

The molecular basis and downstream immune consequences of mycobacteria-host cell interactions

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To cite this version:

Wassim Daher, Virginia Pichler, Jona Karam, Olivier Neyrolles, Laurent Kremer. The molecular basis and downstream immune consequences of mycobacteria-host cell interactions. FEMS Microbiology Reviews, 2023, 47 (2), pp.fuad009. 10.1093/femsre/fuad009. hal-04720923

HAL Id: hal-04720923 <https://hal.science/hal-04720923v1>

Submitted on 4 Oct 2024

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ABSTRACT

 Pathogenic mycobacteria gain entry to their hosts by inhalation or ingestion where they adhere to different cell types and are subsequently internalized by professional phagocytic cells, such as macrophages or dendritic cells. Multiple pathogen-associated molecular patterns present on the mycobacterial surface are recognized by and interact with a diverse panel of phagocytic pattern recognition receptors, representing the first step of the infection process. This review summarizes the current knowledge on the numerous host cell receptors and their associated mycobacterial ligands or adhesins. It further discusses the downstream molecular and cellular events resulting from the engagement of the various receptor-mediated pathways, leading to either intracellular survival of mycobacteria or to activation of host immune defenses. The content presented herein on adhesins and host receptors may serve as a resource for those developing novel therapeutic approaches, e.g., in the design of anti-adhesin molecules to prevent bacterial attachment and infection. The collection of mycobacterial surface molecules highlighted in this review may also provide potential new therapeutic targets, diagnostic markers, or vaccine candidates to combat these notoriously challenging and persistent pathogens.

INTRODUCTION

 Mycobacterium is a genus of the Actinobacteria phylum representing over 190 species, comprised mostly of non-pathogenic species, such as *Mycobacterium smegmatis*. Other species are opportunists or obligate pathogens, including *Mycobacterium tuberculosis*, the causative agent of tuberculosis (TB) in humans (Meehan *et al.* 2021). Inhalation or ingestion of bacilli are the most common modes of entry where after the bacteria are engulfed by professional phagocytes at the site of infection as been observed in alveolar macrophages for *M. tuberculosis*-infected lungs (Shim, Kim and Shin 2020) or intestinal macrophages and dendritic cells (DCs) for *Mycobacterium avium* subsp*. paratuberculosis* (MAP)-infected animals (Rees *et al.* 2020).

 Successful infection requires adhesion of the pathogen to host cell, colonization of tissues/organs, bacterial multiplication and eventual dissemination to other tissues and/or persistence within the host. Bacteria exploit adhesins/invasins or other macromolecular complexes to trigger an intricate host- pathogen crosstalk that leads to the subversion of cellular functions and establishment of disease. Playing a role in this attachment, the mycobacterial cell envelope is composed of complex network of glycopolymers, lipids, glycolipids, proteins, and of the mycolyl-arabinogalactan-peptidoglycan skeleton (Dulberger, Rubin and Boutte 2020). Bacterial attachment to a substrate may be mediated by adhesins, which are surface-localized molecules capable of binding specific host molecules (Kline *et al.* 2009). In mycobacteria, these adhesins are comprised of a diverse range of glycopolymers, DNA, lipids and proteins. Adhesion facilitates biofilm formation, an essential step for bacterial colonization of environmental niches and for the establishment of infection, and endows bacteria with resistance to immune effector mechanisms, bacteriolytic enzymes and antibiotics (Stones and Krachler 2016; Schulze *et al.* 2021). The ubiquity of biofilm formation across most mycobacterial species, as has been seen in fast-growing non-tuberculous mycobacteria adhering to household plumbing and shower heads (Williams *et al.* 2009) and on clinical biomaterials by slow-growers, such as *M. tuberculosis* (Esteban and García-Coca 2018), points to an advantageous mechanism during pathogenesis.

 Following attachment, mycobacterial entry into host cells is mediated by two different membrane receptor-dependent mechanisms: non-specific macropinocytosis and phagocytosis. Macropinocytosis is characterized by an invagination of the membrane, forming an endosome, which then fuses with microbicidal lysosome compartments to degrade the enclosed microorganisms. Though considered a secondary pathway when phagocytosis receptors are already saturated, this process is also employed by INF-γ-activated macrophages to clear bacteria (Bosedasgupta and Pieters 2014). Conversely, the primary pathway engages multiple phagocytosis pattern recognition receptors (PRR) that recognize specific pathogen-associated molecular patterns (PAMP) present on the surface of the bacilli **(Table S1, Supporting Information)**. PRR are PAMP-specific based on their location and include cellular receptors (found in the plasma membrane, endosomal compartments, and the cytosol; reviewed in part I) and the extracellular host matrix, including mucosal surfaces (reviewed in part II) (Vinod *et al.* 2020). Recognition occurs in either a non-opsonic or opsonic fashion, the latter of which depends on bacteria coated with complement proteins or immunoglobulins to enhance binding affinity with phagocytes *via* 86 complement receptors or FcyR immunoglobulin receptors, respectively. Non-opsonic phagocytosis involves other classes of receptors, including Toll-like receptors (TLR) and C-type lectin receptors (CLR). The interaction between PPR and PAMP triggers signaling cascades that lead to the restructuring of the actin cytoskeleton. Depending on the receptor engaged, the plasma membrane subsequently remodels in one of two ways: 1) invagination, or 2) the formation of membrane protrusions that encompass the microorganism, known as pseudopods (Caron and Hall 1998).

 Immune cells are central to mounting an adequate protective response; however, they, with other cells types, including pneumocytes, epithelial, endothelial, neuronal and intestinal cells, also provide a favorable niche for mycobacterial multiplication and dissemination. Through the development of adaptive mechanisms, mycobacteria use these cells to enable colonization. Although it is known that the fate of mycobacteria within host cells is largely dependent on the entry pathway, with some enhancing host protection and others promoting infection, the mechanisms contributing to the latter are currently not fully understood. Unpacking the interaction between mycobacteria and host cells during pathogenesis is of paramount importance to leverage into improved and innovative therapeutic approaches. This review discusses the processes employed by mycobacteria to hijack host cells and

- tissues, their broader significance in both immune evasion and bacterial survival, and the features that may contribute to reduced bacterial growth and pathogenicity.
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RECEPTOR-MEDIATED RECOGNITION OF MYCOBACTERIA BY DIFFERENT CELL TYPES (Part I)

Innate immune receptors

 The innate immune system, which comprises effector cells, antimicrobial peptides, soluble mediators and cell receptors, represents the first line of defense against invading microbial pathogens. The response is rapidly activated through the recognition of conserved PAMP by PRR (membrane-bound or cytosolic). Each PRR isspecific to a diverse set of PAMP, ensuring the appropriate downstream activation 110 of the adaptive immune response.

Toll-like receptors

 TLR are type I transmembrane glycoproteins composed of extracellular, transmembrane and intracellular signaling domains (Gay and Gangloff 2007). The extracellular domains contain repeated modules of leucine-rich repeats (LRR) and are responsible for binding to PAMP (Medzhitov 2001). Each PAMP type is engaged by different TLR. Di- and tri-acylated lipopeptides and lipoproteins are the defined ligands of TLR2 (Jin and Lee 2008) while lipopolysaccharides (LPS) and microbial DNA are recognized by TLR4 and TLR9, respectively (Uematsu and Akira 2008). Ligand-induced dimerization of TLR triggers the recruitment of adaptor proteins to the intracellular Toll/Interleukin-1 receptor (TIR) domains to initiate signaling (O'Neill and Bowie 2007). Signaling cascades *via* TIR domains are mediated by specific adaptor molecules such as MyD88 (O'Neill and Bowie 2007). MyD88 is essential for TLR signaling (Medzhitov, Preston-Hurlburt and Janeway 1997) and, with the exception of TLR3 and TLR4 (its signaling is composed of at least two distinct pathways, a MyD88- and TRIF-dependent pathway), all TLR require MyD88 for downstream signaling (Kawai *et al.* 1999; Kawai and Akira 2010). The MyD88 adaptor protein mediates many biologically important signal transduction pathways in innate immunity (Warner and Núñez 2013) and is important in the regulation of inflammation during bacterial infection (Wang *et al.* 2014). Mutations in MyD88 are associated with immunodeficiencies that predispose patients to recurrent life- threatening bacterial infections, as observed in MyD88-deficient mice susceptible to a variety of pathogens (von Bernuth *et al.* 2008, 2012). *M. tuberculosis* infection in these mice is lethal as MyD88 signaling is required to elicit an adequate innate and acquired immune response (Fremond *et al.* 2004; Hölscher *et al.* 2008; Berod *et al.* 2014). Phagocytosis, in turn, is essential for an optimal response to MyD88-dependent bacteria (Ip *et al.* 2010). In addition to playing a central role in phagocytosis, MyD88 is crucial for downstream TLR activation and signaling that occurs after bacterial degradation in the phagosome of human monocytes (Cervantes *et al.* 2013) and murine macrophages (Ip *et al.* 2010). Bacteria must be phagocytosed and it is in the acidic environment of the phagosome that endosomal

 TLR recognize their bacterial ligands. Once the bacterial ligands are released, a TLR-dependent response can be initiated from the phagosome (Ip *et al.* 2010; Kagan and Iwasaki 2012; Cervantes *et al.* 2014). Furthermore, MyD88 signaling in DCs and macrophages is essential to control the mycobacterial burden and prevent their persistence (Scanga *et al.* 2004; Berod *et al.* 2014). MyD88-KO mice infected with *M. tuberculosis* develop granulomatous lung lesions with enhanced neutrophil infiltration as compared to wild-type mice (Sugawara *et al.* 2003). These massive cellular infiltrations accompanied by extensive granuloma necrosis lead to high susceptibility of MyD88-KO mice to TB infection (Hölscher *et al.* 2008). Consequently, higher bacterial loads in the lungs and spleen are found in MyD88-KO mice (Sugawara *et al.* 2003; Hölscher *et al.* 2008). Furthermore, an aberrant inflammatory response ensues when MyD88 is absent, due to the fact that MyD88 acts as a negative signaling factor to stop NF-κB activation (Burns *et al.* 2003), a mechanism necessary to prevent excessive inflammation and return to homeostasis (Ruland 2011). In the following section, we will discuss the current knowledge about TLR, focusing on 148 their role in mycobacterial infections.

TLR2

 Establishment of an effective immune response against intracellular mycobacteria depends on the rapid detection of the invading pathogen by the innate immune system and the coordinated activation of the adaptive immune response. TLR are adept at detecting and restricting infection by pathogenic microorganisms, including mycobacteria. The interaction is complex and involves distinct mycobacterial cell wall components and multiple members of the TLR family. Numerous studies have shown that TLR2, acting alone or in concert with other TLR, can recognize several secreted or surface- associated mycobacterial components and help mounting an effective defensive response against *M. tuberculosis*. In macrophages, recognition of the *M. tuberculosis* 19-kDa glycolipoprotein (LpqH) by TLR2 induces apoptosis *via* the caspase-8 pathway, limiting intracellular proliferation of the bacilli **(Figure 1)** (López *et al.* 2003). Since lipoproteins/lipopeptides are detected by TLR2 at physiological picomolar concentrations, the activity of other putative bacterial compounds reported in the literature as TLR2 agonists may, eventually, be due to the presence of highly active natural lipoproteins and/or lipopeptides. It remains possible that recombinant proteins other than *bona fide* TLR2 ligands described in some studies interact with activating lipopeptides, which may explain their observed effects (Zähringer *et al.* 2008). Based on co-structure studies described in the literature (TLR2 in complex with lipoproteins and lipopeptides), further studies reporting various mycobacterial proteins, such as Rv0350 or Rv0577, interacting with TLR2 should be cautiously considered as structural evidence is not yet available. TLR2 is also found in other cell types, including human endothelial cells, where it has been shown to activate the key immune regulatory NF-κB pathway when interacting with *M. tuberculosis*' Hsp70 (Rv0350) protein (Bulut *et al.* 2005). In DC, TLR2 seems to recognize the secreted Rv0577 protein,

 involved in the methylglyoxal detoxification pathway, to induce pro-inflammatory cytokines, including TNF-α, IL-1β, IL-6 and IL-12p70 in a MyD88-dependent manner, as well as mitogen-activated protein (MAP) kinases and NF-κB **(Figure 1)**. It has been shown that Rv0577-treated DC have the capacity to 174 activate naïve T cells, polarize CD4⁺ and CD8⁺ T cells to secrete IFN-γ and IL-2, and induce T cell 175 proliferation. Moreover, this mechanism has been observed to induce the proliferation of memory CD4⁺ 176 and CD8⁺ CD44^{high}CD62L^{low} T cells in the spleen of *M. tuberculosis*-infected mice. Collectively, these observations suggest the close association of TLR2 and Rv0577 in the protective regulation of both the innate and adaptive immune responses to *M. tuberculosis* infection (Byun *et al.* 2012). Conversely, TLR2 may also play a harmful role in IL-10-producing B cells. Upon the interaction of TLR2 and *M. tuberculosis*' mannose-capped lipoarabinomannan (ManLAM), the MyD88/PI3K/AKT/Ap-1 and NF-κB signaling pathways stimulate both B cell proliferation and their IL-10 production, causing the excessive cytokines to diminish immune cell activity and increase infection susceptibility **(Figure 2)** (Yuan *et al.* 2019). While there are many analyses that point to the role of TLR2 in *in vitro* model systems, investigations into the importance of TLR2 in aerosolized *M. tuberculosis* infection of mice *in vivo* have yielded contradictory results. In this context, some reports have found no individual role for TLR2 in establishing effective immunity to growth-limiting *M. tuberculosis* after low- or high-dose aerosol infections (Reiling *et al.* 2002; Bafica *et al.* 2005). Another study, conversely, suggested TLR2 to play a non-redundant role in providing protective immunity during long-term infection. Indeed, TLR2-deficient mice show reduced bacterial clearance, a defective granulomatous response, and the development of chronic pneumonia, causing them to prematurely succumb to infection within 5 months. The range of interactions of TLR2 with diverse ligands highlights its critical role in immune regulation, particularly as its absence yields an exaggerated inflammatory response (Drennan *et al.* 2004). The underlying reasons for these discrepancies are not known but may be explained by the loss of functionality of a single TLR in *M. tuberculosis* aerosol infection models having a negligible effect on the development of the immune response *in vivo* and is easily compensated by other receptors. However, seminal studies performed after *M. tuberculosis* infection in TLR2/4/9- and MyD88-deficient mice, showed that only the latter succumbed rapidly to uncontrolled mycobacterial growth, while the former controlled the infection (Fremond *et al.* 2004, 2007; Scanga *et al.* 2004; Hölscher *et al.* 2008). This demonstrates that only MyD88, but not TLR2, TLR4 and TLR9, is essential for triggering the macrophage effector mechanisms that are central to anti-mycobacterial defense.

 As described above, TLR2 plays a crucial role in the recognition of mycobacteria by their cell wall 202 components. These agonists activate macrophages by initiating NF-KB through TLR2 ligation. However, prolonged TLR2 signaling could help *M. tuberculosis* escape immune surveillance. For example, extended exposure of macrophages to LpqH, LprG, LprA, LM and PIM results in the expression of IL-10, IL-4 and TGF-β, which inhibits macrophage activation (Saraav, Singh and Sharma 2014). Furthermore, prolonged TLR2 signaling activated by LpqH and LprG inhibits the expression of MHC class II molecules and the processing of exogenous antigens for presentation to CD4⁺ T cells, providing a basis for *M. tuberculosis* immune evasion (Hu and Spaink 2022).

TLR heterodimers

 Effective response to mycobacteria by heterodimeric TLR acting in concert has also been described in the literature. In human monocytes, stimulation of TLR2/TLR1/CD14 by the LpqH lipoprotein triggers a cascade that induces the production of the antimicrobial peptide cathelicidin. Cathelicidin paired with other components of the vitamin D pathway, including Cyp27b1 hydroxylase and AMP-activated protein kinase (AMPK), to increase intracellular calcium concentration, and mitogen- activated protein kinase (MAPK) to induce Cyp27b1 expression to trigger cellular autophagy **(Figure 1)** (Shin *et al.* 2010). Influencing adaptive immune functions as well, the lipoproteins LprG and LpqH 218 interact with TLR2/TLR1 heterodimers to activate NF-κB in primary human CD4⁺ T cells. Thus, these lipoproteins serve as important stimuli for immune system regulation in both the innate immune system, *via* cytokine and co-stimulatory molecule secretion, and the adaptive immune system, *via* memory T cell activation, during *M. tuberculosis* infection (Lancioni *et al.* 2011). Another study showed that LprG, ManLAM, and LM bind to TLR2 in the absence of TLR1. Nevertheless, trimolecular interactions were 223 revealed by binding of TLR2-LprG or TLR2-PIM₆ complexes to TLR1, whereas binding of TLR2 to TLR1 was not detected in the absence of the lipoprotein or glycolipid. In addition, ManLAM has a low affinity for TLR2 compared with PILAM, LM, and LprG, accounting for its reduced ability to induce TLR2-mediated ERK signaling pathway activation and TNF-α secretion by macrophages (Shukla *et al.* 2018). In contrast, LM from *Mycobacterium bovis* BCG induces both macrophage activation and pro-inflammatory cytokine production through TLR2 ligation. This pro-inflammatory activity has been attributed to the tri- and tetra-acylated forms of LM. Tri-acyl-LM, a TLR2/TLR1 agonist, promotes IL-12p40 and nitric oxide (NO) secretion by macrophages through the adaptor proteins MyD88 and TIRAP **(Figure 1)** (Doz *et al.* 2007).

 To evaluate the role of other TLR heterodimers, the independent function of TLR9 and cooperative behavior with TLR2 in *M. tuberculosis* infection were elucidated using knock-out mice. Infected *Tlr9*-/- 233 mice exhibited a defect in IL-12p40 and IFNy production, whereas double knock-out *Tlr2^{-/-}/Tlr9^{-/-}* mice were markedly more susceptible to infection due to defects in pro-inflammatory cytokine production 235 and diminished *M. tuberculosis*-specific IFN_V responses, resulting in increased pulmonary pathology, i.e., widespread inflammation and focal necrosis (Bafica *et al.* 2005). *In vitro,* cooperation between TLR9 and 237 TLR2 was demonstrated by a reduced IL-12 response in DC and macrophages from *Tlr2^{-/-}/Tlr9^{-/-}* mice as compared to control cells. These findings reveal TLR9 plays a functional role both independently and in tandem with other TLR members in host resistance to mycobacterial infections (Bafica *et al.* 2005).

TLR4

 In addition to TLR1/2/9, TLR4-mediated signaling also contributes to the protective response against *M. tuberculosis*. TLR4 is the key receptor involved in LPS recognition and signal initiation (Soares *et al.* 2010). In fact, LPS induces dimerization of the TLR4-MD-2 complex (Park and Lee 2013). A hydrophobic pocket of MD-2 houses most of the lipid portion of LPS, however, one of the six acyl chains 246 of LPS is left outside the pocket and interacts with the ectodomain of a neighboring TLR4 molecule (Płóciennikowska *et al.* 2015). Viable and attenuated strains of *M. tuberculosis* have been shown to activate murine macrophages that overexpress TLR4 (Means *et al.* 1999). In contrast, expression of a dominant negative TLR4 protein in macrophages partially blocked *M. tuberculosis*-induced NF-κB activation (Means *et al.* 2001). Interestingly, the lipid A antagonist E5531 specifically inhibited *M. tuberculosis*-induced TNF- α production in macrophages and, thus, apoptosis (Means *et al.* 2001). As agonists, several mycobacterial proteins, including Hsp65 and Hsp70, interact with TLR4 and stimulate the NF-κB cascade in human endothelial cells (Bulut *et al.* 2005). In DC, TLR4 recognizes the ribosomal 254 protein Rv0652, which induces cellular maturation and the pro-inflammatory cytokines TNF- α , IL-1 β and IL-6 following activation of the MyD88 and TRIF signaling pathways **(Figure 1)** (Lee *et al.* 2014). These 256 newly activated DC in turn activate naïve T cells and efficiently polarize CD4⁺ and CD8⁺ to secrete IFN_Y and induce cell-mediated cytotoxicity to eliminate infected cells (Lee *et al.* 2014). The peptidoglycan hydrolase RipA activates the NF-κB signaling pathway and triggers the production of the pro- inflammatory cytokines TNF-α, IL-6, and IL-12 through ligation to TLR4. Homology modelling, docking and MD simulations suggest that the C-terminal globular domain of RipA monomers inserts into the ligand binding pocket of the TLR4 dimer (Shariq *et al.* 2021). Unlike other mycobacterial ligands interacting with TLR4, RipA activates the PI3K-AKT-mTORC1 signaling cascade, ultimately resulting in inhibition of the autophagy-initiating kinase ULK1 **(Figure 2)** (Shariq *et al.*, 2021). This inhibition results in efficient intracellular survival of recombinant *M. smegmatis* expressing *M. tuberculosis* RipA in macrophages (Shariq *et al.*, 2021). RipA also targets host cell mitochondria and inhibits the production of oxidative phosphorylation enzymes to promote mycobacterial replication in macrophages **(Figure 2)**. In addition, RipA also inhibits caspase-dependent programmed cell death in macrophages, thereby preventing an effective innate antibacterial response **(Figure 2)** (Shariq *et al.*, 2021). Collectively, RipA contributes to the creation of a permissive replication niche in host cells by altering autophagy and apoptosis. In addition to proteins, the tetra-acylated LM-containing fraction from *M. bovis* BCG activates macrophages in a MyD88-dependent manner through TLR4 (Doz *et al.* 2007) while PIMs induce TLR2- and TLR4-dependent signaling, thus possibly influencing protective immunity (Abel *et al.* 2002). However, the use of bacterial expression systems and the resulting protein agonists may contribute in minute amounts (pico- to nanogram) of LPS, which are sufficient to induce the activation of phagocytes. Resolution of co-structures are needed to definitively validate the described interactions between TLR4 with its different bacterial substrates. The role of TLR4 in host resistance to *M. tuberculosis* was also evaluated in C3H/HeJ mice (harboring a point mutation within the coding region of the *tlr4* gene) after aerosol infection (Qureshi *et al.* 1999). C3H/HeJ mice showed a reduced ability to clear mycobacteria 279 from the lungs, favoring the spread of the infection in the spleen and liver and accelerating mortality (Abel *et al.* 2002). The lungs of these animals showed signs of chronic pneumonia and deficits in pulmonary production of TNF-α, IL-12p40 and chemoattractant protein-1 (Abel *et al.* 2002). However, careful interpretation is required when using the C3H/HeJ strain as a model of TLR4-deficient mice as there are significant allelic differences between C3H/HeJ and other C3H mouse substrains. Taken with caution, the data suggest that TLR4 may not be sufficient for optimal immunity against *M. tuberculosis* (Kamath *et al.* 2003). It is likely that TLR4 signaling does not contribute to the initiation of protective responses against low-dose airborne infection to *M. tuberculosis* (Reiling *et al.* 2002; Shim, Turner and Orme 2003). These divergent results may indicate that subtle, but as yet unknown differences in experimental conditions (including the type of mice used, the respective microbiome of these mice and the different specific pathogen-free standards in the animal houses) may be instrumental in determining whether TLR4 functionality is of significance in *M. tuberculosis* infection.

Lectin domain-containing receptors and opsonins

293 C-type lectin receptors (CLR) are Ca²⁺-dependent glycan-binding proteins, which adopt a C-type lectin fold structure with a highly variable primary protein sequence and possess similarities in the primary and secondary structures of their carbohydrate-recognition domain (CRD). CLR are widely expressed in living organisms (Drickamer 1999) and are made up of a diverse components, including phagocytic receptors and proteoglycans. Adopting both secreted, soluble forms and anchored forms in the plasma membrane, they frequently oligomerize into homodimers, homotrimers and higher ordered oligomers. 299 These structures lend to the interaction with multivalent ligands and recognition of diverse glycans, owing to the unique carbohydrate composition and structure found on the surface of pathogens (Hsu, Pilobello and Mahal 2006). Functionally, CLR can act as adhesion molecules or phagocytic and/or signaling receptors in the innate immune response to microbes and have been highly conserved throughout evolution (Cummings and McEver 2015). Understanding of CLR family-mycobacterial ligand interactions has expanded in recent years and will be discussed below.

Collectins

307 Collectins are soluble PRR. They belong to a group of collagenous $Ca²⁺$ -dependent defensive lectins found in animals and function to bind oligosaccharides or lipids present on the surface of microorganisms. Following binding to collectins, microbes may be eliminated through aggregation, complement activation, opsonization, phagocytosis activation, or growth suppression.

 The CLR, including human pulmonary surfactant protein A (SP-A, a member of the collectin family produced by lung epithelial cells of the distal and proximal air spaces), have been identified as key players in the early recognition of invading pathogens and initiation of host defense responses. SP-A decorates the surface of *M. tuberculosis* to enhance macrophage adhesion **(Figure 3)** (Ferguson *et al.* 1999). Although ManLAM is considered as the ligand of several CLR including DC-SIGN, MR and CR3, the Apa glycoprotein has also been shown to interact with SP-A in a calcium-dependent fashion (Ragas *et al.* 2007). Through the interaction with cell wall-associated mycobacterial components, the human lung SP- A acts as an effective opsonin to facilitate attachment of bacilli to macrophages. The surfactant protein D (SP-D) is another collectin produced in the distal airspaces of the lungs. Capable of recognizing carbohydrates through its CRD, SP-D regulates interactions between *M. tuberculosis* and macrophages through the recognition of mannosylated compounds, such as ManLAM (Ferguson *et al.* 1999). Specific binding of SP-D to *M. tuberculosis* causes bacterial agglutination, reduces adhesion to macrophages and decreases its intracellular growth **(Figure 3)** (Ferguson *et al.* 1999; Carlson *et al.* 2009). Together, these observations reveal that SP-A and SP-D play opposite roles in the host innate response to *M. tuberculosis* in the lungs.

 Another member of the collectin family, the mannose-binding lectin (MBL, produced by the liver and circulating throughout the body) recognizes various slow-growing mycobacteria (e.g., *M. tuberculosis*, *M. bovis*, *M. kansasii*, and *M. gordonae*) as well as *M. smegmatis*. The molecular recognition of ManLAM and the antigen 85 complex (Ag85) leads to activation of the lectin pathway of the complement system and increases phagocytosis **(Figure 3)** (Bartlomiejczyk *et al.*, 2014, Świerzko *et al.*, 2016). Given MBL's ability to bind fibronectin, it may play an additional role in the interaction of the Ag85 complex with the extracellular matrix. Finally, MBL binding could also favor the uptake of *M. africanum* by macrophages, thereby promoting infection and TB-imposed natural selection that could have fostered the spread of functional MBL-G57E variant in *M. africanum* endemic regions (Thye *et al.* 2011).

 While extensive research focus has been given to the interaction of *M. tuberculosis* with phagocytic cells, less is understood about the molecular basis underlying mycobacterial binding and entry with non-phagocytic cells. Among the different cell types investigated, Chinese hamster ovary (CHO) fibroblasts and primary porcine aortic endothelial cells were reported to successfully interact with *M. tuberculosis in vitro*. Binding markedly increases in the presence of 10% to 20% human or bovine 341 serum, suggesting that the bacteria benefit from the coating of serum opsonins (Hoppe *et al.* 1997). Pre- incubation with individual opsonins revealed that recombinant serum-derived human mannose-binding protein (MBP, belonging to the collectin family, possessing one lectin domain and produced in the liver during infection) also improved binding **(Figure 3)**. Using PIM-specific antibodies to demonstrate a partial blocking of *M. tuberculosis* and *M. smegmatis*, these surface molecules were found to play a role

 in binding to CHO and endothelial cells (Hoppe *et al.* 1997). Furthermore, binding of PIM-coated beads to CHO cells wassignificantly enhanced after addition of MBP-enriched serum (Hoppe *et al.* 1997). These findings confirm that PIM can function as adhesins to bind to non-phagocytic cells both directly and after opsonization with serum MBP.

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Serum amyloid A-opsonin-dependent uptake

 The serum amyloid A1 (SAA1) protein belongs to the family of apolipoproteins associated with high-density lipoproteins (HDL). These proteins play several roles, including the transport of cholesterol to the liver for secretion into the bile, the recruitment of immune cells to inflammatory sites and the induction of enzymes to degrade the extracellular matrix. The interaction between *M. tuberculosis* and SAA1 occurs through the membrane effectors AtpA (Rv1308), the ABC transporter (Rv2477c), the ESX-1 substrate EspB (Rv3881c), the antigen TB18.6 (Rv2140c), and the phosphomethylpyrimidine synthase ThiC (Rv0423c) **(Figure 3)** (Kawka *et al.* 2021). Opsonization of *M. tuberculosis* by SAA1 promotes bacterial entry into phagocytes, stimulates intracellular growth and survival **(Figure 3)** (Kawka *et al.* 2021). Despite the protective opsonic behavior of SAA1, the interaction with *M. tuberculosis* inadvertently promotes the infection of host macrophages and modulates the functional response of the pathogen.

Mincle and Dectin

 Mincle is principally expressed on myeloid cells, including macrophages and DC (Marakalala and Ndlovu 2017). It is composed of a CRD, a transmembrane (TM) domain and a short cytoplasmic tail with a positively-charged residue, which engages with the adaptor molecule FcRγ to trigger intracellular signaling *via* the Syk/CARD9 pathway **(Figure 1)** (Marakalala and Ndlovu 2017). Mincle is an essential receptor for the glycolipid trehalose-6,6'-dimycolate (TDM, also known as cord factor) (Heitmann *et al.* 2013), which activates macrophages and downstream inflammatory cytokines and NO **(Figure 1)** (Ishikawa *et al.* 2009). It is also a known adjuvant for Th1/Th17 vaccination that activates Syk-Card9 signaling in antigen-presenting cells (APC). Experimental genetic disruption of Mincle showed the complete elimination of TDM-induced macrophage activation and stimulation of T cell immune responses to a TB vaccine (Ag85B-ESAT-6). Moreover, macrophages lacking Mincle or FcRγ exhibit impaired inflammatory responses to *M. bovis* BCG (Schoenen *et al.* 2010). Administration of TDM in wild-type mice triggered elevated inflammatory cytokine levels in sera and lung inflammation associated with granuloma formation (Ishikawa *et al.* 2009), whereas Mincle-deficient mice were still able to mount an effective granulomatous and protective immune response after infection with both low and high doses of *M. tuberculosis* (Heitmann *et al.* 2013). These findings suggest that the loss of Mincle *in vivo* can be fully compensated and a protective inflammatory immune response remained during *M.*

 tuberculosis infection. Mincle has been shown to further induce an immune response in mice following interaction with other mycobacterial ligands, such as trehalose-monomycolate (TMM), glucose- monomycolate (GMM) and arabinose-monomycolate (AraMM). Stimulation with these ligands activate 384 bone marrow-derived DC to produce IL-6, TNF- α and reactive oxygen species (ROS) and stimulate the NLRP3 inflammasome to promote Th1 and Th17 responses (Tima *et al.* 2017). The murine bone marrow- derived DC may also be activated through Mincle signaling after exposure to *M. tuberculosis'* immunogenic β-gentiobiosyl diacylglycerides (Richardson *et al.* 2015). Lastly, unique to the human immune response, Mincle interplays with glycerol-monomycolate (GroMM) to stimulate macrophages for inflammatory cytokines production (Hattori *et al.* 2014).

 Signaling through Dectin receptors activates the Syk/CARD9/BCL-10/MALT1 cascade **(Figure 1)**, resulting in the production of pro-inflammatory cytokines and the induction of T cell-mediated immunity (Marakalala and Ndlovu 2017). Adopting several forms, Dectin-1, Dectin-2 and Dectin-3 have been linked to antimycobacterial immunity. Dectin-1 is a glycosylated TM protein with an extracellular CRD and a cytoplasmic immunoreceptor tyrosine-based activation motif (ITAM)-like domain that supports intracellular signaling **(Figure 1)** (Marakalala and Ndlovu 2017). Dectin-1 is primarily expressed on macrophages, DC, neutrophils and a subset of T cells. Dectin-1 recognizes *M. tuberculosis* and less virulent mycobacterial species, although its mycobacterial ligand(s) remaining largely unknown. Dectin- 1-dependent infection of BMDM, DC, A549 cells, PBMC, MDC, neutrophils or monocytes with varied 399 mycobacterial species leads to the production of antimicrobial peptides, ROS and cytokines, such as TNF- α, IL-6, G-CSF, RANTES, IL-12p40, IL-17A, IL-1β, and IL-23 **(Figure 1)** (Yadav and Schorey 2006; Rothfuchs *et al.* 2007; Lee *et al.* 2009; Zenaro, Donini and Dusi 2009; van de Veerdonk *et al.* 2010; Romero *et al.* 2016; Bisiaux *et al.* 2017). Furthermore, DC activated by a Dectin-1 agonist stimulates naïve CD4⁺ T cells to upregulated IFNγ and IL-17 (Zenaro, Donini and Dusi 2009). *Dectin-1*-KO mice infected with *M. tuberculosis* had a significantly decreased lung bacillary loads but developed histological signs of pneumonia (Marakalala *et al.* 2011). Additionally, the loss of Dectin-1 did not result in any significant variations across the pulmonary cytokine expression profiles when compared to control mice (Marakalala *et al.* 2011). Thus, Dectin-1 does not appear to play a major role in immunity against *M. tuberculosis in vivo*, understanding limited applicability due to the use of a murine model. The structure of Dectin-2 consists of a CRD, a TM and a short cytoplasmic tail and is mainly expressed on macrophages, certain subsets of DC and peripheral blood monocytes (Marakalala and Ndlovu 2017). Surface- associated Dectin-2 specifically recognizes ManLAM in BMDC, resulting in the production of pro- and 412 anti-inflammatory cytokines (Figure 1), and these effects are reversed in *Dectin-2^{-/-}* BMDC (Yonekawa *et al.* 2014). Upon mycobacterial infection, *Dectin-2^{-/-}* mice exhibit increased lung pathology, demonstrating that this receptor is a key factor in host immunity against mycobacterial infection, at least in the mouse model. The remaining type of Dectin, Dectin-3, recognizes TDM, stimulates Mincle

 expression through the CARD9-Bcl10-MALT1 complex, and binding of NF-κB to the Mincle promoter enhances host immunity to mycobacterial infection. Consistent with these findings, Dectin-3- or CARD9- deficient mice produce significantly less pro-inflammatory cytokines and KLH-specific antibodies after immunization with a TDM-containing adjuvant (Zhao *et al.* 2014).

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Dendritic cell immune activating receptor

 DC immune activation receptor (DCAR) is expressed on peritoneal macrophages and monocyte- derived inflammatory cells in the lungs and spleen. It lacks an immunoreceptor tyrosine-based inhibitory motif (ITIM) in its intracellular domain (Toyonaga *et al.* 2016; Omahdi *et al.* 2020). However, it possesses a positively-charged amino acid in its TM, allowing protein-protein interactions with FcRγ, which supplies the immunoreceptor tyrosine-based activation motif (ITAM) required for DCAR-dependent signaling (Omahdi *et al.* 2020). Macrophages and monocytes produce the MCP-1 chemokine upon exposure to 428 PIM, a function that is modulated through DCAR, which interacts directly with acylated PIM (Ac₁PIM₁, AcPIM² and Ac2PIM2) (Toyonaga *et al.* 2016; Arai *et al.* 2020). In the absence of DCAR or FcRγ, MCP-1 production is halted, as was observed in DCAR-deficient mice (Toyonaga *et al.* 2016). Upon mycobacterial infection, *Dcar*-KO mice showed reduced numbers of monocyte-derived inflammatory cells at the site of infection, decreased IFNγ production by T cells and increased bacterial loads, thus revealing that an adequate T cell response against mycobacteria requires DCAR (Toyonaga *et al.* 2016).

DC-SIGN and its murine homologs

 Interactions between DC and the *M. tuberculosis* complex play a key role in anti-mycobacterial immunity. *M. tuberculosis* gains entry to DC through the interaction between DC-SIGN and ManLAM or LAM (Maeda *et al.* 2003; Tailleux *et al.* 2003), with the acyl chains of the ManLAM's mannosylphosphatidylinositol anchor and the mannooligosaccharide caps acting as the primary interface (Maeda *et al.* 2003). Although mannose-capped LAM molecules are present across mycobacterial species, DC-SIGN discriminates between these permutations and selectively recognizes *M. tuberculosis.* For instance, *M. smegmatis*-derived LAM, capped with phosphatidylinositol (PILAM), has a limited ability to bind DC-SIGN in the presence of *M. tuberculosis*. Furthermore, DC-SIGN interacts poorly with PILAM and with the uncapped AraLAM molecules from *M. fortuitum* or *M. chelonae*, respectively, or with *M. avium* single mannose residue-capped ManLAM (Maeda *et al.* 2003). Despite this, the removal of the mannose caps in a Δ*pimE* mutant (PimE/Rv1159 catalyzes the transfer of the 447 fifth mannose to PIM₄ to generate PIM₅) fails to reduce the interaction of whole mycobacteria with DC- SIGN (Driessen *et al.* 2009), suggesting that the receptor is likely to interact with additional ligands. Indeed, DC-SIGN has also a strong affinity for hexamannosylated PIM⁶ **(Figure 2)** (Driessen *et al.* 2009; Ehlers 2010). *M. bovis* BCG mutants lacking PIM⁶ (single mutant) or PIM⁶ and mannose capping on LAM

 (double mutant) (Driessen *et al.* 2009) still show similar binding affinity to DC-SIGN and DC and induce comparable levels of IL-10 and IL-12p40 as the wild-type strain. Furthermore, infection studies with these strains have established that the ManLAM/PIM-DC-SIGN interaction was not critical for protective 454 immunity in mice (Ehlers 2010), strengthening the view that while ManLAM and PIM₆ are true ligands of DC-SIGN, additional ligands are likely to govern the interaction between mycobacteria and DC *in vivo*. This notion is further supported by other studies reporting the binding of multiple ligands to DC-SIGN, including LM, PIM2, α-glucan (a dominant capsular polysaccharide), the 19-kDa or the 45-kDa mannosylated Apa glycoproteins **(Figure 2)** (Pitarque *et al.* 2005; Torrelles, Azad and Schlesinger 2006; Geurtsen *et al.* 2009; Sawettanai *et al.* 2019).

 The consequences of DC-SIGN-mediated interactions between mycobacterial ligands and DC are multifold. *M. tuberculosis* and *M. bovis* BCG (through ManLAM) bind to DC-SIGN, halting DC maturation, impeding IL-12 release and inducing IL-10 secretion (Geijtenbeek *et al.* 2003; Gagliardi *et al.* 2005; Wu *et al.* 2011). Similarly, binding of the *M. tuberculosis* α-glucan to DC-SIGN stimulatesimmunosuppressive IL-10 production by DC **(Figure 2)** (Geurtsen *et al.* 2009). This behavior is mirrored during ManLAM or 465 PIM₆ interactions with DC-SIGN in immature DC and macrophages, impairing DC maturation and 466 modulating cytokine secretion by phagocytes and DC, leading to overall suppressed protective immunity to TB (Ehlers 2010). Furthermore, IFNγ levels have been showed to be significantly down-regulated in the supernatants of naïve T cells after co-culture of ManLAM-primed DC (Wu *et al.* 2011). The same phenotype was described in a clinical study reporting that overexpression of DC-SIGN in TB patients decreased DC activation, elevated secretion of IL-10 by DC, decreased induction of T cell proliferation and impaired the immune response (Zhang, Guo and Luo 2009). Nevertheless, *M. tuberculosis* infection of human DC-SIGN-transgenic mice revealed that DC-SIGN can promote host protection by limiting tissue pathology (Ehlers 2010). DC can also target and eliminate *M. tuberculosis*-infected apoptotic neutrophils following the association between neutrophil Mac-1 protein (CD11b/CD18) and DC-SIGN, thereby reducing inflammation (Hedlund *et al.* 2010). Reduced inflammation was further shown in an *in vivo* experiment exposing DC to synthetic mannodendrimers mimicking the ManLAM of *M. tuberculosis,* revealing the cells' pro-inflammatory cytokine production to be inhibited in a DC-SIGN-dependent manner, limiting acute neutrophil influx in mice lungs (Blattes *et al.* 2013).

 In *M. leprae*, the etiological agent of leprosy, infection severity is a function of DC-SIGN expression levels and the interaction with ManLAM. When treated with *M. leprae*-specific ManLAM, DC upregulate DC-SIGN expression, resulting in an increased nuclear translocation of NF-κB and potent IL-10 production. This promotes an immunosuppressive environment during leprosy progression, creating an optimal niche for bacterial persistence in the host (Kumar *et al.* 2013a). Overall, pathogenic mycobacteria capitalize on the DC-SIGN-ManLAM interaction through the prevention of DC maturation and induction of the immunosuppressive IL-10, permitting enhanced survival and persistence **(Figure 2)**.

 To further understand the function of DC-SIGN in anti-TB immunity, parallel murine studies were undertaken. Among the eight murine homologs (SIGNR1-8), SIGNR1 and SIGNR3 are the closest analogs to DC-SIGN. SIGNR1 is expressed by macrophages only, and interacts with *M. tuberculosis* through ManLAM, similar to DC-SIGN (Koppel *et al.* 2004; Wieland *et al.* 2007). Peritoneal macrophages from *Signr1*-KO mice produce less IL-10 upon stimulation with ManLAM than those from wild-type mice, suggesting that the interaction of ManLAM with SIGNR1 may result in similar immunosuppression observed in the human equivalent (Wieland *et al.* 2007). Another *in vivo* study showed that SIGNR1 upregulates SOCS1 expression during *M. tuberculosis* infection, impairs IL-12 production and promotes *M. tuberculosis* survival (Srivastava *et al.* 2009). Moreover, upon stimulation of murine DC with C-type lectin ligand LAM, SIGNR1 significantly suppresses NF-κB activation as well as TNFα, IL-6 and IL-12p40 production (Ohtani *et al.* 2012). In contrast to the observations in *Signr1*-KO mice, *Signr3*-KO mice were the only group to display dampened resistance to *M. tuberculosis*. SIGNR3 is expressed by lung phagocytes during infection and interacts with *M. tuberculosis* surface glycoconjugates to induce, in 499 synergy with TLR2, the secretion of inflammatory cytokines critical for host defense, including TNF and IL-6, confirming the protective role of murine SIGNR3 during the infection (Tanne *et al.* 2009; Tanne and Neyrolles 2010).

Mannose receptor

 The mannose receptor (MR) is an eight lectin-domain transmembrane protein capable of binding carbohydrate ligands including terminal mannose-containing glycoconjugates, fucose and GlcNAc (Martinez-Pomares 2012). MR recognizes mycobacterial surface ManLAM **(Figure 2)**, LAM, AraLAM, acylated PIMs, LM, glycosylated and acylated 19-kDa antigen and PstS-1 (a 38-kDa mannosylated glycolipoprotein) (Schlesinger, Hull and Kaufman 1994; Diaz-Silvestre *et al.* 2005; Torrelles, Azad and Schlesinger 2006; Esparza *et al.* 2015). The MR facilitates the adhesion of *M. tuberculosis* strains to human MDM. Playing a role in adhesion, MR facilitates non-opsonic phagocytosis of *M. smegmatis* by binding to surface glycopeptidolipids (GPL) **(Figure 2)** (Schlesinger 1993; Villeneuve *et al.* 2005). MR was recently shown to internalize fluorescent beads coated with the triglycosylated form of GPL (GPL-3) through the internal and external rhamnose residues linked to the alaninol residue (Daher *et al.* 2022). After phagocytosis, maturation of the phagosome **(Figure 2)** only takes place at the point of fusion with the lysosomal Hck compartment (a Src family tyrosine kinase used as a marker of lysosome-phagosome fusion in human cells), providing an opportunity for mycobacteria to inhibit this process through MR- ManLAM interaction **(Figure 2)** (Astarie-Dequeker *et al.* 1999; Kang *et al.* 2005). Specifically, it is the ManLAM mannose cap structures that prevent the phagosome-lysosome fusion, and experimentally, it has been shown that the fully intact ManLAM molecule is required to maintain this phenotype (Kang *et al.* 2005). The arrest of phagosome-lysosome fusion has also been observed in *M. avium* serovar 4

 through the GPL-MR interaction **(Figure 2)** (Shimada *et al.* 2006), causing downstream suppression of EEA1 and Ca2+ /calmodulin kinase II recruitment in THP-1 cells (Shimada *et al.* 2006). Internalization *via* the MR not only inhibits phagosome-lysosome fusion but also blocks the production of cytokines that target mycobacteria. ManLAM, after cross-linking with MR, inhibits TLR2-induced IL-12 production in human DC (Nigou *et al.* 2001). A subsequent study confirmed the ManLAM-MR engagement reduces inflammation by both inducing the production of anti-inflammatory factors IL-10 (IL-1R antagonist) and IL-1R type II, and suppressing IL-12 secretion by human DC (Chieppa *et al.* 2003). In THP-1 cells, the induction of matrix metalloproteinase-9 (MMP-9) production by MR in response to *M. tuberculosis* and LAM is also a contributing factor to lung tissue damage during *M. tuberculosis* infection (Rivera-Marrero *et al.* 2002). Overall, these studies demonstrate that MR plays a multi-faceted role in promoting a favorable mycobacterial infection niche in phagocytes.

Complement receptor type 3 (CR3)

 CR3 is a heterodimeric surface receptor that belongs to the integrin superfamily, comprising CD11b and CD18 **(Figure 4)**. It has multiple binding sites located in the C-terminal lectin domain, which can mediate both opsonic and non-opsonic phagocytosis(Velasco-Velázquez *et al.* 2003). Several studies have evaluated the role of CR3 in mycobacterial infections, highlighting its involvement in early binding events during infection **(Figure 4)** (Stokes, Thorson and Speert 1998; Velasco-Velázquez *et al.* 2003). Monoclonal antibodies against CR3 inhibit adhesion and phagocytosis of virulent *M. tuberculosis* by human monocytes. Thermally inactivated serum similarly reduced *M. tuberculosis* adhesion, and replenishment of component C3 or factor B (part of the alternative complement pathway, cleaved by factor D to yield a protease that associates with C3b to form the C3 convertase) increased adhesion 543 (Schlesinger *et al.* 1990; Schlesinger 1993). This was also observed *in vivo* in *Itgam^{-/-}* (CR3 negative) mice where non-opsonic binding and serum-mediated opsonic attachment of *M. tuberculosis* to resident macrophages was significantly reduced (Melo *et al.* 2000; Rooyakkers and Stokes 2005). Downstream of internalization, *M. tuberculosis* survival and replication in infected macrophages and mice were not significantly affected by the absence of ITGAM/CD11b, suggesting that CR3-mediated uptake is not a major factor contributing to intracellular survival (Hu *et al.* 2000; Melo *et al.* 2000). Consistently, MDM exhibit enhanced adherence of BCG and *M. leprae* and the attachment process is CR3- and/or serum- dependent, i.e. requiring thermolabile serum components (Schlesinger and Horwitz 1990, 1991; Launois *et al.* 1992). Mechanistically, the C-terminal lectin domain of CR3 recognizes LAM, PIM₂ and polar GPL **(Figure 4)** (Villeneuve *et al.* 2005). In addition, Ag85C promotes the uptake of BCG and *M. tuberculosis* by monocytes through ligation to CR3 **(Figure 4)** (Hetland and Wiker 1994). Furthermore, Rv0180c promotes the infection initiation in the lungs of mice and facilitates entry into macrophages through CR3 (Payros *et al.* 2021). The cooperation between CR3 and TLR2 appears fundamental to inhibit the

 release of peroxidase by eosinophils, which in turn modulate the innate immune response to mycobacteria (Driss *et al.* 2012). Thus, CR3 is important in mycobacterial uptake but is not needed for the induction of the microbicidal machinery and thus favors the survival of intracellular bacteria.

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Oxidized low-density lipoprotein receptor-1 (LOX-1)

 The LOX-1 receptor is a TM protein that structurally belongs to the C-type lectin family (Zeya, Arjuman and Chandra 2016). GroEL2, often found associated with the mycobacterial cell wall, has been identified as a potential ligand for the macrophage LOX-1 receptor **(Figure 4)** based on the decreased uptake of GroEL2-coated latex beads by macrophages following treatment with the LOX-1 inhibitor polyinosinic acid (Vinod *et al.* 2021). This remains only a putative interaction, but may contribute to the internalization of bacteria in macrophages.

Galectin receptors

 Galectins are a large class of proteins serving multiple cellular roles including signaling and adhesion. They are considered S-type lectins due to the presence of disulfide bonds, which function to provide stability and the binding of carbohydrates, including nitrogen- or oxygen-linked β-galactoside sugars. Found in a variety of species, there are 15 mammal-specific galectins, which are further subdivided into three forms: chimera, tandem, and dimeric. Although most lectins exist as membrane- bound proteins, galectins are unique in their soluble state. Tandem galectins, such as Galectin-9, possess two distinct CRD whereas the chimeric Galectin-3 exists as a monomer or a multivalent form. Galectin- 3's multifunctionality lends itself to be found both primarily in the cytoplasm and additionally on the cell surface of immune cells. At the surface, it is known to recognize mycolic acids (MA), the major lipid of the mycobacterial cell envelope, yet the nature of this interaction is still not fully understood (Barboni, Coade and Fiori 2005). More has been discovered regarding the biological role of Galectin-9, particularly with its physical interaction with the essential cell wall polysaccharide, arabinogalactan (AG), during mycobacterial infection **(Figure 2)**. Structural-functional relationship analyses indicate that the high- affinity interaction between AG and Galectin-9's CRD2 causes the latter to associate with transforming growth factor β-activated kinase 1 (TAK1) to trigger the activation of extracellular signal-regulated kinase (ERK) and the induction of matrix metalloproteinases (MMP) expression **(Figure 2)** (Wu *et al.* 2021). These pathways contribute to AG-induced damage in the lungs and have been shown to aggravate the *M. tuberculosis* infection in mice by promoting bacilli survival **(Figure 2)** (Wu *et al.* 2021). Therefore, interaction between AG and Galectin-9 may serve as a viable target for therapeutic development to reduce the severity of TB pathology (Wu *et al.* 2021).

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Other receptors

Nucleotide-binding oligomerization domain-like receptors

 Following internalization, mycobacteria typically inhabit the phagosomal compartment, however, sporadic escape into the cytoplasm (Houben *et al.* 2012) exposes the bacteria to intracellular receptors, including the nucleotide-binding oligomerization domain (NOD)-like receptors (NLR). The NLR member NOD2 detects the N-glycolyl-muramyl dipeptide (MDP) component of peptidoglycan in the mycobacterial cell wall **(Figure 1)** (Coulombe *et al.* 2009). More specifically, NOD2 is stimulated by the N-acetyl muramic acid hydroxylase, NamH, which converts MDP into a N-glycolylated form (Coulombe *et al.* 2009). Accordingly, disruption of *namH* in *M. smegmatis* and *M. tuberculosis* abrogates NOD2- mediated TNF-α secretion in macrophages (Coulombe *et al.* 2009; Hansen *et al.* 2014) and NOD2- dependent immune responses were confirmed to be contingent on the presence of NamH in a murine study (Coulombe *et al.* 2009). Further still, N-glycolyl MDP promotes the secretion of pro-inflammatory cytokines (TNF-α, IL-1β, IL-6) **(Figure 1)** and induces T-cell immunity in a NOD2-dependent manner (Coulombe *et al.* 2009; Juárez *et al.* 2012). During *M. tuberculosis* infection, NOD2 induces expression of 605 the antimicrobial peptide LL37, recruits the autophagy proteins IRGM, LC3, and ATG16L1 to the bacteria- containing autophagosome **(Figure 1)** (Juárez *et al.* 2012), and increases NO production upon NF-κB activation **(Figure 1)** (Landes *et al.* 2015). Synergistic effect of MDP combined to Hsp70 increases IL-6, IL-12p40, and TNF-α production in BMDC, enhances DC maturation and promotes T cell IFNγ production, while accordingly these effects were diminished in NOD2-deficient BMDC (Kim *et al.* 2015). In mice, intraperitoneal injection of MDP together with Hsp70 increased the seric production of IL-6, CXCL-1, and CCL2 (Kim *et al.* 2015), suggesting these combined proteins could be harnessed for an effective vaccination strategy. NOD2 has also been identified in the pathogenesis of other mycobacterial infections, including *M. leprae*, where the induction of IL-32 and differentiation of monocytes into DC in the innate immune response occurs in a NOD2-dependent manner (Schenk *et al.* 2016). Similarly, new insights into the potential roles of NOD2 during innate immune activation against *M. abscessus* lung infections have recently emerged. The production of pro-inflammatory cytokines and NO to limit intracellular growth, eliminate bacteria and ultimately ameliorate lung pathology in *M. abscessus*- infected mice has been shown to hinge on the presence of NOD2 (Lee *et al.* 2017). These collective data demonstrate that NLR, and frequently NOD2, are central to the host defense and reduction of mycobacterial survival.

The cyclic GMP-AMP synthase (cGAS) receptor

 The recognition of microbial components in the cytosol is critical for initiating an innate immune response against intracellular pathogens. The cytosolic DNA sensor cyclic GMP-AMP synthase (cGAS) is essential for triggering STING-dependent signaling and initiating type I interferons (IFN-I) IFN-α and IFN-

 β as central messengers in the host response against bacterial infections. Cyclic GAMP (cGAMP) synthesis is stimulated by the association of cGAS with cytosolic *M. tuberculosis* DNA **(Figure 1)** (Wassermann *et al.* 2015). The ESX-1 mycobacterial secretion system is required for the cytosolic surveillance pathways to be activated during *M. tuberculosis* infection, which results in the generation of IFN *via* the STING/TBK1/IRF3 pathway **(Figure 1)** and in interleukin-1β (IL-1β) synthesis (Wassermann *et al.* 2015; Watson *et al.* 2015). In this way, cGAS promotes autophagic targeting and clearance of *M. tuberculosis* (Watson *et al.* 2015). Similarly, in DC, type I IFN and its cognate receptor (IFNAR), in concert with the cGAS signaling pathway, act against *M. bovis* infection by promoting phenotypic maturation 634 and functional activation of DC and also by increasing CD4⁺ T cell proliferation with DC (Li *et al.* 2019). However, not all mycobacteria species stimulate the cGAS pathway to trigger IFN production. In comparison to *M. smegmatis*-infected macrophages, those infected with *M. avium sbsp. paratuberculosis* (MAP) produce much less IFN-β (Ruangkiattikul *et al.* 2017). This could be explained by the fact that TBK1 is phosphorylated at higher rates in *M. smegmatis* and that there is more extracellular bacterial DNA present in the cytosol (most likely as a result of bacterial autolysis, which releases more DNA needed to effectively activate the cGAS/STING cascade). This is also true in a mouse model, where *M. smegmatis*-induced high IFN-β production and bacterial clearance are correlated. But MAP only slightly increases IFN-β expression, which is associated with bacterial persistence and enhanced hepatic granuloma formation (Ruangkiattikul *et al.* 2017). As predicted, *M. smegmatis* survival was increased in 644 mice lacking IFNAR, although MAP survival was equivalent in *Ifnar^{-/-}* and wild-type mice (Ruangkiattikul *et al.* 2017). Overall, cGAS is as an innate sensor of mycobacteria and contributes to the elimination of the bacilli.

CD43 receptor

 Found on the surface of all hematopoietic cells, CD43/SPN (sialophorin) is a large sialylated glycoprotein essential in the general immune response to mycobacteria and the optimal uptake by macrophages. *M. tuberculosis* engages various chaperones, Cpn60.2/Hsp65/GroEL and to a lesser extent DnaK/Hsp70, as bacterial adhesins that bind to CD43 on the surface of human macrophages **(Figure 1)** (Hickey *et al.* 2010). CD43 is required for optimal uptake and inhibition of *M. tuberculosis* growth both *in vitro* and *in vivo*. Mechanistically, binding of Cpn60.2 to CD43 stimulates macrophages to produce TNF-α, IL-12, and IL-6 to control *M. tuberculosis* infection **(Figure 1)** (Randhawa, Ziltener and Stokes 2008; Torres-Huerta *et al.* 2017). The signaling pathway leading to TNF-α production upon interaction with Cpn60.2 necessitates the Src family kinases, phospholipase C-γ (PLC-γ), phosphatidylinositol 3- kinase (PI3K), p38, and Jun N-terminal protein kinase (JNK) in both BMM and THP-1 cells **(Figure 1)** (Torres-Huerta *et al.* 2017). Furthermore, CD43 is involved in the inflammatory response to *M. tuberculosis* and, through the induction of pro-inflammatory mediators, regulates apoptosis to control

 intracellular bacterial growth (Randhawa, Ziltener and Stokes 2008). Similarly, the absence of CD43 in 662 M. tuberculosis-infected mice (Spn^{-/-}) increases the bacterial loads during the acute and chronic phases of infection and the rapid development of granulomas (Randhawa *et al.* 2005). Furthermore, macrophage CD43 is required for optimal induction of TNF-α production by *M. avium* (Fratazzi *et al.* 2000). This emphasizes the importance of CD43 in promoting a stable interaction of mycobacteria with cells allowing the host to respond primarily through TNF-α production.

Scavenger receptors

 Scavenger receptors (SR) are a diverse group of cell surface receptors. They are involved in a variety of processes, including pathogen clearance. SR are mainly found on myeloid cells and are organized into several different classes. Class A receptors, such as MARCO, are mainly expressed on macrophages and bind to ligands *via* their collagen-like domain. Macrophages expressing MARCO receptors secrete pro-inflammatory cytokines in response to TDM by cooperation between MARCO and TLR2/CD14 **(Figure 1)**. Indeed, MARCO is used to tether TDM to the macrophage and to activate the TLR2 signaling pathway that also requires CD14 **(Figure 1)** (Bowdish *et al.* 2009). As expected, macrophages from *Marco* -/- mice are defective in the activation of extracellular signal-related kinase 1/2 (ERK1/2) and subsequent production of pro-inflammatory cytokines in response to TDM or *M. tuberculosis* infection **(Figure 1)** (Bowdish *et al.* 2009). In diabetic mice, the expression level of MARCO is reduced, which restricts *M. tuberculosis* internalization by macrophages and indirectly contributes to a defective sentinel function of alveolar macrophages, promoting susceptibility to TB (Martinez *et al.* 2016).

 CD36 is classified as a scavenger B receptor (SR-B) and possesses two TM domains with an extracellular loop. CD36 recognizes mycobacterial ligandssuch as LprA (Drage *et al.* 2009) or diglycerides (Martin *et al.* 2011) and serves as a co-receptor for TLR2 by enhancing the recognition of specific bacterial-derived diacylglycerides (Jimenez-Dalmaroni *et al.* 2009). In contrast to MARCO, CD36 plays a permissive function to mycobacterial infection and may enhance mycobacterial uptake (Philips, Rubin and Perrimon 2005). CD36 interacts with the surfactant lipid (composed of 90% lipids, particularly phospholipids, and 10% proteins) to mediate uptake by human macrophages and, therefore, *M. tuberculosis* exploits this function for its growth **(Figure 2)** (Dodd *et al.* 2016). In addition, treatment of macrophage with ManLAM and its deacylated form promotes TNF-α production and inhibits NO secretion by engaging CD36 **(Figure 2)** (Józefowski *et al.* 2011). *In vivo*, CD36 plays a critical role in cellular events involved in granuloma formation that promote early bacterial expansion and dissemination. In *Cd36^{-/-}* mice, mycobacterial loads are reduced in the liver and spleen and infection is associated with reduced granuloma density and decreased levels of circulating TNF-α (Hawkes *et al.* 2010). However, these observations were countered by another study demonstrating the functional redundancy between SR other PRR, which may cooperate in a coordinated response to support the complete immune control of *M. tuberculosis* infection. Therefore, dual deficiency of SR-A/CD204 and CD36 had a limited effect on mycobacterial uptake by macrophages, TNF response, and long-term control of *M. tuberculosis* infection (Court *et al.* 2010).

Fcγ receptors

 Fcγ receptors (FcγR) belong to the immunoglobulin superfamily and are known to induce phagocytosis of opsonized pathogens. This family includes several members, FcγRI (CD64), FcγRIIA (CD32A), FcγRIIB (CD32B), FcγRIIIA (CD16a), FcγRIIIB (CD16b), which differ in their affinity to antibodies. The role of FcꝩR in mycobacterial infections is not completely elucidated but a few studies showed either a restrictive or a permissive impact on bacilli survival. As an example of restriction, during the chronic 707 phase of TB, PPD-specific IgG1 antibodies (which bind to FcyR) are upregulated and contribute significantly to increased pro-inflammatory cytokine secretion by monocytes (Hussain *et al.* 2001). In addition, antibodies opsonized against live *M. tuberculosis* have been shown to induce elevated intracellular calcium release, which promotes maturation and acidification of bacilli-containing phagosomes, reducing the intracellular viability of *M. tuberculosis* **(Figure 1)** (Malik, Denning and Kusner 712 2000). Therefore, both studies indicate that Fcy receptor expression provides control of infections caused by pathogenic mycobacteria. In contrast, CD32B engagement attenuates the Th1 response, IL- 12 production, APC activation, and increases susceptibility to *M. tuberculosis* infection **(Figure 2)**. Upon *M. tuberculosis* infection, CD32B-deficient C57BL/6 mice exhibited enhanced mycobacterial clearance and reduced immunopathology compared with wild-type controls. These outcomes are consistent with increased pulmonary Th1 responses and production of large amounts of IL-12 (Maglione *et al.* 2008). 718 The CD32B-induced signaling pathway also interferes with those of Mincle and FcyR and, consequently, causes a delay in phagosome maturation, thereby promoting mycobacterial survival in host macrophages (Patin *et al.* 2017).

TREM2 receptor

 The TREM2 receptor is a TM protein that possesses an extracellular region (also called ectodomain). The ectodomain of TREM2 can bind to glycoproteins and lipids. The intracellular component of TREM2 does not contain any signaling ability on its own but rather works in tandem with the activator proteins 10 and 12 (DAP10, DAP12) to elicit a downstream signal **(Figure 2)**. TREM2 is found in myeloid cells, such as macrophages, monocytes and DC. Mycobacteria use mycolic acids (MA) to control host immunity *via* TREM2. Indeed, macrophages respond to glycosylated MA in a Mincle/FcRγ/CARD9-dependent manner to produce inflammatory cytokines and recruit inducible nitric oxide synthase (iNOS)-positive mycobacterial macrophages to clear the mycobacterial infection **(Figure**

 2) (Iizasa *et al.* 2021). To counteract this effect, macrophages respond to non-glycosylated MA in a TREM2/DAP12-dependent manner to recruit iNOS-negative macrophages (Iizasa *et al.* 2021). Therefore, TREM2-DAP12 signaling counteracts Mincle-FcRγ-CARD9-mediated anti-mycobacterial immunity to evade the immune response.

CD14 receptor

 CD14, primarily produced by macrophages, helps detect bacteria by binding to various PAMP. In mycobacteria, the LM or LAM lipid anchor and Cpn60.1 bind to CD14 (Yu *et al.* 1998; Lewthwaite *et al.* 2001; Elass *et al.* 2007). Mycobacteria have developed strategies to exploit CD14 in order to evade the host immune system. Among these, *M. tuberculosis*-derived PG and ManLAM expand a subset of CD14⁺ DC with a low capacity to produce IL-12p70 (Søndergaard *et al.* 2014). This process blocks the ability of naïve CD4⁺ T cells to efficiently produce IFNγ, abrogates IL-12p70 production by *M. tuberculosis*- challenged DC and disrupts the synergic action between *M. tuberculosis*-infected macrophages, IFN-γ-744 producing CD4⁺ T cells and IL-12p70-producing DC (Søndergaard *et al.* 2014). Through binding to PIM₁ 745 or PIM₂, mycobacteria inhibit TNF release and host inflammatory responses in a CD14-dependent manner **(Figure 2)** (Court *et al.* 2011). *M. tuberculosis* stimulates also CD14 monocytes to increase the production of two hyaluronan and IL-10, which promote bacillary growth or modulate the immune response (Shams *et al.* 2003; Dhiman *et al.* 2011). However, by acting with other receptors, CD14 plays 749 a restrictive role in the course of infection. Stimulation of TLR2/1/CD14 by the lipoprotein LpqH activates antibacterial autophagy through activation of vitamin D receptor signaling and induction of cathelicidin **(Figure 1)** (Shin *et al.* 2010). Furthermore, MARCO-expressing macrophages secrete pro-inflammatory cytokines in response to TDM through cooperation between MARCO and TLR2/CD14 **(Figure 1)** (Bowdish *et al.* 2009). Other studies suggest that LM from *M. chelonae* or *M. kansasii* induce TNF-α and IL-8 secretion through a CD14∕TLR2-dependent mechanism (Vignal *et al.* 2003). AraLAM has the ability to induce, in a CD14-dependent manner, monocyte chemotaxis that could be detrimental to mycobacteria *in vivo* by maximizing the recruitment of additional alveolar macrophages or peripheral blood monocytes to the infection site (Bernardo *et al.* 1998). Although a significant role for CD14 in antimycobacterial protection *in vivo* has not been substantiated (Ehlers *et al.* 2001), CD14 contributes to pulmonary inflammation and mortality during murine TB. During chronic infection, *Cd14*-KO mice are protected from lethality due to a reduced inflammatory response (Wieland *et al.* 2008). This conclusion is supported by another study indicating that LM may play a functional role in the immunopathology of TB through CD14-dependent secretion of MMP-9, which is directly involved in tissue destruction in TB patients (Elass *et al.* 2007). Additionally, CD14 facilitates also the internalization of the bacilli by host cells **(Figure 4)**. In THP-1 and CHO cells, a cross-talk between CD14 and CR3 promotes phagocytosis of mycobacteria (Sendide *et al.* 2005). In addition, *M. bovis* strain TMV 401 selectively infects alveolar

macrophages subpopulations, particularly in those expressing high levels of CD14 (Khanna *et al.* 1996).

CD14 may facilitate also the entry of *M. tuberculosis* into brain macrophages (Peterson *et al.* 1995).

CD40 receptor

770 CD40 is a member of the TNF-receptor superfamily found on [antigen-presenting cells,](https://en.wikipedia.org/wiki/Antigen-presenting_cell) including DC, [B cells,](https://en.wikipedia.org/wiki/B_cells) an[d macrophages.](https://en.wikipedia.org/wiki/Macrophages) In [macrophages](https://en.wikipedia.org/wiki/Macrophage), the primary signal for activation is IFNy from Th1-type [CD4](https://en.wikipedia.org/wiki/CD4)⁺ [T cells.](https://en.wikipedia.org/wiki/T_cell) The secondary signal is CD40L (CD154) on the Th1 cell, which binds to CD40 on the [macrophage](https://en.wikipedia.org/wiki/Macrophage) cell surface. As a result, the macrophage expresses more CD40 and [TNF](https://en.wikipedia.org/wiki/Tumor_necrosis_factors) receptors on its surface, which contributes to the increased level of activation, high production of microbicidal substances, including ROS and NO, and destruction of the ingested microbe. Specific to *M. tuberculosis* infection, mucosal T- helper cells producing IFNγ (Th1) and IL-17 (Th17) are important for protecting against TB. To this end, *M. tuberculosis* alters CD40 expression on DC and restricts Th1 and Th17 responses. As a result, CD40- deficient DC are unable to induce antigen-specific IL-17 responses after infection (Sia *et al.* 2017). Intratracheal instillation of *M. tuberculosis*-infected DC treated with CD40LT (a multimeric CD40 agonist) significantly enhanced antigen-specific Th17 responses in mice (Sia *et al.* 2017). Furthermore, enhanced CD40-CD40L interactions promote better control of lung bacterial loads after aerosol challenge with *M. tuberculosis* (Sia *et al.* 2017). Thus, targeting the CD40-CD40L pathway represents a novel strategy to improve adaptive immunity against TB. Another CD40-dependent pathway is also important for combatting *M. tuberculosis* infections, based on the stimulation by CD40 and TLR-4 that induces DC to increase their production of IL-12, IL-6, and TNF-α and to upsurge autophagy (Khan *et al.* 2016). *M. tuberculosis* Hsp70 elicits IL-12 and RANTES production by DC and serves as a ligand for CD40 **(Figure 1)** (Wang *et al.* 2001; Lazarevic *et al.* 2003). This stimulation is an effective host-directed therapy against 788 M. tuberculosis because it amplifies the pool of memory CD4⁺ T cells as well as CD8⁺ T cells and effectively contributes to reducing the bacterial burden in the lungs **(Figure 1)** (Khan *et al.* 2016). Moreover, CD40 stimulation of DC enhances immune responses to *M. tuberculosis* infection. Importantly, BCG-infected 791 DC stimulated with CD40 show an increased ability to release bioactive IL-12 and activate IFNy-producing T cells *in vitro* (Méndez-Samperio, Ayala-Verdin and Trejo-Echeverria 1999; Demangel *et al.* 2001). Additionally, when C57BL/6 mice are immunized with these DC and challenged with aerosol containing *M. tuberculosis*, increased levels of IL-12, IL-18, and IFNγ transcripts were found in the draining mediastinal lymph nodes (Demangel *et al.* 2001). As for *M. tuberculosis*, CD40 is also required for optimal protective immunity against *M. avium* (Flórido *et al.* 2004) and *M. bovis* BCG (Méndez-Samperio, Ayala- Verdin and Trejo-Echeverria 1999). Indeed, *Cd40*-KO mice are more susceptible to *M. avium* infection 798 due to the generation of a poorer IL-12 and IFNy response (Flórido *et al.* 2004). Nevertheless, bacilli are capable of countering the CD40-dependent immune response that jeopardizes their survival. For example, MDM infected with *M. avium* subspecies *paratuberculosis* fails to upregulate the expression

 of iNOS and IL-12 in response to CD40 stimulating pathway (Sommer *et al.* 2009). In addition to CD40, 802 its partner CD40L also helps to induce an antimicrobial response against several species. CD40L and IFNy have been shown to activate the vitamin D-dependent antimicrobial pathway and to trigger antimicrobial activity, through upregulation of antimicrobial peptides and induction of autophagy, against intracellular *M. tuberculosis*, contributing to human host defense against intracellular infection **(Figure 1)** (Samten *et al.* 2000; Klug-Micu *et al.* 2013). Finally, MDM expressing CD40L inhibit *M. avium* growth by stimulating IL-12 production (Hayashi *et al.* 1999). In conclusion, the CD40-CD40L axis plays an important role in the host immune response against mycobacterial infections.

Aldolase

 The aldolase catalyzes a reversible reaction that cleaves the aldol, fructose 1,6-bisphosphate, into the triose phosphates dihydroxyacetone phosphate (DHAP) and glyceraldehyde 3-phosphate (G3P). The fructose-bisphosphate aldolase occupies a central position in glycolysis and gluconeogenesis. Beyond its role in central metabolism, it appears also implicated in other biological functions and is exploited as a receptor by pathogenic mycobacteria. In HEp-2 or A549 epithelial cells, the aldolase, present in the membrane and cytosolic compartment, binds to the *M. avium* superoxide dismutase (SOD) (Reddy and Suleman 2004). This interaction allows *M. avium* to adhere, gain entry and multiply inside epithelial cells **(Figure 4)**. In addition, the pathway that allows *M. avium* to colonize the gastrointestinal tract of patients has been identified. Studies on mouse intestinal mucus identified fructose-1-6-bisphosphate aldolase B as a host receptor interacting with the SOD and the heparin- binding hemagglutinin (HBHA) **(Figure 4)** (Reddy, Suleman and Hayworth 2004). In conclusion, MAC binds to the intestinal mucus aldolase, plausibly facilitating intestinal colonization of the organism.

THE EXTRACELLULAR MATRIX PLATFORM (Part II)

 The extracellular matrix (ECM) is a three-dimensional network of macromolecules and minerals that provides structural and biochemical support to surrounding cells. The composition of the ECM varies among multicellular structures; however, cell adhesion, intercellular communication and differentiation 828 are common functions of the ECM. ECM components are produced intracellularly by resident cells and 829 secreted into the ECM by exocytosis. Once secreted, they aggregate to the existing matrix. The ECM is composed of an interlocking meshwork of fibrous proteins and glycosaminoglycans (GAG) such as proteoglycans, heparan sulfate, hyaluronic acid, collagen, fibronectin, and laminin. The ability of pathogenic microorganisms to adhere to host cells and avoid removal by the host immune system is the initial and the most decisive step leading to infection. Mycobacteria have developed different means to 834 attach to various host surface structures. One important strategy consists of adhering to the ECM components that are abundant in connective tissue and basement membranes. Mycobacteria express

 variable outer membrane adhesins to attach to these components and understanding the molecular mechanisms of mycobacterial adhesion is a prerequisite for inhibiting these interactions using "anti-838 ligand" strategies to prevent/reduce host colonization.

Integrins

841 Integrins are TM receptors that facilitate cell-cell and cell-ECM interactions. When bound to a ligand, integrins activate signal transduction pathways that transmit various cellular signals. The role of integrins in mycobacterial infections is not yet fully elucidated but two functions are known to benefit pathogenic mycobacteria. On the one hand, the peptidyl prolyl isomerase A (PPiA) interacts with the integrin α5β1, aids in *M. tuberculosis* survival and disease progression by exploiting host-associated factors, such as upregulation of multiple host matrix metalloproteinases **(Figure 2)** (Dubey *et al.* 2021). While PPiA deletion compromises granuloma-like formation and promotes host cell death through ferroptosis, its overexpression enhances the bacilli burden and exacerbates pulmonary pathology in mice (Dubey *et al.* 2021). On the other hand, host integrins also facilitate the attachment of *M. avium* subsp. *paratuberculosis* to intestinal epithelial M cells. Internalization is primarily mediated by the formation of a fibronectin (FN) bridge formed between FAP-P (fibronectin attachment protein homologue) of *M. avium* subsp. *paratuberculosis* and integrins on M cells **(Figure 4)** (Secott, Lin and Wu 2004). Thus, host integrins facilitate host-pathogen interactions and disease progression.

Collagens

 Collagens are the most abundant proteins in the ECM, present as fibrillar proteins and providing structural support to resident cells. Using a collagen-sepharose affinity chromatography approach, the *M. bovis* BCG collagen-binding protein was characterized as a laminin-binding histone-like protein (LBP/Hlp), a highly conserved protein associated with the mycobacterial cell wall **(Figure 4)** (Dias *et al.* 2012). Moreover, the C-terminal domain of *M. leprae* LBP/Hlp was found to bind to collagen I (Dias *et al.* 2012). Exogenous collagen I supplementation cross-linked *M. bovis* BCG to improve the interaction with pneumocytes and macrophages (Dias *et al.* 2012).

Plasmin(ogen)

 Plasmin is a serine protease that acts to dissolve fibrin blood clots. In addition to fibrinolysis, plasmin cleaves various proteins of the ECM, including fibronectin and laminin. The ability of a pathogen to interact with and infect host tissues directly determines the spread of infection. Adherence due to host-pathogen interactions and in-depth traversal within infected organs are involved in the process. *M. tuberculosis* surface-associated and secreted glyceraldehyde-3-phosphate dehydrogenase (GAPDH) not only recruits and serves as a dual receptor for both plasminogen and plasmin, but it also gives bacilli the

 ability to break down physical tissue barriers during systemic bacterial dissemination **(Figure 4)** (Gani *et al.* 2021). Soluble GAPDH can re-associate with bacilli to promote plasmin(ogen) recruitment and thus improves bacterial adhesion and passage through lung epithelial cells (Gani *et al.* 2021). GAPDH association with ECM proteins, together with its ability to recruit plasmin(ogen), may confer capacity for directed proteolytic activity by the bacilli, vital for tissue infection (Gani *et al.* 2021).

Hyaluronic acid

 Hyaluronic acid (HA) is a polysaccharide consisting of alternating residues of D-glucuronic acid and N-acetylglucosamine. HA present in the extracellular space endows the tissue with stability to resist compression by providing an antagonistic turgor force by absorbing large amounts of water. The *M. tuberculosis* protease Rv3194c (residues 91-110) functions as an adhesin by binding to HA present on the surface of pneumocytes **(Figure 4)** (Zhao, Lin and Xu 2020). *M. smegmatis* overexpressing Rv3194c leads to persistent infections and pulmonary lesions in mice (Zhao, Lin and Xu 2020). Subsequent intratracheal treatment with the Rv3194c peptide 91-110 to infected mice showed a growth suppression of *M. smegmatis* and reduced lung pathology, attributable to the unavailable HA binding sites once saturated with the peptide 91-110 (Zhao, Lin and Xu 2020). As Rv3194c functions as a HA-binding adhesin, the 91-110 peptide may offer possibilities to reduce or prevent mycobacterial infections.

Syndecans

 Syndecans are single TM proteins carrying three to five chains of heparan sulfate and chondroitin sulfate, *i.e.* they are proteoglycans, which allow interactions with a variety of ligands, such as fibronectin. The mechanisms of attachment and internalization of *M. tuberculosis* to non-professional phagocytes, like epithelial cells, remain incompletely understood. Syndecan 4 (Sdc4) has been identified 894 as a mycobacterial attachment receptor on alveolar epithelial cells interacting with the mycobacterial HBHA (Zimmermann *et al.* 2016) **(Figure 4)**. Sdc4 knockdown in alveolar epithelial cells or blocking with an anti-Sdc4 antibody showed reduced mycobacterial attachment and internalization. *In vivo*, Sdc1/Sdc4 double-KO mice appeared more resistant to lung colonization by *M. tuberculosis* (Zimmermann *et al.* 2016), thus unraveling an important role for distinct Sdcs in promoting mycobacterial entry into alveolar epithelial cells.

Laminin

 Laminin, an extracellular matrix protein, is thought to play a role in the attachment, migration and organization of cells in tissues during embryonic development by interacting with other components of the extracellular matrix. The alpha, beta and gamma subunits are linked together by disulfide bonds to form a cross-shaped molecule. The laminin-2 isoform on the Schwann cell-axon unit serves as the

 initial neural receptor for *M. leprae* by interacting with ML-LBP21/Hlp (*M. leprae* laminin-binding protein 21-kDa/21-kDa histone-like protein) (Shimoji *et al.* 1999; de Melo Marques *et al.* 2000) **(Figure 4)**. The role of ML-LBP21 in Schwann cell adhesion and internalization was investigated using fluorescent polystyrene beads coated with rML-LBP21. Although beads coated with rML-LBP21 alone specifically adhered to and were ingested by primary Schwann cells, these processes were significantly enhanced 911 when the rML-LBP21-beads were pre-incubated with exogenous α 2 laminins (most likely exogenous α 2- laminins bridge rML-LBP21 to unoccupied laminin receptors on Schwann cells and subsequently mediates the ingestion) (Shimoji *et al.* 1999). *M. smegmatis* produces a paralog, designated MS-LBP, which is attached to the bacterial surface and, interacting with host laminin, is responsible for laminin- mediated mycobacterial adhesion to human pneumocytes and macrophages (Pethe *et al.* 2001). Deletion of the *hlp* gene fails to affect the capacity of mycobacteria to bind to neuronal cells, suggesting that alternative adhesins and/or pathways are exploited by mycobacteria for adhesion to Schwann cells (de Melo Marques *et al.* 2000). Verifying the involvement of malate synthase's (MS) (catalyzes the condensation of acetyl coenzyme A and glyoxylate to form malate) in the entry of the bacilli into nerve cells could help elucidate this process (Kinhikar *et al.* 2006) **(Figure 4)**. Computational models suggest putative interactions between as yet uncharacterized *M. tuberculosis* adhesins and laminin (Kumar *et al.* 2013b). Together, these studies underscore the multiplicity of mycobacterial adhesins that interact with a single receptor. Overall, ML-LBP21 functions as a critical surface adhesin that facilitates uptake of *M. leprae* into Schwann cells and as a contributing factor to the pathogenesis of *M. leprae*-mediated nerve damage.

Heparan sulfate

 Heparan sulfate (HS) is a linear polysaccharide in which two or three chains are attached in close proximity to the cell surface or to ECM proteins. HS binds to a variety of ligands, regulates a wide array 930 of biological functions and serves as a cellular receptor for mycobacteria. Importantly, ML-LBP21/Hlp, besides laminin, binds also to heparin and HS (Soares de Lima *et al.* 2005). The interaction between ML- LBP21/Hlp with heparin is mainly driven by the C-terminal domain of the protein, also involved in mediating bacterial binding to human Schwann cells (Soares de Lima *et al.* 2005) **(Figure 4)**. These findings reinforce the participation of ML-LBP21/Hlp in mycobacterial infection and define its highly positively charged C-terminal region as the major adhesive domain of this protein. Apart from LBP, the Lys/Pro-rich C-terminal region of HBHA also binds to sulfated carbohydrates and functions as an adhesin for epithelial cells (Menozzi *et al.* 1998; Pethe *et al.* 2000) **(Figure 4)**. Consequently, binding of HS chains to HBHA promotes adhesion to epithelial cells and may be necessary for extrapulmonary dissemination of *M. tuberculosis*. While HBHA induces a reorganization of the actin filament network in confluent endothelial cells, it does not affect their tight junctions (Menozzi et al. 2006). In addition, the

 transcellular migration of endocytic vacuoles containing HBHA-coated particles suggests that HBHA induces epithelial transcytosis, representing a macrophage-independent mechanism of extrapulmonary dissemination leading to systemic infection (Menozzi *et al.* 2006). Both LBP and HBHA are also considered as major adhesins for the attachment of *M. leprae* to epithelial cells (Silva *et al.* 2013).

Fibronectin

 Fibronectin (FN) is a high molecular weight glycoprotein of the ECM that binds to integrins. FN also binds to other ECM proteins such as collagen, fibrin and HS proteoglycans, like syndecans. FN is targeted by a large set of bacterial adhesins. A number of bacterial FN-binding proteins have been reported as FN interactants playing diverse roles in bacterial colonization, virulence and bacterial-host interactions. Studies have shown that mycobacteria attach to various FN-producing cells by engaging various adhesins (Ratliff *et al.* 1993). The p55/FAP protein of *M. bovis* BCG and *Mycobacterium vaccae* binds to FN and inhibits the attachment of the bacilli to host cells **(Figure 4)** (Ratliff *et al.* 1993). Moreover, the *M. leprae* fibronectin attachment protein (FAP) adhesin binds to FN and significantly enhances the attachment and ingestion of bacilli by epithelial and Schwann cells **(Figure 4)** (Schorey *et al.* 1995), representing an important step in the initiation of *M. leprae* infection *in vivo*. The RWFV motif is required for the FN binding function of mycobacterial FAP proteins (Zhao *et al.* 1999). Furthermore, MAC and *M. smegmatis* adhere to FN-containing epithelial cells *via* FAP (Middleton *et al.* 2000; Secott, Lin and Wu 2002). The other characterized ligand interacting with FN is the Ala/Pro rich protein (Apa), a secreted antigen, which binds to the cell-binding domain of FN **(Figure 4)** (Kuo *et al.* 2019). In addition, the secreted Ag85 complex favors the attachment of mycobacteria in the lung or during hematogenous spread by acting as a stress-sensitive adhesin **(Figure 4)** (Viljoen, Alsteens and Dufrêne 2020). The C- terminal domain of the glycine-rich PE-PGRS proteins such as PE-PGRS81 of *M. tuberculosis* exhibit FN binding properties **(Figure 4)** (Espitia *et al.* 1999). In this context, the cell wall-localized MS of *M. tuberculosis* has adapted to function as an adhesin by binding to FN, enhancing bacterial attachment to lung epithelial cells **(Figure 4)** (Kinhikar *et al.* 2006). Evidence of *in vivo* expression of *M. tuberculosis* MS during active infection in humans show that a housekeeping enzyme of *M. tuberculosis* contributes to its arsenal of virulence factors (Kinhikar *et al.* 2006). Moreover, computational strategy using different algorithms has predicted putative bindings between human FN with various *M. tuberculosis* adhesins (Rv2599, N-acetylmuramoyl-L-alanine amidase, L,D-transpeptidase) (Kumar *et al.* 2013b). This approach, through further experimental investigations, could expand the number of known *M. tuberculosis* adhesins. Lastly, binding and ingestion of *M. avium* subsp. *paratuberculosis* (MAP) by host cells is dependent on both FN and the bacterial elongation factor Tu (EF-Tu) **(Figure 4)** (Viale *et al.* 2014). This supports the view that human FN plays a primary role in the internalization of several mycobacterial species and contributes to the infection process.

DRP-2 and GAPDH

 MAP is the causative agent of Johne's disease, a chronic and fatal enteritis that affects ruminant populations. Oral transmission of MAP occurs when young animals consume bacteria from infected dams' colostrum and milk. Raw milk exposure has a dramatic effect on MAP, resulting in a more invasive and virulent phenotype. Post-exposure, expression of the *MAP1203* gene is up-regulated more than 28- fold and plays a role in increased binding and uptake by bovine MDBK epithelial cells during the early phase of infection **(Figure 4)** (Everman *et al.* 2018). Furthermore, MAP1203 is a MAP surface-exposed protein that interacts with the host proteins dihydropyrimidinase-related protein 2 (DRP-2) and GAPDH, both of which are found on the epithelial cell membrane **(Figure 4)** and are involved in cytoskeletal remodeling (Everman *et al.* 2018). Hence, MAP1203 plays a role in the initiation of MAP infection of bovine epithelial cells.

MECHANISMS BEYOND PRR and ECM (Part III)

 Despite the identification of a large set of receptors interacting with bacterial surface glycolipids, a paucity of knowledge still exists around the host partners of certain mycobacterial ligands. A few bacterial adhesins play an important role in the internalization and pathogenesis of mycobacteria but the molecular mechanisms underlying these processes remain unknown. *M. leprae* is frequently encountered inside human microvascular endothelial cells (HMVEC) surrounding Schwann cells at the site of peripheral nerve damage in patients with lepromatous leprosy. Based on this observation, it was thought that *M. leprae* uses the nasal mucosa as an entry pathway and that HMVEC serves as an important reservoir for the bacteria before they interact with Schwann cells. An elegant study demonstrated that the first 72 amino acids of the Mce1A protein play an important role in *M. leprae* uptake by HMVEC and that antibodies against this region prevent the entry of *M. leprae* into HMVEC (Idris *et al.* 2019). In *M. tuberculosis* and *M. bovis* BCG, cell wall-associated PE/PE-PGRS proteins play an important role in establishing macrophage infectivity (Brennan *et al.* 2001). As a result, PE-PGRS proteins influence mycobacterial interactions with macrophages. Finally, the *M. tuberculosis* protein product encoded by *Rv3312A* has been shown to be an adhesin/invasin of epithelial cells and macrophages, as well as an entry factor for *M. tuberculosis* (Ramsugit and Pillay 2014; Ramsugit, Pillay and Pillay 2016). *M. tuberculosis* strains lacking Rv3312A showed a significant reduction in their ability to adhere to and enter A549 pulmonary epithelial cells and THP-1 macrophages (Ramsugit and Pillay 2014; Ramsugit, Pillay and Pillay 2016).

 The aryl hydrocarbon receptor (AhR) is a transcription factor that senses environmental toxins, among other substances, thereby modulating immune cell responses (Moura-Alves *et al.* 2014). AhR recognizes pigmented bacterial virulence factors as ligands, namely naphthoquinone phthiocol from *M.*

 tuberculosis (Moura-Alves *et al.* 2014). After ligand binding, AhR activation leads to virulence factor degradation and regulates production of cytokines and chemokines. The importance of the AhR in host defense is underlined by the increased susceptibility of AhR-deficient mice to *M. tuberculosis* (Moura- Alves *et al.* 2014). Thus, the AhR is an intracellular PRR that senses bacterial pigments and controls antibacterial responses.

 Host factors can also facilitate phagocytosis of mycobacteria. In this context, sphingolipid biosynthesis inhibition has experimentally been shown to significantly reduce *M. tuberculosis* and *M. marinum* uptake by a panel of macrophages and DC (Niekamp *et al.* 2021). Microscopic analysis revealed that sphingolipid-deficient macrophages can recognize bacilli and assemble actin at the site of contact, but they are unable to remodel the actin cytoskeleton, which is required for complete internalization of the bacilli **(Figure 5)**. Furthermore, sphingolipid-deficient macrophages failed to exclude the CD45 tyrosine phosphatase from the receptor-pathogen contact site or nascent phagosome, a critical step in phagocytosis progression (Niekamp *et al.* 2021). At the host-pathogen interaction sites, this impairment is accompanied by poor Rho-GTPase activation and a substantial reduction in phosphoinositide turnover (Niekamp *et al.* 2021). These observations highlight the importance of sphingolipid production in *M. tuberculosis* phagocytic uptake and identifies a possible target for future antimycobacterial treatments.

 Finally, very little is known about the dissemination of *M. tuberculosis* from the lungs but it seems that specific adhesins are also involved in this process. Indeed, the dissemination of *M. tuberculosis* from the primary site of infection is critical to TB pathogenesis. While bacterial trafficking to regional lymph nodes is required for the development of a protective T cell-mediated immune response, entry into the circulatory system presents the risk of extrapulmonary dissemination, yielding some of the most lethal clinical consequences of TB. While the mechanism of exiting the lungs across the alveolar epithelium has yet to be fully characterized, some features have been identified **(Figure 6)**. At the epithelial layer, *M. tuberculosis*' HBHA facilitates binding to sulphated glycoconjugates on epithelial cells. When HBHA is blocked, a marked decrease in dissemination from the lungs to the spleen has been observed **(Figure 6)** (Krishnan, Robertson and Thwaites 2010). Following attachment, the early secretory antigenic target 6-kDa (ESAT-6) and culture filtrate protein 10-kDa (CFP-10), encoded by the RD1 locus, have been linked to cell lysis and to internalization into the alveolar epithelium **(Figure 6)** (Krishnan, Robertson and Thwaites 2010). Work in embryonic zebrafish suggests that ESAT-6 may additionally contribute to early spreading of the bacteria by stimulating the trafficking of infected macrophages within granulomas, indicating that *M. tuberculosis* has evolved granuloma-dependent mechanisms for macrophage recruitment, infection, and subsequent bacterial dissemination (Krishnan, Robertson and Thwaites 2010). In the absence of both ESAT-6 and HBHA, a notable reduction of bacterial migration across the alveolar barrier has been observed (Ryndak, Chandra and Laal 2016). More complete characterization of these proteins and their interactions with host cells may offer a potential for novel therapeutic targets.

CONCLUDING REMARKS AND PERSPECTIVES

 Adhesion molecules, found on the surface of most bacteria, facilitate the interaction with host cells, aid in colonization and uptake, and trigger the host's immunological response during infection. The precise interactions observed between pathogenic mycobacterial surface molecules and host receptors affirms the favorable and exploitable niche of the intracellular environment. The purpose of a multi-entry strategy may lie in the hijacking of macrophages and other host cells to cross the pulmonary and epithelial barriers. This is performed by macrophages that directly ingest inhaled mycobacteria or by monocytes, macrophages, and/or neutrophils that migrate to the initial infection site in response to chemokines secreted by infected macrophages. Bacterial entrance in macrophages alters transcriptional gene expression, permitting the stimulation genes that inadvertently support bacterial survival, growth, and intercellular spread. This is mirrored in the increased cytotoxicity to respiratory epithelial cells caused by *M. tuberculosis* emerged from intracellular environments *versus* those grown in cell-free media, suggesting that processes in the intracellular environment offer an advantage to aid in the breaching of epithelial barriers and spreading to distant sites (McDonough and Kress 1995). Furthermore, *M. avium* and *M. intracellulare* may spend time in macrophages to initiate specific virulence mechanisms (Bermudez, Parker and Goodman 1997; Cirillo *et al.* 1997). Additional work is still needed to fully understand the potential impact of the internalization pathway on intracellular trafficking of phagosomes and whether host cell responses differ according to the receptors engaged and mycobacterial species involved. Mycobacterial interactions with both opsonic and non-opsonic receptors on host cells are complex and not yet fully understood. Receptor studies are often performed in artificial *in vitro* systems, while more biologically representative *in vivo* results may only be cautiously interpreted due to their high variability across different experimental conditions. Despite best practices, inconsistencies in *Mycobacterium*-receptor function studies can be influenced by several technical conditions. Bacterial species, genetic diversity of strains of the *M. tuberculosis* complex (lineage 2 vs lineage 4 vs Lineage 1, etc.) (Brites and Gagneux 2017; Gisch *et al.* 2022; Zha *et al.* 2022), genetic diversity in humans, host cell types, infection sites and cell preparation are all considerations to be taken into account when monitoring the characteristics of host-pathogen interactions. Mycobacteria culture conditions are also important aspects to consider. For instance, the use of detergents when culturing mycobacteria strongly affects the mycobacterial surface properties and, consequently, subsequent adhesion and interaction with the host (Pietersen *et al.* 2020; Lim *et al.* 2022). For these reasons, approaching near-natural experimental conditions will yield the most physiologically-meaningful results. However, this is made more complicated by the nature of mycobacterial internalization by host cells *via*

 multiple receptor-mediated mechanisms. Experimentally, many of the receptors do not appear to be independently essential, suggesting compensatory alternatives. Furthermore, synergism between the various receptor families and the impact on mycobacteria-caused diseases requires additional attention. The abundance of mycobacterial surface ligands also contributes to this complexity, adopting several downstream permutations by binding receptors on diverse cell types, engaging multiple receptors in tandem or conversely blocking sufficient receptor clustering for cellular cross-talk and signaling. It is currently well-established that the type of interaction correlates with infection outcome. The LAM cap structure spans both ends of immunomodulation through PILAM as a pro-inflammatory molecule that 1087 stimulates the production of TNF- α and IL-12 and ManLAM as an anti-inflammatory molecule that 1088 stimulates the production of IL-10 while blocking the production of IL-12 and TNF- α . These immunomodulatory processes will be influenced by a number of factors, including the expression and availability of certain receptors and their downstream responses.

 Better understanding the initial features of host-pathogen interactions *via* adhesion and internalization could reveal future targets for prophylactic strategies in preventing mycobacterial internalization. Current efforts are focused on unpacking the immunogenicity of surface-localized adhesins for application in vaccine development, as previously discussed for HBHA (Temmerman *et al.* 2004). The synthesis of chemical scaffolds or peptides that mimic adhesin-receptor binding sites are also being pursued as alternative therapies to limit infection. Some success has been observed with anti- adhesion therapies against pathogenic mycobacteria and may show improved outcomes when administered alone or with antibiotics (Ofek, Hasty and Sharon 2003). Finally, as additional mycobacterial adhesins continue to be identified, it is now more critical than ever to employ cutting- edge techniques such as super-resolution imaging or atomic force microscopy to clarify the intricacies of their functionality (Kreve and Reis 2021; Tabusi *et al.* 2021).

SUPPLEMENTARY DATA

Supplementary data are available at FEMSRE online.

FUNDING

 This work was supported by the Agence National de la Recherche [SUNLIVE-19-CE15-0012-01; DCIR-TB- 18-CE44-0005] and by the "Equipe FRM EQU202103012588" to LK. In addition, the Neyrolles laboratory is also supported by the Fondation Bettencourt Schueller, MSDAVENIR, and the Fondation pour la Recherche Médicale (FRM).

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ACKNOWLEDGMENTS

- JK wishes to thank the foundation IHU Méditerranée Infection for her doctoral fellowship and GP
- acknowledges the Friedman Award for Scholars in Health.
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- **CONFLICT OF INTEREST**
- None declared.
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