytes (Ref. 82) induces activation of Th1 cells and IFN- $\gamma$ , which in turn enhances IL-12 production in positive-feedback loops. In response to TLR activation, released TNF- $\alpha$  and IL-1 might act as secondary auto/paracrine mediators through their cognate receptors TNFR-1 and IL-1R, respectively, to further activate and recruit various immune cells, thus contributing to exaggerated immune responses that contribute to inflammatory diseases.

However, TLR activation might also lead to tissue repair: necrosis-induced inflammation and tissue damage provide nonself danger signals that might function as major inducers of tissue repair gene responses via TLRs (Ref. 83). The actual TLR ligands released from necrotic cells have not yet been identified. In addition, numerous pro-inflammatory genes encoding chemokines (Ref. 86), complement proteins and adhesion molecules (Ref. 87) might also be activated in response to different TLR ligands. Nitric oxide (NO) secretion and cyclooxygenase 2 (COX-2) gene expression, which play pathophysiological roles in intestinal inflammation, might be induced via TLRs (Refs 88, 89). All of these various downstream effects are critically involved in the control of pathogen elimination and the transition to adaptive immune responses.

### Tolerance and prolonged survival as keys to effective mucosal host defence

In the intestine, tolerance represents an essential mucosal defence mechanism that maintains hyporesponsiveness to harmless luminal bacterial antigens. However, it is unclear how the intestinal epithelium discriminates between the numerous, nonharmful, indigenous microbial commensals and invasive pathogens. The molecular mechanisms underlying how IECs maintain microbial tolerance, yet efficiently react with immediate immune responses to harmful

luminal bacteria during infection, are poorly defined but might involve altered TLR function combined with blockage of central downstream signalling events through IRAK.

Induction of tolerance has been shown to be associated with suppression of TLR expression (Refs 90, 91). TLR2 and TLR4 are normally only present in small amounts on IECs in vivo, thus minimising recognition of luminal bacterial in the healthy intestine (Ref. 14). As shown by Abreu et al. (Ref. 8), decreased expression of TLR4 surface protein and the absence of cofactor MD-2 correlate with inhibition of downstream cytokine production in the tolerance of IECs to LPS. Continuous exposure to LPS leads to suppression of downstream immune responses in IECs in vitro (Refs 10, 92, 93). IL-1 $\beta$ , but not TNF- $\alpha$ , induces a LPS-refractory state in vivo (Ref. 94), suggesting that common downstream signalling molecules of both the IL-1R and TLR pathways might be targeted in tolerance. IRAK has recently been identified as an important negative regulator of TLR signalling (Refs 95, 96), with microbial tolerance correlating with downregulation of IRAK expression (Ref. 97) and inhibition of the release of IRAK from TLRs (Ref. 98) in host cells. Disruption of the IRAK response might also lead to 'cross-tolerance' (Ref. 99) between a variety of microbial components differentially affecting MyD88-dependent pathways (Ref. 100).

Conversely, a cytokine-induced imbalance in inflammation might lead to intestinal 'intolerance' by altering TLR expression and downstream signalling events that could play a role in promoting disease (Fig. 3). For instance, pro-inflammatory cytokines, such as IFN- $\gamma$ , could counteract LPS-induced downregulation of TLR4 (Ref. 101) and modulate IRAK function by upregulating its expression, inhibiting its degradation and promoting its association with MyD88. This would effectively prevent the induction of tolerance (Ref. 102) and instead prime hyper-reactivity to LPS (Ref. 101).

Pathogenic bacteria have evolved various strategies to overcome recognition and develop resistance against the host. Enteric bacteria can directly block antibacterial peptide synthesis (Ref. 103). Conversely, nonpathogenic bacteria can help the host to maintain mucosal homeostasis by directly suppressing inflammatory responses and inhibiting specific intracellular signal transduction pathways. It was recently shown that nonpathogenic *Salmonella pullorum* is capable of

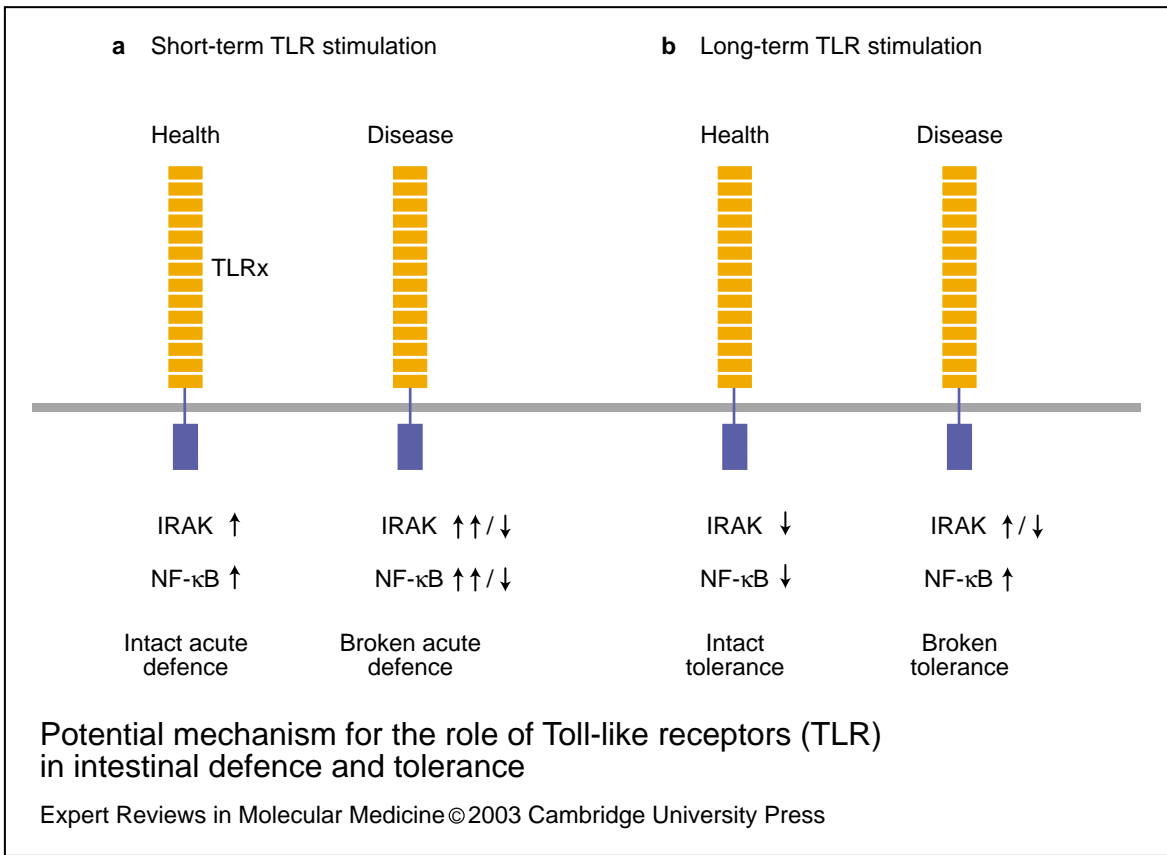
attenuating IL-8 secretion by blocking NF- $\kappa$ B activation elicited by pathogenic *Salmonella typhimurium* (Ref. 104).

Commensal-associated bacterial cell wall components might even enhance survival of the host against deleterious threats of the lumen by activating TLR signalling pathways that convey signals to transcription factors that orchestrate the inflammatory response. Indeed, it has recently been demonstrated that exposure to PGN results in significant phosphorylation of Akt, an essential factor in the phosphatidylinositol 3-kinase (PI3K)/Akt signalling pathway via TLR2 and involves downstream substrates such as forkhead transcription factor (FKHR) and glycogen synthase kinase 3 $\beta$  (GSK3 $\beta$ ) (Ref. 105). Furthermore, LPS phosphorylates Akt, which in turn reduces the ubiquitination of  $\beta$ -catenin, resulting in its nuclear accumulation and transcriptional activity (Ref. 106). Inhibition of this pathway by wortmannin (a PI3K inhibitor) leads to the predominance of LPS-induced stress responses via MAPKs and NF- $\kappa$ B (Ref. 107). Rac1/Akt controls NF- $\kappa$ B activation via TLR2 (Ref. 108). Similarly, it was recently shown that *Bacteroides vulgatus* induces NF- $\kappa$ B transcriptional activity via TLR4 in a PI3K/Akt-dependent pathway in IECs (Ref. 11). PI3K also facilitates the interaction of CpG DNA with TLR9 in endocytic vesicles (Ref. 109).

Apoptosis of IECs has been implicated in the generation and resolution of inflammation in response to bacterial pathogens, and TLR activation might transiently promote caspase-dependent apoptosis through MyD88 (Refs 110, 111), possibly interconnecting with Fas-associated death domain (FADD) protein via their death domains (Ref. 112). The TLR-PI3K/AKT- $\beta$ -catenin innate survival mechanism might enable IECs to resist induction of apoptosis by pathogenic bacteria or other pro-inflammatory challenges and thereby maintain mucosal homeostasis in vivo. In this context, it will be essential to define how an imbalance in signalling events induced by pathogenic versus nonpathogenic bacteria could lead to impaired survival and exaggerated inflammatory responses of the mucosal immune system in intestinal disease.

### Clinical and therapeutic implications

Chronic recurrent intestinal inflammation in inflammatory bowel disease (IBD) might result from stimulation of the mucosal immune system



**Figure 3. Potential mechanism for the role of Toll-like receptors (TLRs) in intestinal defence and tolerance.** Interleukin 1 receptor (IL-1R)-associated kinase (IRAK) appears to be an important negative regulator of TLR signalling. Thus, following short-term TLR stimulation (a), expression of IRAK and NF-κB might be appropriately upregulated, thereby rapidly and efficiently defending the host against an acute threat; this acute defence mechanism might be dysregulated in disease, leading to exaggerated immune responses. Following long-term TLR stimulation (b), expression of IRAK and NF-κB might be appropriately downregulated, maintaining hyporesponsiveness in health; again, this might be dysregulated in disease (**dfig003ece**).

by products of commensal bacteria in the lumen. Bacteria might penetrate through the impaired mucosal barrier, leading to direct interaction with immune cells of the lamina propria, such as lymphocytes, monocytes and DCs (Ref. 113). Normal and IBD tissues exhibit low significant TLR2 expression in IECs, and TLR5 is not significantly modulated in acute intestinal inflammation in IBD (Ref. 14). However, TLR2 and TLR4 are highly upregulated in inflammatory cells of the lamina propria in active IBD (Refs 14, 16), including monocytes, macrophages and lymphocytes, suggesting that these immune cells are primarily involved.

‘Healthy’ intestinal mucosa expresses a low concentration of TLR2 or TLR4 protein in vivo (Refs 14, 16, 80). However, there is emerging evidence that intestinal TLR expression is

selectively altered in patients with IBD (Refs 14, 16). It has recently been demonstrated that TLR4 is significantly increased in IECs throughout the lower gastrointestinal tract in active disease of both Crohn’s disease (CD) and ulcerative colitis (UC) (Ref. 14). However, others have failed to detect any TLR4 expression in IECs during inflammation (Ref. 16). These contrasting results might be partially due to different technical conditions used [e.g. cell-permeabilising fixation with Triton X-100 (Ref. 14) versus fixation without Triton X-100 (Ref. 16)]. In addition, it remains to be shown whether upregulated TLR4 expression simply reflects a loss of the appropriate immune response in host defence.

In acute dextran sulfate sodium (DSS)-induced colitis, bacteria and/or bacterial products play a major role in the initiation of inflammation



(Ref. 114). C3H/HeJ mice (which possess a spontaneous TLR4 mutation corresponding to Pro712His) do not develop spontaneous colitis but show increased susceptibility to DSS- and trinitrobenzenesulfonic acid (TNBS)-induced colitis in comparison with C3H/SnJ mice (no TLR4 mutation) (E. Cario and D.K. Podolsky, unpublished), suggesting that homeostasis between indigenous intestinal flora and the host response might be broken in TLR4 dysfunction. It remains to be determined whether TLR polymorphisms might occur more frequently in patients with IBD and could be linked with differences in the inflammatory response of the intestinal mucosa elicited by PAMPs, and thereby could potentially play a role in the pathogenesis of IBD.

Characterisation of the regulation of TLR expression in different cell types of the intestinal mucosa will be of considerable interest in order to understand tissue distribution and function in health and disease. Of note, both IL-4 and IFN- $\gamma$ , which play key roles in mediating colonic inflammation in IBD, have already been shown to regulate TLR activation. IL-4 downregulates TLR4 expression in monocytes (Ref. 115) and IECs (Ref. 116), suggesting that Th2-type adaptive immune responses might inhibit TLR activation. Conversely, IFN- $\gamma$  might upregulate intestinal epithelial TLR4 expression (Ref. 116), priming cells to LPS-dependent IL-8 secretion (Ref. 80).

The factors and mechanisms regulating TLR expression in IBD remain to be elucidated further. In active IBD, variant alleles in the gene encoding TLRx (where x indicates any TLR) and downstream signalling partners could induce functional dysregulation of responses to its/their ligands. Impaired function could exacerbate intestinal inflammation by uncontrolled clonal expansion and activation of mucosal immune cells to resident antigens in IBD and other inflammatory disorders of the gut. TLR dysfunction could also derive from secondary effects of nonbacterial ligands, either endogenously or exogenously induced, which have not yet been identified.

There is emerging evidence that dysregulation of the innate immune response via TLRs might contribute to many different immunological disorders, such as autoimmune diseases or chronic inflammatory responses. Targeting the TLR signalling pathways to blunt harmful cellular responses during such diseases such as IBD

could provide a new therapeutic avenue. So far, neutralising antibodies against specific TLRs have mainly been used in assay systems *in vitro*, preventing ligand-induced activation of downstream signalling (Refs 24, 35); unfortunately, large-scale production of such antibodies for *in vivo* approaches would be enormously costly. Ligand-induced TLR activation might also have a beneficial effect in cancer treatment by triggering a desired antitumor immune response (Ref. 117). Soluble TLRs that bind the respective class of ligands, thus preventing recognition through the host, could also be an alternative to modulate sensing.

At present, not enough is known about the functional roles of TLRs and their downstream cascades under physiological and pathophysiological conditions to be able to define an optimal therapeutic strategy for the treatment of human disease caused by dysregulation of the innate immune response. However, initial research has started to exploit the potential adjuvant properties of TLR signalling in the modulation of colonic inflammation. It has recently been demonstrated that pretreatment with the TLR9 ligand CpG DNA ameliorates both chemically induced and spontaneous colitis in mice by inhibiting the induction of various pro-inflammatory cytokines and chemokines (Ref. 118). IECs express functional TLR9 (Ref. 64), but it remains to be verified whether CpG DNA-induced anti-inflammatory immune responses are indeed mediated via TLR9 in the intestinal mucosa. An improved understanding of the precise mechanisms leading to protective cellular immunity in the intestinal mucosa following DNA vaccination could help in the design of novel DNA constructs containing immunostimulatory features that target one or more of these signalling mechanisms via TLRs, potentially preventing exaggerated immune responses in IBD.

### Conclusions and outstanding questions

In the five years that have followed the discovery of human Toll, enormous progress has been made in characterising TLR regulation and function in different cell types and animal models, mainly in identifying new TLR ligands and downstream signalling pathways. There is an emerging understanding of the complex mechanisms through which dysregulated innate immune responses might lead to disease. Definitive understanding of TLR dysfunction in active IBD and other intestinal disorders will require

elucidation of the structural diversity of numerous luminal bacteria and their specific differential immunomodulatory activities via the innate immune system. Some pathogenic bacteria seem to have developed elaborate ways to escape TLR recognition. Furthermore, it is likely that others might directly limit TLR activation, effectively desensitising the mucosal immune system towards constant exposure to luminal commensals. Thus, in disease, tolerance might essentially be broken. Other pathogenic bacteria might acutely induce TLR hyper-responsiveness, possibly in self-sustaining cycles via feedback regulators of the adaptive immune system, leading to exaggerated inflammatory immune responses. There is increasing evidence that TLRs not only recognise 'nonself' but also abnormalities of mammalian 'self'. Further in-depth evaluation of inter-dependent host-microbial, as well as host-host, cross-talks via the innate immune system could provide insight into disease pathophysiology, potentially leading to new therapeutic targets to fight microbe-associated gastrointestinal disorders such as IBD.

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### Further reading, resources and contacts

A useful list of links (some of which do not provide free access) to websites related to various clinical aspects of immunology, including inflammatory bowel disease, is provided by the Clinical Digital Libraries Project of the University of Alabama at Birmingham:  
<http://uasom-dl.slis.ua.edu/clinical/immunology/general.htm>

Every February, *Current Opinion in Immunology* provides a special issue of reviews on 'hot' topics in innate immunity, including Toll-like receptors (see issues 2000, 2001 and 2002):  
<http://www.current-opinion.com/jimm/about.htm?jcode=jimm>

A collection of excellent reviews on various topics on innate immunity can be found in the 2002 edition of *Annual Reviews in Immunology*, Volume 20:  
<http://immunol.annualreviews.org/>

A helpful table on the essentials of the family of TLRs has been created by Naohiro Inohara, Dept of Pathology, University of Michigan Medical School:  
<http://www-personal.umich.edu/~ino/List/TOLLRE.htm>

Medzhitov, R. (2001) Toll-like receptors and innate immunity. *Nat Rev Immunol.* 1, 135-145, PubMed: Figures from this article are provided online as slides at:  
[http://www.nature.com/nri/journal/v1/n2/slideshow/nri1101-135a\\_F5.html](http://www.nature.com/nri/journal/v1/n2/slideshow/nri1101-135a_F5.html)

### Features associated with this article

Figure 1. Toll-like receptors (TLRs): structure and heterodimerisation (dfig001ece).  
Figure 2. Toll-like receptor (TLR) signalling is mediated by at least two distinct pathways (dfig002ece).  
Figure 3. Potential mechanism for the role of Toll-like receptors (TLRs) in intestinal defence and tolerance (dfig003ece).

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