CD1b tetramers bind αβ T cell receptors to identify a mycobacterial glycolipid-reactive T cell repertoire in humans


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Microbial lipids activate T cells by binding directly to CD1 and T cell receptors (TCRs) or by indirect effects on antigen-presenting cells involving induction of lipid autoantigens, CD1 transcription, or cytokine release. To distinguish among direct and indirect mechanisms, we developed fluorescent human CD1b tetramers and measured T cell staining. CD1b tetramer staining of T cells requires glucose monomycolate (GMM) antigens, is specific for TCR structure, and is blocked by a recombinant clonotypic TCR comprised of TRAV17 and TRBV4-1, proving that CD1b–glycolipid complexes bind the TCR. GMM-loaded tetramers brightly stain a small subpopulation of blood-derived cells from humans infected with Mycobacterium tuberculosis, providing direct detection of a CD1b-reactive T cell repertoire. Polyclonal T cells from patients sorted with tetramers are activated by GMM antigens presented by CD1b. Whereas prior studies emphasized CD8+ and CD4−CD8− CD1b-restricted clones, CD1b tetramer-based studies show that nearly all cells express the CD4 co-receptor. These findings prove a cognate mechanism whereby CD1b–glycolipid complexes bind to TCRs. CD1b tetramers detect a natural CD1b-restricted T cell repertoire ex vivo with unexpected features, opening a new investigative path to study the human CD1 system.

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Ulrichs et al., 2003; Gilleron et al., 2004; Layre et al., 2009; Montamat-Sicotte et al., 2011). However, existing experimental models for study of group 1 CD1 function rely on activation assays that destroy the responding cells or focus on a limited number of in vitro–derived human T cell clones, which may not accurately reflect the in vivo phenotype. Consequently, information about the precise frequencies, effector functions, and possible host-protective effects of group 1 CD1–restricted T cells remain unknown. In contrast, the biological functions of CD1d and NKT cells have been broadly studied through mice deficient in CD1d or invariant Vα14 or Jα18 T cell receptors, as well as CD1d tetramers (Benlagha et al., 2000; Matsuda et al., 2000; Karadimitris et al., 2001; Gumperz et al., 2002). Tetramers take advantage of multimerization to generate high avidity fluorescent staining reagents that bind to individual clonotypic TCRs and selectively track antigen–specific T cells within much larger T cell populations (Altman et al., 1996). Tetramers can identify even rare antigen–specific T cells (Moon et al., 2007) for functional analysis, and CD1d tetramers have allowed single-cell analysis of NKT cells during infection, autoimmunity, and cancer (Benlagha et al., 2000; Matsuda et al., 2000; Karadimitris et al., 2001; Gumperz et al., 2002; Lee et al., 2002; Jahng et al., 2004; Arrenberg et al., 2010). Germline deletion of group 1 proteins is not currently feasible, so development of CD1 tetramers represents a promising method to study fresh antigen–specific T cells at the population level.

The basic principle of tetramer staining requires that TCRs bind to the antigen-presenting molecule and that this physical interaction is mediated by a groove-bound cognate antigen that physically ligates CD1 to the TCR. For CD1d, lipids like synthetic α-galactosylceramides mediate the trimolecular complex of CD1d–antigen–TCR (Borg et al., 2007), so an analogous function of glycolipids in mediating TCR contact with group 1 CD1 proteins is a leading model. However, recent studies have emphasized three alternate mechanisms whereby TCRs bind to CD1 or activate T cells but do not physically ligate CD1 and TCR. Lipopolysaccharide stimulates iNKT cell activation, not as a CD1d–ligand for CD1 proteins is not currently feasible, so development of CD1 tetramers represents a promising method to study fresh antigen–specific T cells at the population level.

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However, initial attempts to stain were unsuccessful, even after confirming monomer purity, biotinylation, and multimerization of CD1b proteins, as well as successful staining of NKT cells with control CD1d tetramers (Fig. S1 a and Fig. S2). Tetramer staining requires that key aspects of the cellular loading mechanism, which is particularly stringent for CD1b, be replicated in vitro. Therefore, we tested the sufficiency of in vitro conditions for antigen loading. In particular, the absence of cellular loading cofactors like saposin C (Winau et al., 2004) and the lack of essential cellular processing might alter structures in ways that are required for binding. After optimizing the time, pH, and chain length of the antigen, we were able to see high-level T cell activation with a plate bound CD1b monomer loaded with a C32 GMM antigen. This result confirmed that cellular processing and loading cofactors are not absolutely required and proved proper CD1b folding (Fig. 1 b).

**CD1b tetramers bind to T cells**

Using optimized conditions for loading CD1b with C32 GMM (Fig. S1 b), we observed CD1b tetramer staining of LDN5 (Fig. 1 c). Although CD1d tetramers bound to the synthetic superagonist α-galactosylceramide brightly stain CD1d-restricted T cells, self-antigens such as isogloboside 3 or sulfatide result in absent or moderate tetramer staining (Jahng et al., 2004; Zhou et al., 2004; Arrenberg et al., 2010). Therefore, it is notable that GMM, a natural foreign antigen, gives bright staining, such that the mean fluorescence intensity increases 10–100-fold after loading in optimized conditions (Fig. 1 c). To determine whether staining is specific for the structure of the antigen or is a result of nonspecific hydrophobic interactions resulting from the presence of lipids, we exposed CD1b to natural and synthetic antigens that recapitulate certain aspects of the C32 GMM structure. Whereas natural bacterial C32 GMM contains two chiral centers in the R conformation at the C2 and C3 positions of the mero­mycolate chain GMM (2R, 3R), synthetic C32 GMM dia­stereomers containing an S configuration at either position GMM (2R,3S + 2S,3R; Fig. 1 a) are nonantigenic (Moody et al., 2000a). Only C32 GMM (2R, 3R) mediated tetramer staining, indicating that chiral carbons, which determine the orientation of the glucose head group and β-hydroxyl unit relative to the TCR, are required for staining (Fig. 1 c).

In contrast, three preparations of natural bacterial GMMs containing a mean chain length of 32, 54, or 80 carbons and having 2R,3R configuration mediate bright staining (Fig. 1 d). Thus, C48 differences in overall lipid length can be tolerated, leading to high avidity binding. Whereas the length and conformation of the alkane chain hidden within the CD1d groove can significantly influence NKT cell activation (McCarthy et al., 2007), our results strongly suggest that CD1b-restricted TCR binding depends critically on head group positioning but can tolerate very large differences in lipid chain length. These results support and extend prior work suggesting that C80 lipids fill the entire groove, whereas shorter lipids partially fill the groove, allowing smaller spacer lipids to fill in the remaining volume (Gadola et al., 2002; Batuwangala et al., 2004; Garcia-Alles et al., 2006).

**CD1b tetramers bind the TCR-αβ complex**

The cognate model predicts that the surface target of tetramer binding is the heterodimer of rearranged TCR-α and -β chains normally expressed on the LDN5 T cell clone, TRAV 17, and TRBV4-1. However, a physical interaction of TCRs with any group 1 CD1 protein has not been previously observed. In addition to any alternate surface ligands on T cells that are unknown and might bind to CD1b, NK receptors (Carbone et al., 2000) and immunoglobulin-like proteins (ILT; Li et al., 2009) have been implicated in binding CD1 proteins. Therefore, we designed experiments to test the presence and specificity of a proposed interaction between CD1b with the clonotypic αβ TCR. CD1b tetramers made from the same type of construct failed to stain LDN5 but did stain the CD1d-restricted T cell clone J3N.5, implicating CD1 isoform–specific sequences in tetramer staining (Fig. S2).

Preincubation with anti-CD1b or anti-TRBV4-1 blocked tetramer staining to background (Fig. 2 a and Fig. S3 a). These
studies were consistent with interaction between CD1b and TCR VB4-1, if binding of monoclonal antibodies directly interfered with contact between TCR-β and the distal surface of CD1b. However, antibodies might have blocked staining in indirect ways involving sequestration of TCRs or CD1b proteins. To definitively test the role of the distal domains of TRBV4-1 and TRAV17 in physical contact with CD1b-GMM complexes, we produced soluble leucine-zipped TCRs comprised of the distal domains of the TCR-α and -β chains from LDN5 (sLDN5) and from CD8-2 (sCD8-2), a TRAV3, TRBV3-1 heterodimer which recognizes CD1a (Fig. 2 b and Fig. S3 b). Preincubation with sCD8-2 TCR did not inhibit tetramer staining, but sLDN5 TCR reduced tetramer staining to background levels (Fig. 2 c). Thus, the clonotypic TCR is necessary for CD1b-GMM binding to cells, proving a cognate TCR interaction with the CD1b-antigen complex, which is TCR specific and necessary for cellular binding.

CD1b tetramers detect GMM-specific T cells during TB infection

Development of tetramers for study of patient blood in the setting of an infectious disease requires low background among all types of cells present in PBMCs. To evaluate tetramer specificity, we mixed LDN5 T cells with CD1d-restricted NKT cells and found that GMM-loaded CD1b tetramers selectively stained the TRBV4-1+ clonotypic T cells, with no detectable staining over background of T cells with another TCR (Fig. S3 c). Also, titration of GMM-specific LDN5 T cells into fresh PBMC at known frequencies demonstrated that clonotypic T cells could be sensitively detected at the level of 0.01% of CD3+ cells. A discrete population of brightly staining cells was detected at frequencies near to their actual abundance when titrated into PBMC, so tetramers were not binding to T cells with diverse TCRs (Fig. S3 d). The potential problem of low but detectable background staining on increased interferon-γ responses in tuberculosis patients, indicating that lipid-reactive T cells likely expand during infection (Moody et al., 2000a; Ulrichs et al., 2003; Gilleron et al., 2004; Layre et al., 2009; Montamat-Sicotte et al., 2011). However, group 1 CD1-restricted T cells have never been detected directly ex vivo without stimulation. Tetramer detection is desirable because it rules out false positive results from cytokine production by non-T cells, indirect stimulation of cells by lipid adjuvants, or activation of MHC-restricted cells by contaminating peptide antigens. Also, tetramer-based sorting allows live cell capture for diverse functional and phenotypic studies. Among four subjects with positive intradermal purified protein derivative tests, we observed a similar pattern: a small percentage of blood T cells (~< 0.01%) stained brightly such that they were well separated from the pool of nonstaining cells (Fig. 3 a). The absolute frequency of cells was detected at similar rates among patients with latent (patients 1, 2, and 4) and active tuberculosis (patient 3), but staining was not observed in three healthy controls (Fig. S4 c). The detected frequency of T cells from individual patients was similar to one another and highly reproducible among experiments using blood from the same patient to assess different aspects of function and phenotype (Fig. 3, a and b; and Fig. 4, a and b).

To determine whether cells staining with CD1b-GMM complexes functionally recognized CD1b and GMM, we sorted CD3+ cells into tetramerhigh and tetramerlow populations (Fig. 3 b and Fig. S4 b). After recovery, total cells were tested in γ-interferon ELISPot using K562 cells that do or do not express CD1b (de Jong et al., 2010). Only tetramerhigh cells produced interferon-γ in response to GMM, and this response required CD1b expression (Fig. 3 b). Thus, CD1b tetramers directly identify populations of foreign glycolipid-reactive T cells in the blood of human tuberculosis patients that constitute a natural sub-repertoire of human αβ T cells. A precursor frequency of 0.01% is similar to that of human NKT cells identified using CD1d tetramers (Gumperz et al., 2002).
resulted from methods that depleted CD4 T cells in cultures to reduce MHC class II alloreactivity during cloning procedures. This was a key intervention that allowed the discovery of CD1-restricted T cells, but unbiased study of the CD1b and GMM repertoire now suggests that the CD4+ population dominates.

Identification of the CD1b and GMM reactive repertoire as TCR-αβ+CD4+ provides basic information about the CD1b-restricted T cell subset, which raises new questions about potential infection of these cells by HIV as well as a possible role of CD4 in development and effector function of this T cell subset. Furthermore, these results illustrate how any phenotypic question can be approached without confounders relating to in vitro growth or contaminating peptide antigens. Whereas NKT cells can be studied in CD1d- or Jα18-altered mice with human or mouse tetramers, there is no widely used small animal model for CD1b. Therefore, CD1b tetramers open a broad window for detailed study of the immunobiology of these cells. In contrast to highly polymorphic MHC proteins, which require haplotype matching for donors, the low rates of CD1 polymorphism in human populations allow one CD1b sequence in tetramer form to be readily applied to almost any human donor in ways that facilitate population studies. Prior clinical studies indicate that group 1 CD1 T cell responses are frequent in human tuberculosis patients (Moody et al., 2000a; Ulrichs et al., 2003; Gilleron et al., 2004; Layre et al., 2009; Montamat-Sicotte et al., 2011), so CD1 tetramers might be developed as a means of immunodiagnosis. Future studies will take advantage of this technology to determine whether the CD4+ T cell populations described in this

Distinct features of the CD1b-GMM repertoire

The first and subsequent studies of group 1 CD1-restricted clones show expression of either γδ or αβ TCRs (Porcelli et al., 1992; Spada et al., 2000) in combination with CD4, CD8, or neither co-receptor. We found that CD1b tetramerhigh T cells uniformly stain with antibody against invariant components of αβ TCRs in all four patients tested (Fig. 4 a). CD4 and CD8 represent key subset markers for NKT cell and MHC-restricted T cells because they strongly influence thymic selection and, thereby, determine effector functions. CD1b-restricted T cell clones can express CD4 or CD8 or neither co-receptor (Porcelli et al., 1992; Moody et al., 1997; Stenger et al., 1998), but any general view of co-receptor expression is limited by the small number of clones studied and the possibility of selective outgrowth in vitro. Given the large number of CD4+CD8- and CD8+ clones isolated in early work on CD1b, it was unexpected to observe that CD4 single-positive cells dominate the population of tetramer+ T cell populations cells in all four patients studied (Fig. 4 b). The absence of CD4 positivity in early clone-based studies likely
paper may be expanded in the blood and tissues of tuberculo­sis patients and express effector functions that contribute to control of mycobacterial infection, like interferon-γ, TNF-α, and granulysin (Stenger et al., 1998), or instead have un­expected roles in immunosuppression or immunopathology.

MATERIALS AND METHODS

Generation of soluble CD1b proteins. Soluble biotinylated CD1b monomers were produced in lentivirus-transduced HEK293 T cells by the National Institutes of Health Tetrramer Core Facility (Emory University, Atlanta, GA) and tetramerized with fluorescently labeled streptavidin. In brief, human β-2-microglobulin and the extracellular domain of CD1b were cloned into the expression vector pCMJ(4 (gift from J. Jacob, Emory University, Atlanta, GA). Lenti­viral particles were made in a second generation pack­aging system (Naldini et al., 1996). The light and heavy chains are expressed under control of the CMV promoter and are separated by the 2A-TcA pep­tide to generate two separate proteins from a single mRNA. The chains are followed by a C-terminal acidic or basic leucine zipper which stabilizes the complex and is used for affinity purification using the 2H11 monoclonal antibody (E. Reinherz, Harvard, Boston, MA). Purified monomers were enzymatically biotinylated at the BirA site at the C terminus of the heavy chain. Monomer purity and composition were confirmed by PAGE, and biotinyla­tion was confirmed by streptavidin bead pulldown assay. Functional activity was assayed by affixing biotinylated monomers at final concentration of 3 μg/ml onto 96-well streptavidin plates (Thermo Fisher Scientific) in PBS, pH 7.4, for 24 h at 37°C. Lipid antigens were sonicated in PBS for 2 min, added to the wells, and incubated for 24 h at 37°C before washing three times with 200 μl/well sterile PBS. 10^6 LDN5 cells were added in a total volume of 200 μl/well medium per well (RPMM). The plate was incubated for 24 h at 37°C after which culture supernatants were collected for HT2 bioassay.

Generation of soluble clonotypic TCR–αβ complexes. The cDNAs of the α and β chains of TCR (LDN5 and CDS.2) were cloned into the baculo­virus transfer vector pAcUW51 (BD). Honey Bee Melittin and envelope glycoprotein gp67 were used as signal peptides to optimize secretion of the α and β chains. The C terminus of the α chain has a thrombin cleavage site followed by an acidic zipper and hexahistidine tag. The β chain also has a thrombin cleavage site followed by a basic zipper and Strep-tag II (WSHPQFEK). The TCRs were expressed using the baculovirus cotransfec­tion method and the protein was secreted by SF9 insect cells. The secreted TCR, from the supernatant was purified using Nickel beads (QIAGEN), and a Strep-Tactin column (IBA), followed by gel-filtration chromatography. The pooled protein was concentrated to ~1 mg/ml in 20 mM Tris-HCl and 100 mM NaCl, pH 8.0, for purity by gel electrophoresis, and stored at ~80°C in small aliquots.

Loading CD1b monomers with GMM. GMM with differing average chain lengths produced by Rhodococcus equi (C32), Nocardia farcinica (C54), or Mycobacterium phlei (C80) was isolated as previously described (Moody et al., 2002); Antigen identity and purity were confirmed by biochemical analysis including thin layer chromatography and electrospray ionization mass spectrometry in the positive mode (LXQ Linear Ion Trap Mass Spectrometer; Thermo Fisher Scientific). Loading conditions were guided by results from T cell activation by monomorphic proteins and optimized by staining T cells after loading under conditions ranging in pH 5–7.4, temperature (20–37°C), concentration (10–100-fold excess antigen), and time (~2–4 h). Optimal staining was seen with GMM sonicated into 50 mM sodium citrate at pH 5.0 for 2 min, added at 40-fold molar excess to CD1b monomers, and incubated in a 37°C water bath for 2 h with vortexing every 15 min, followed by incuba­tion at room temperature for an additional 2 h before neutralization to pH 7.4 with 10 μl TRIS, pH 9. The duration of antigen loading and the purity of antigen preparations were critical for obtaining bright staining of T cells. After loading, CD1b monomers wereimerized using fluores­cently labeled streptavidin (Invitrogen) at a 1:5 molar ratio.

CD1b tetramer staining of clones. CD1b tetramers were validated by stain­ing the clone LDN5 (Moody et al., 1997). In brief; 2 × 10^5 T cells were treated with human AB serum for 10 min, washed, and then suspended in FACS buffer (PBS with 2% fetal calf serum;Gemini) and stained with 1 μg of fluorescently labeled CD1b tetramer for 60 min at room temperature in the dark. Cells were acquired in a FACS Canto flow cytometer (BD) and analyzed using FlowJo (Tree Star) software with doublet exclusion based on forward and side scatter in the presence or absence of anti-CD1b or recombinant TCRs.

Tetramer staining of human PBMC. After informed consent, 50 ml of blood were collected from healthy controls, asymptomatic tuberculin-positive subjects with no clinical or radiographical evidence of active tuberculosis, and active tuberculosis patients overseen by the institutional review boards of the Lemuel Shattuck Hospital (00000786) and Partners Healthcare (2002­P-000661) and the Harvard Committee on Microbiologic Safety (08–184). PBMCs were separated by Ficoll density gradient centrifugation. After thaw­ing, one million PBMCs were treated with human AB serum and stained with 1 μg tetramer for 40 min at room temperature in the dark, after which they were stained with violet fluorescent reactive dye (Invitrogen) to exclude dead cells. Cells were stained with monoclonal antibodies including CD3 (BD), CD14 (BD), and CD19 (eBioscience) for an additional 20 min and then fixed in 2% formaldehyde before FACS analysis. Cells from patient 1 were stained in 12 experiments; cells from patients 2, 3, and 4 were each stained four times. For functional assays, unfixed tetramer-positive cells were sorted using a FACS Aria flow cytometer and tested for antigen specificity using untransfected or CD1b–transfected K562 cells as antigen presenting cells in ELISpot assays (de Jong et al., 2010). Tetramer-positive cells were stained with TCR–αβ FITC (BD) or CD4–PE (BD).

Online supplemental material. Fig. S1 shows optimization of tetramer staining of the T cell clone LDN5. Fig. S2 shows a comparison of CD1b and CD1d tetramer staining. Fig. S3 shows tetramers staining clonotypic T cell receptors. Fig. S4 shows FACS gating strategies and tetramer staining of healthy controls. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20110665/DC1.

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