

# The evolved functions of CD1 during infection

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CD1 proteins display lipid antigens to T cell receptors. Studies using CD1d tetramers and CD1d-deficient mice provide important insight into the immunological functions of invariant NK T cells (iNKT) during viral and bacterial infections. However, the mouse CD1 locus is atypical because it encodes only CD1d, whereas most mammalian species have retained many CD1 genes. Viewed from the perspective that CD1 is a diverse gene family that activates several of classes of T cells, new insights into lipid loading and infection response are emerging.

## Addresses

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CD1 antigen presentation was discovered using human T cells that recognize CD1a, CD1b, or CD1c proteins [1,2]. Separately, a distinct population of CD3<sup>+</sup> cells that persist in MHC knockout mice were designated 'invariant NK T cells' (iNKT) based on their (nearly) invariant TCR V $\alpha$ 14 chains and V $\beta$  chains, as well as natural killer (NK) locus encoded markers [3,4]. Later, mouse iNKT cells were found to recognize CD1d, so that the previously separate fields of CD1 and NKT cells merged [5]. Human T cells with V $\alpha$ 24 TCRs were found to have the same molecular recognition properties as V $\alpha$ 14 mouse iNKT cells [6,7] as well as a shared lineage-specific transcription factor, promyelocytic leukemia zinc finger (PLZF) [8<sup>\*\*</sup>]. In addition, certain mouse and human T cells recognizing CD1d were found to lack the conserved TCRs [9] and antigen reactivity [10,11], that normally characterize iNKT, so that the NKT definition was expanded to include also 'diverse' NK T cells.

Here, we review recent advances in understanding the role of these various populations of CD1-reactive T cells

during infection. Increasingly, differences in the cellular expression patterns, subcellular trafficking, antigen-binding grooves, and phenotypes of the responding T cells make the case that CD1a, CD1b, CD1c, CD1d, and CD1e proteins have distinct functions. Further, new insights into nonhuman CD1 genes show that CD1 gene families are large and vary from species to species. These studies emphasize that CD1-restricted T cells and NK T cells are not synonymous, and make the case that understanding the functions of CD1 involves looking at and beyond NKT.

## CD1 presents lipids to the TCR

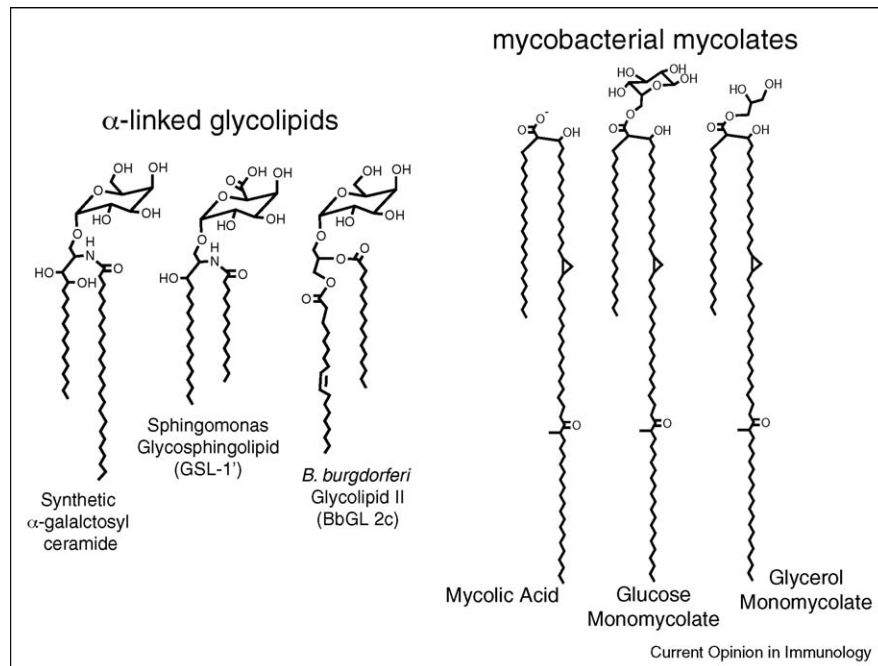
Many crystal structures of CD1 proteins bound to lipid antigens show that the alkyl chains are inserted into a hydrophobic groove, allowing presentation of carbohydrate, peptidic, or inorganic components of amphipathic antigens [12]. Recent studies of ternary complexes show how the T cell receptor  $\alpha$  and  $\beta$  chains of iNKT contact the CD1–glycolipid complex to form a binding footprint [13<sup>\*\*</sup>,14]. The NKT footprint is quite different from that of TCRs contacting peptide-MHC [15]. The iNKT TCRs are rotated and pushed laterally so that the  $\alpha$  chain binds near the center of CD1d, and the TCR  $\beta$  chain makes limited contact at the margin of CD1d.

These new crystal structures explain in detail why certain V $\alpha$  and V $\beta$  chains are conserved in natural iNKT populations. The CDR3 $\alpha$  loop plays the dominant role in binding to the CD1d platform, and the direct contacts with the protruding galactose unit are mediated by J $\alpha$ 18 residues. On the basis of mutational studies [16], molecular models [14], and other data [17], the global orientation of the TCR and other aspects of the recognition event visualized in these crystal structures are also likely conserved for natural  $\alpha$ -linked glycolipid antigens (Figure 1) [17–19]. Whether this rotated and laterally displaced footprint is used by diverse TCRs that recognize the glycolipid, lipid, and lipopeptide antigens presented by CD1a, CD1b, CD1c, or CD1d, remains to be seen.

## New bacterial targets

Unlike CD1a, CD1b, and CD1c, the CD1d protein is expressed in the liver and on certain gastrointestinal epithelia. Recent studies implicate CD1d and iNKT cells in controlling bacterial colonization of the gastrointestinal tract of mice [20]. Small intestinal colonization with both Gram-negative and Gram-positive organisms was increased in CD1d knockout mice, and organisms translocated across the intestinal epithelium. NKT cells

Figure 1



Structural homologies among CD1 ligands. Invariant NKT cells recognize structurally related glycolipid antigens that differ in the composition of their lipid anchors, but shared an  $\alpha$ -linked galactose unit. Three types of mycobacterial mycolate antigens are recognized by CD1b-restricted T cells. These foreign molecules have lipid anchors (C72–86) that are much larger than most self diacylglycerols or sphingolipids. CD1b is the only CD1 protein that is known to have a groove large enough to accept this type of antigen.

triggered CD1d-expressing Paneth cells to secrete antimicrobial peptides [20].

Invariant NKT cells respond to *Borrelia burgdorferi*, the causative agent of Lyme disease. Mice that are usually resistant to infection become more susceptible when the CD1d gene is deleted [21], and levels of protective *Borrelia*-specific IgM are reduced [22]. An antigenic target of the response was identified as the *B. burgdorferi* glycolipid II (BbGL-II), an  $\alpha$ -galactosyl diacylglycerol that constitutes 12% of lipid in this pathogen [17]. This antigen has obvious structural homology to  $\alpha$ -galactosyl ceramide (Figure 1), and BbGL-II loaded CD1d tetramers stain liver NKT cells during infection, indicating that the molecular mechanism of activation involves CD1–glycolipid–TCR contact. Infection of J $\alpha$ 18-deficient mice with *B. burgdorferi* resulted in prolonged arthritis and bacterial persistence, raising the possibility that lipid recognition by iNKT is relevant to a chronic syndrome [23]. Lastly, the recognition of *Borrelia* antigens by mouse NKT cells may be relevant to human Lyme disease because human NKT cells recognize a variant of BbGL-II [17], and unpublished studies have identified CD1 gene expression in human skin affected by acute borrelial infection (Yakimchuk and Moody, unpublished).

For CD1a, CD1b, and CD1c proteins, the most extensively studied bacterial pathogens are *Mycobacterium tuberculosis*

and *Mycobacterium leprae*. Following the discovery of free mycolic acid [24] and glucose monomycolate antigens [25], glycerol monomycolate isolated from *Mycobacterium bovis* was recently found to stimulate a human CD4+ T cell clone (Figure 1) [26]. Additionally, polyclonal mononuclear cells from humans latently infected with *M. tuberculosis* produced IFN- $\gamma$  in response to glycerol monomycolate at a higher frequency than cells from noninfected controls or actively infected tuberculosis patients. Along with studies of mannosyl phosphomycoketides, mycolic acids, glucose monomycolates, and sulfated trehalose lipids [27–29], this patient study supports the hypothesis that tuberculosis infection promotes expansion of human lipid reactive T cells *in vivo*. However, whether or not such responses are durable and subject to recall, such that vaccination might provide protection from infection, remains unknown.

### CD1 responses to viruses

NKT cells respond to viral infections involving HIV [30] HSV [31], and influenza [32]. These new observations raise the question of whether the mechanism of virus recognition involves cognate recognition of a virally produced antigen by the TCR, indirect recognition of cellular changes induced by viruses, or both. To date, no virally derived CD1 ligands have been identified. However, new evidence shows that CD1c presents an N-terminally acylated lipopeptide similar in sequence to HIV nuclear envelope factor (Nef) [33]. This finding

supports the hypothesis that cellular lipidation of viral proteins may generate antigens presented by CD1 [34]. In addition, viruses trigger Toll-receptors and cause other cellular changes in ways that can activate NKT cells indirectly via IL-12, altered CD1d expression, or increased production of endogenous sphingolipids [18,35,36]. For example, TLR ligation affects glycosphingolipid biosynthesis by dendritic cells and is associated with increased IFN- $\gamma$  release by NKT cells [37,38].

### Microbes upregulate CD1 expression

CD1d is constitutively expressed on thymocytes, B cells, monocytes, macrophages, and myeloid dendritic cells (DC) at various stages of maturation. In contrast, CD1a, CD1b, and CD1c proteins are absent on blood monocytes in the circulation, and two new studies help explain why. Serum immunoglobulin (Ig) and activators of the peroxisome proliferator activator receptor- $\gamma$  (PPAR- $\gamma$ ) are present in the serum and tonically inhibit CD1a, CD1b, and CD1c on human monocytes [39,40]. A human patient with common variable immunoglobulin deficiency expressed CD1a, CD1b, and CD1c, and this expression was downregulated after restoring immunoglobulin (Ig) to physiologic levels. Thus seems to be Ig necessary and sufficient for control of CD1 expression on circulating monocytes [39].

When monocytes exit the circulation, they are presumably released from inhibitory signals found at high concentrations in the serum, and they also encounter stimuli that increase CD1a, CD1b, or CD1c gene expression when present in tissues, as seen in patients with autoimmune disease [41] or infection [42]. The localized upregulation of CD1a, CD1b, and CD1c proteins on maturing myeloid DCs at sites of inflammation may allow CD1-expressing DCs and CD1-restricted T cells to generate proinflammatory positive feedback loops [43]. These CD1-inducing signals involve GM-CSF, IL-4, Toll-like receptor (TLR) 2, and TLR 5 [44,45]. Mycobacteria produce both ligands for CD1 proteins and signals that induce CD1, so they might provide dual signals to promote CD1-restricted T cell activation at the site of infection [46].

### Microbes downregulate CD1 expression

Several studies of monocyte derived DCs have found that CD1a-expressing, CD1b-expressing, and CD1c-expressing cells decline in number after exposure to mycobacteria in culture [47–50]. These *in vitro* studies led to the speculation that drastic losses of CD1 expression might occur at the site of mycobacterial infection *in vivo* and might represent a physiological means of immune evasion. However, other *in vitro* studies failed to confirm CD1 downregulation [44,51]. More importantly, studies of CD1 expression in the lungs, lymphoid tissues, and skin of humans with tuberculosis and leprosy do not support the immune evasion hypothesis because

CD1a-expressing, CD1b-expressing, and CD1c-expressing cells are found at high levels at sites of infection [42,45,52]. Although mycobacteria do not prevent CD1 expression in a general way in all humans, a subset of humans with the lepromatous form of leprosy have reduced levels of CD1 expression at the site of infection [42,53].

Viral infection also downregulates cell surface expression of CD1. The HIV peptide Nef interacts with human CD1d, leading to decreased expression on the cell surface and diminished activation of CD1d-restricted NKT cells [54]. Kaposi sarcoma-associated herpesvirus and herpes simplex virus 1 downregulate CD1 surface expression using distinct mechanisms involving ubiquitination and lysosomal targeting, respectively [31,55]. The detailed molecular mechanisms of rerouting identified here, as well as the precedent of virally mediated MHC class I immune evasion, now provide a rationale to examine CD1d expression during *in vivo* infection with viruses.

### CD1 beyond NKT cells

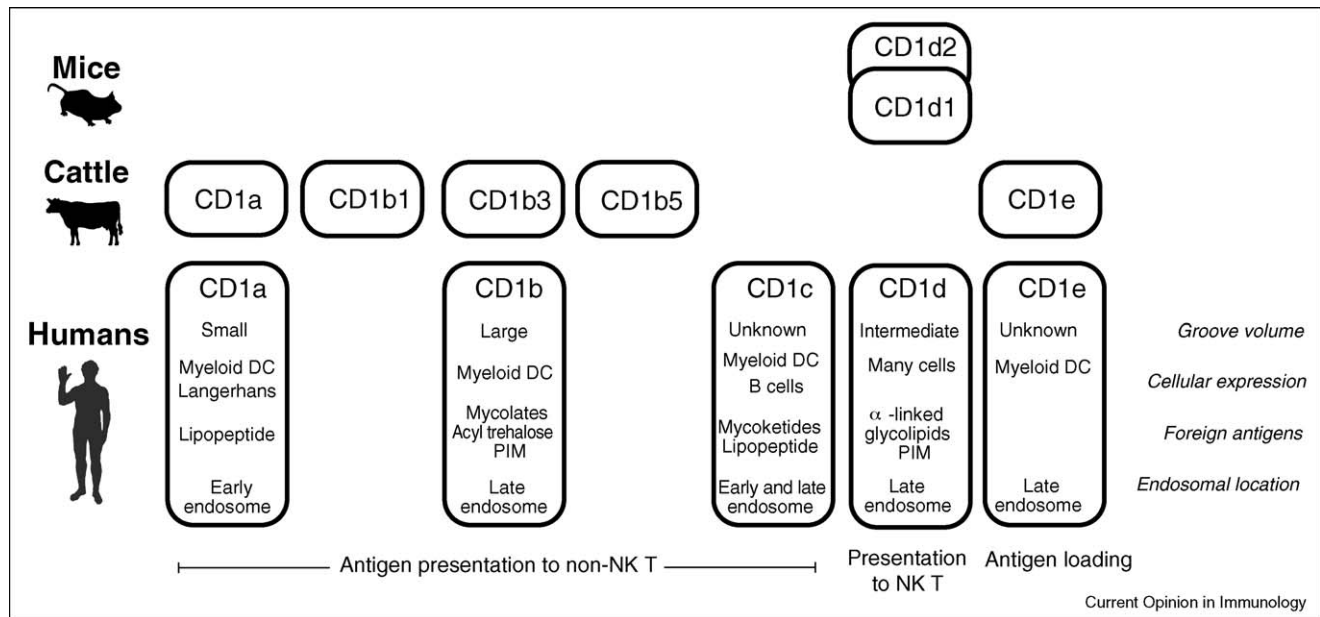
T cells recognizing human CD1a, CD1b, and CD1c or their mammalian orthologs do not fall under historical or modern definitions of NKT cells because they are not known to commonly express NK receptors or invariant TCRs, and they do not recognize CD1d (Figure 2). Lacking a catchy jargon term like iNKT, they are designated according to a simple, descriptive, and accurate naming convention: CD1x-restricted T cells, where x is the identifying CD1 gene (Figure 2). Many CD1-restricted T cells have functions that are distinct from iNKT cells because they express diverse TCRs, present chemically diverse antigens and recognize different types of cells (Figure 2). Also, the study of gene induction patterns on myeloid DCs makes clear that CD1a, CD1b, CD1c, and CD1e are linked to one another, whereas CD1d is different [44,56].

### Emerging pictures of isoform-specific function

Further, each of the five CD1 human proteins is emerging to have a distinct personality (Figure 2). Such gene-specific functions can be most readily understood for CD1e. After exiting the endoplasmic reticulum to the golgi apparatus, CD1e is diverted directly to endosomes without evidence of expression at the surface, suggesting that CD1e does not display antigens at the cell surface [57]. Recent studies show that unlike other CD1 proteins, CD1e is released into the lumen by proteolytic cleavage [58], where it can float freely and promote the molecular trimming of phosphatidylinositol antigens and their subsequent presentation by CD1b [59,60].

CD1b is emerging as the CD1 isoform that focuses on presenting large, exogenous foreign antigens that are

Figure 2



Humans, cows, and mice reflect differing patterns of CD1 gene conservation among mammalian species. Among CD1-restricted T cells, humans have NKT and non-NKT cells, whereas mice have only NKT cells, and cows have only non-NKT cells. Recent data suggest that the average number of CD1 genes in mammalian species is higher than in humans, so the mouse and other muroid rodents are distinctly atypical. CD1d1 and CD1d2 are highly homologous, but the three bovine genes that belong to the CD1b group have differing cytoplasmic tail sequences and differences in  $\alpha 1$  and  $\alpha 2$  domains that likely affect groove structure. This figure does not show the two bovine CD1b pseudogenes and the two bovine CD1d pseudogenes because they are predicted not to be translated into proteins.

taken up into lysosomes. With an interior volume of approximately 2300 cubic angstroms, the CD1b groove is much larger than that in CD1d and nearly twice the volume of the CD1a groove [61]. Correspondingly, the polyacylated trehaloses and mycolates, including the new glycerol monomycolate antigen, are lipids in the size range of C70–80, much larger than the C18–48 lipids presented by other CD1 isoforms. In fact, the longest C84–86 mycobacterial mycolates exceed the predicted volume of the CD1b groove and may protrude through a small opening at the bottom of the groove in the C' pocket [62]. The insertion of such large lipids into CD1b may be more dependent on lipid transfer proteins and acid-mediated steric changes than seen for other CD1 proteins [59,63,64]. CD1a and CD1c proteins show fewer requirements for acid-mediated loading and less prominently accumulate in the most acidic lysosomal compartments [65,66]. These biophysical properties of CD1b suggest that it is specialized to capture exogenous long chain foreign lipids in preference to shorter self-phosphodiacylglycerols, sphingolipids, and other self-lipids that comprise mammalian membranes (Figure 2). Correspondingly, T cells autoreactive to CD1b have been less frequently observed than those directly recognizing CD1a or CD1c [1,41,67,68].

### Surprising patterns of CD1 evolution

The discovery of an avian CD1 gene [69,70] and new evidence that it folds to form an antigen-binding pocket [71] proves that the CD1 system predates the emergence of mammals. However, unlike classical MHC class I molecules, which are present in all jawed vertebrates including fish, CD1 has not been identified in fish [72]. Also, recent studies suggest that CD1d proteins and NKT cells are apparently lacking in ruminants [73,74]. Figure 2 illustrates how modern species have survived while lacking any one of the five CD1 gene types. However most mammalian species have preserved large gene families, with up to 12 CD1 genes. Also, no mammalian species lacking all CD1 proteins has been identified since the discovery of the CD1 locus more than 20 years ago, implying that CD1 has an indispensable role in the mammalian immune system [75].

Thus, it appears CD1d and NKT cells per se are not universally conserved, but instead that the CD1 family is represented in some form in all amniote species. If all mammalian species express at least one CD1 protein, this implies that CD1 proteins have important immunological functions that were positively selected by evolutionary forces. Because one of the main functions of CD1 proteins is to present lipid antigens from pathogens, we speculate

that the size and composition of CD1 genes present in any given species reflects the results of pathogen exposure and selection pressure on an evolutionary time scale.

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