Check for updates

RESEARCH ARTICLE

REVISED The lipid transfer protein Saposin B does not directly bind CD1d for lipid antigen loading [version 2; peer review: 3 approved]

Maria Shamin [iD] [1,2], Tomasz H. Benedyk[2], Stephen C. Graham [iD] [2], Janet E. Deane [iD] [1,3]

[1]Cambridge Institute for Medical Research, University of Cambridge, Cambridge, CB2 0XY, UK
[2]Department of Pathology, University of Cambridge, Cambridge, CB2 1QP, UK
[3]Department of Clinical Neurosciences, University of Cambridge, Cambridge, CB2 0QQ, UK

Abstract

Background: Lipid antigens are presented on the surface of cells by the CD1 family of glycoproteins, which have structural and functional similarity to MHC class I molecules. The hydrophobic lipid antigens are embedded in membranes and inaccessible to the lumenal lipid-binding domain of CD1 molecules. Therefore, CD1 molecules require lipid transfer proteins for lipid loading and editing. CD1d is loaded with lipids in late endocytic compartments, and lipid transfer proteins of the saposin family have been shown to play a crucial role in this process. However, the mechanism by which saposins facilitate lipid binding to CD1 molecules is not known and is thought to involve transient interactions between protein components to ensure CD1-lipid complexes can be efficiently trafficked to the plasma membrane for antigen presentation. Of the four saposin proteins, the importance of Saposin B (SapB) for loading of CD1d is the most well-characterised. However, a direct interaction between CD1d and SapB has yet to be described.
Methods: In order to determine how SapB might load lipids onto CD1d, we used purified, recombinant CD1d and SapB and carried out a series of highly sensitive binding assays to monitor direct interactions. We performed equilibrium binding analysis, chemical cross-linking and co-crystallisation experiments, under a range of different conditions.
Results: We could not demonstrate a direct interaction between SapB and CD1d using any of these binding assays.
Conclusions: This work strongly indicates that the role of SapB in lipid loading does not involve direct binding to CD1d. We discuss the implication of this for our understanding of lipid loading of CD1d and propose several factors that may influence this process.

Keywords
CD1, prosaposin, lipid transfer protein, lipid antigens, lipid loading, lipid exchange, lipid binding proteins, sphingolipid storage disorder

Corresponding author: Janet E. Deane (jed55@cam.ac.uk)

Author roles: Shamin M: Conceptualization, Formal Analysis, Funding Acquisition, Investigation, Methodology, Visualization, Writing – Original Draft Preparation, Writing – Review & Editing; **Benedyk TH**: Methodology, Writing – Review & Editing; **Graham SC**: Funding Acquisition, Investigation, Methodology, Writing – Review & Editing; **Deane JE**: Conceptualization, Formal Analysis, Funding Acquisition, Investigation, Methodology, Project Administration, Supervision, Validation, Writing – Original Draft Preparation, Writing – Review & Editing

How to cite this article: Shamin M, Benedyk TH, Graham SC and Deane JE. **The lipid transfer protein Saposin B does not directly bind CD1d for lipid antigen loading [version 2; peer review: 3 approved]** Wellcome Open Research 2019, **4**:117 (https://doi.org/10.12688/wellcomeopenres.15368.2)

First published: 02 Aug 2019, **4**:117 (https://doi.org/10.12688/wellcomeopenres.15368.1)

REVISED **Amendments from Version 1**

We thank the reviewers for their insightful comments. We have revised the manuscript following their helpful suggestions as follows:

We acknowledge that the lack of a detectable interaction does not necessarily mean that there is no interaction. We have edited the abstract and discussed why an interaction too weak to be detected by the assays used in this study is unlikely to be physiologically relevant. This is supported by the fact that strong direct protein-protein interactions are crucial for several different lipid transfer pathways as detailed in the Discussion.

We have performed an additional equilibrium binding experiment where SapB was pre-loaded with the lipid α-GalCer while CD1d remained loaded with the endogenous human lipids with which it co-purifies. In agreement with our earlier results, no interaction was detected in this new experiment. This additional data is now included as part of Figure 2.

We have clarified the nature and relevance of the lipids expected to be associated with CD1d and SapB in the experiments reported in this manuscript and clarified that glycosylation of SapB is not required for lipid loading of CD1d.

Any further responses from the reviewers can be found at the end of the article

Introduction

The presentation of antigenic molecules is fundamental to host defence and immune regulation. The MHC class I and II molecules present peptide antigens to T cells and the molecular mechanisms of peptide loading and editing are relatively well understood[1–3]. However, the mechanism by which lipid antigens are loaded onto the CD1 family of antigen-presenting molecules remains poorly understood. CD1 molecules have structural similarity to MHC class I, including association with β-2-microglobulin (β_2m), but unlike MHC molecules, CD1 molecules are non-polymorphic and the antigen-binding grooves of CD1 molecules are extremely hydrophobic, allowing the binding of most classes of lipids including phospholipids, glycerolipids, lysolipids and glycolipids possessing a huge variety of glycosylated head groups[4].

Of the five CD1 family members, antigen presentation by CD1d is best characterised. CD1d undergoes complex cellular trafficking in a manner similar to that of MHC class II. Following synthesis in the endoplasmic reticulum, CD1d traffics via the Golgi apparatus to the plasma membrane, and is then internalised and trafficked through early and late endocytic compartments before being returned to the plasma membrane[5], where CD1d-lipid complexes are recognized by the T cell receptor (TCR) of natural killer T (NKT) cells. Invariant NKT (iNKT) cells, which bear an invariant TCR and are characteristically potently activated by recognition of CD1d loaded with the synthetic glycolipid α-galactosylceramide (α-GalCer), are innate-like T cells involved in the orchestration of immune responses[6].

Lipid antigens are embedded in cellular membranes[7] and thus are not directly accessible to the lumenal, lipid-binding groove of CD1 molecules. The loading of lipid antigen onto CD1 molecules therefore requires the action of lipid transfer proteins (LTPs) for efficient antigen presentation. The loading of lipids onto CD1d can occur in the ER, at the cell surface and in endocytic compartments. Relatively little is known about how lipid specificity is determined, and studies using secreted or recycling, surface-cleavable human CD1d found differences in the lipid repertoire bound to CD1d, reflecting the lipids present in the compartments through which it had trafficked[8–10]. Different LTPs are present in the different cellular locations where lipid antigen loading occurs and are likely to determine the lipid repertoire bound to CD1 molecules[11]. Interestingly, the late endocytic/lysosomal compartment is the site of both glycolipid catabolism and lipid loading of CD1d and the resident LTPs function in both these processes. Importantly, the antigenicity of glycolipids can be regulated by processing of their glycan headgoups prior to presentation to T cells, highlighting the complex interplay between these two pathways[12,13].

The LTPs present in the lysosomal compartments include ganglioside monosialic 2 activator (GM2A), Niemann-Pick type C 2 (NPC2) and four saposin (Sap) proteins. SapA, SapB, SapC and SapD are the products of the proteolytic cleavage of a prosaposin (PSAP) precursor and are each small, non-enzymatic proteins possessing three disulphide bonds that stabilise an extremely heat-resistant helical structure. The saposins can exist in a "closed" monomeric, globular conformation or, at low pH, adopt a more "open" conformation, forming higher-order oligomers enclosing a hydrophobic cavity into which lipid acyl chains can be buried[14–19]. Each saposin functions in conjunction with specific hydrolases to facilitate the degradation of different glycosphingolipids and the loss of saposin function phenotypically resembles the loss of the associated hydrolases[20–25]. There are two proposed mechanisms for how saposins assist in lipid presentation to hydrolases: the "solubiliser" model, whereby saposins encapsulate lipids within a hydrophobic oligomeric complex for presentation to soluble enzymes, and the "liftase" model, where saposins bind directly to membranes destabilising them, allowing membrane-associated hydrolases access to lipid substrates. Structural and cell-based evidence exists to support both these models[19,26–29]. These two models are also relevant for the proposed mechanisms by which saposins load lipids onto CD1 molecules[30]. SapB is thought to behave as a "solubiliser", forming protein-lipid complexes that enhance lipid loading of CD1 molecules, while SapC associates with membranes and may facilitate lipid loading at the membrane surface.

The evidence for saposin-mediated lipid loading of CD1 molecules comes from animal knockout studies, cell-based assays and *in vitro* assays. Knockout of PSAP in mice results in the dramatic loss of presentation of endogenous iNKT cell ligands by CD1d[31]. The presentation of exogenous lipid antigens, such as α-GalCer, is impaired in PSAP knockout or knockdown cells[31–34]. *In vitro* assays have identified that all the saposins, as well as the other lysosomal LTPs, GM2A and NPC2, are capable of transferring lipids onto CD1 molecules[31,35]. However, some LTPs appear to be more efficient than others at loading specific lipid antigens onto different CD1 molecules[30,33,36]. Specificity within the saposin family in this process has been explored via *in vitro* assays identifying SapB as the dominant saposin for the loading of lipid antigens onto CD1d. Specifically, incubation of CD1d with SapB and α-GalCer has been shown to enhance the stimulation of iNKT cells[33,34] and SapB

can mediate lipid binding to CD1d in T cell independent assays[33] suggesting a direct role for this specific saposin in lipid loading of CD1d. The ability of SapB to facilitate and enhance lipid exchange on CD1d has also been monitored *in vitro* via iNKT TCR binding to CD1d following incubation with lipids alone or lipids plus SapB[34]. These *in vitro* assays implicate SapB as a "lipid editor" that facilitates the loading and unloading of lipid antigens onto CD1d.

Due to the hydrophobic property of lipids, their exposure to aqueous solutions is thermodynamically unfavourable. Therefore, lipid transfer between hydrophobic lipid-binding cavities of proteins requires direct interaction of the protein components to provide continuous shielding of the lipid from the aqueous phase[37]. This hypothesis is supported by the fact that other known lipid transfer proteins directly interact with the protein receiving the lipid[38–40]. However, several publications report a failure to detect a direct interaction between saposins and human CD1d[11,33,34]. Unfortunately, these reports do not show any data or detail the approaches used to monitor binding and the implication is that these interactions exist but are weak and very transitory. Therefore we have used a number of robust and sensitive biochemical and structural techniques to monitor direct interactions between SapB and CD1d. Using multiple approaches in a range of conditions we do not observe any evidence of a direct interaction between CD1d and SapB.

Methods
Cloning and cell line production
Codon-optimised cDNA was synthesized (GeneArt) encoding human β_2m (residues 21-119, Uniprot P61769) and the extracellular domain of human CD1d (residues 20-301, Uniprot P15813) with a C-terminal hexahistiding tag (CD1d-H_6). A modified version of the piggyBac target protein plasmid PB-T-PAF[41] was constructed retaining the N-terminal secretion signal but with the Protein A fusion removed. CD1d-H_6 and β_2m were individually cloned into this modified vector, using *Spe*I and *Asc*I restriction-endonuclease sites, to produce PB-T-CD1d-H_6 and untagged PB-T-β_2m. For production of an inducible, stable co-expression cell line, HEK293F cells were quadruple-transfected with PB-T-CD1d-H_6, PB-T-β_2m, PB-RN and PBase using a DNA mass ratio of 5:5:1:1 and transfected cells were selected with geneticin using the established protocol for the piggyBac expression system[41].

Codon-optimised cDNA was synthesized (GeneArt) encoding the segment of human PSAP corresponding to SapB (residues 195-274, Uniprot P07602) and subcloned into the bacterial expression vector pET-15b using *Nco*I and *Xho*I restriction endonuclease sites to produce untagged protein. SapB was also subcloned into the mammalian expression vector pHLsec[42] using the restriction enzymes *Age*I and *Kpn*I to encode a C-terminally H_6-tagged protein.

Protein expression and purification
Protein expression of CD1d-β_2m complex in the HEK293F co-expression cell line was induced with 2 μg/mL doxycycline and expression media was collected over a 2 month period. CD1d-H_6 was purified from conditioned media by nickel affinity

chromatography in phosphate-buffered saline (PBS) pH 7.4 and eluted using PBS containing 300 mM imidazole. CD1d-β_2m was further purified by size exclusion chromatography on a Superdex 200 column (GE Healthcare) equilibrated in cross-linking buffer (20 mM HEPES pH 7.0, 150 mM NaCl) for interaction assays or distinct buffers (described below) for crystallisation experiments. CD1d-β_2m was concentrated to 2 mg/mL and stored at 4 °C for up to one month.

To produce deglycosylated CD1d-β_2m, cells were treated with 5 μM kifunensine at the same time as protein expression was induced. CD1d-β_2m was purified by nickel affinity purification and eluted with 100 mM citrate pH 4. CD1d-β_2m protein was buffer exchanged into 100 mM citrate pH 5.5, using repeated rounds of dilution and concentration using a centrifugal concentrator, concentrated to 2 mg/mL and incubated with 3125 units of Endoglycosidase H (Endo H; New England Biolabs) per milligram of protein for 3 hours at room temperature. Deglycosylated CD1d-β_2m was purified by size exclusion chromatography (as described above).

Untagged SapB was expressed in *Escherichia coli* Origami (DE3) cells and purified as described previously[43]. Briefly, cleared lysate was heat-treated, precipitated proteins were cleared by centrifugation and supernatant containing SapB was dialysed overnight in the presence of 20 μg/mL DNAse against anion exchange buffer (50 mM Tris pH 7.4, 25 mM NaCl). SapB was further purified by anion exchange chromatography (HiTrap QSepharose column) followed by size-exclusion chromatography (HiLoad 16/600 Superdex 75 column) in 50 mM Tris pH 7.4, 150 mM NaCl. Purified SapB was concentrated to 16 mg/mL and stored at 4 °C.

His$_6$-tagged SapB was expressed in HEK293F cells by polyethylenimine-based transient transfection. After 4 days, SapB-H_6 was purified from conditioned media by nickel affinity and size exclusion chromatography with a Superdex 75 column (GE Healthcare) in cross-linking buffer. Prior to crystallisation trials (but not cross-linking assays), the tag was removed by incubation with 1.2 U/mL Carboxypeptidase A-agarose at 25°C overnight followed by incubation with Ni-NTA resin to remove tagged protein. The supernatant containing untagged SapB was separated from Carboxypeptidase A-agarose and Ni-NTA agarose by passing through a gravity flow column.

α-GalCer loading
Endogenously purified lipids were exchanged for the lipid α-GalCer (Avanti Lipids) based on a protocol used to obtain crystal structures of α-GalCer-loaded CD1d[44,45]. Lipid was resuspended in DMSO at 1 mg/mL and dissolved by heating the solution at 80°C for 10 min, with brief sonication and vortexing every 3 minutes. CD1d-β_2m and SapB were incubated with a 3-fold molar excess of α-GalCer in PBS overnight at room temperature. α-GalCer-loaded proteins were then separated from free α-GalCer by size exclusion chromatography with a Superdex 200 10/300 column equilibrated in 20 mM HEPES pH 7.0, 150 mM NaCl. α-GalCer-loaded proteins were used within 24 hours after size exclusion chromatography to avoid significant hydrolysis of the lipid.

Equilibrium binding assay

Ni-NTA agarose beads were loaded with a saturating amount of CD1d-β_2m, and complete capture of CD1d-β_2m was verified by measuring the absorbance of the supernatant at 280 nm. Saturated beads were washed three times in equilibrium assay buffer (50 mM HEPES pH 7.0, 150 mM NaCl, 0.05% digitonin, 2.5 mM CaCl$_2$, 2.5 mM MgCl$_2$). Serial dilutions (1:1) of CD1d-β_2m-saturated beads were made in equilibrium assay buffer supplemented with unloaded Ni-NTA beads to equalize the bead volume across all samples. SapB was added at a final concentration of 680 nM in equilibrium assay buffer. The reaction was incubated with shaking at room temperature for 1 hour. The supernatant containing unbound SapB was separated from the beads by centrifugation (800g, 2 min) followed by separation with a Micro-Spin column (Pierce) (800g, 2 min) to remove all beads. The supernatant was analysed by SDS-PAGE followed by staining with SYPRO Ruby. For analysis of bead samples, these were boiled in SDS-PAGE loading dye, separated by SDS-PAGE and detected by Coomassie staining.

Cross-linking assay

Amine-reactive cross-linking agents disuccinimidyl sulfoxide (DSSO) and PEGylated bis(sulfosuccinimidyl)suberate (BS(PEG)$_5$) were dissolved in DMSO and added to 10 μM CD1d-β_2m alone, 20 μM SapB alone or 10 μM CD1d + 20 μM SapB with final cross-linker concentrations of 0, 200 μM or 1 mM in cross-linking buffer. The reaction was incubated for 30 min at room temperature and terminated by incubation with 20 mM Tris pH 8 for 15 min. The reaction products were analysed by SDS-PAGE followed by Coomassie staining.

Crystallography

Crystallization experiments were performed in 96-well nanolitre-scale sitting drops (200 nL protein plus 200 nL of precipitant) equilibrated at 20°C against 80 μL reservoirs of precipitant. The crystals reported here were grown in drops containing the following components:

Crystal form (i) (Figure 4B) contained glycosylated CD1d-H$_6$-β_2m (13.5 mg/mL) + 2-fold molar excess of unglycosylated SapB (4.7 mg/mL) in 150 mM NaCl, 50 mM Tris pH 7.4 and grew against a reservoir containing 20% w/v polyethylene glycol (PEG) 6000, 0.1 M HEPES pH 7 and 0.2 M calcium chloride.

Crystal form (ii) (Figure 4B) contained glycosylated CD1d-H$_6$-β_2m (12.4 mg/mL) + 2-fold molar excess of glycosylated SapB (after tag removal) (4.3 mg/mL) in 20 mM HEPES pH 7.0, 150 mM NaCl and grew against a reservoir containing 20 mM 1,6-hexanediol, 20 mM 1-butanol, 20 mM 1,2-propanediol, 20 mM 2-propanol, 20 mM 1,4-butanediol, 20 mM 1,3-propanediol, 0.1 M bicine/Trizma base pH 8.5, 12.5% w/v PEG 1000, 12.5% w/v PEG 3350 and 12.5% v/v 2-methyl-2,4-pentanediol.

Crystal form (iii) (Figure 4B) contained α-GalCer-loaded glycosylated CD1d-H$_6$-β_2m (11.9 mg/mL) + 2-fold molar excess of α-GalCer-loaded unglycosylated SapB (4.2 mg/mL) in 50 mM Tris pH 7.4, 150 mM NaCl and grew against a reservoir containing 0.1 M sodium acetate pH 5.0, 20% w/v PEG 6000 and 0.2 M ammonium chloride.

Crystal form (iv) (Figure 4B) contained deglycosylated CD1d-H$_6$-β_2m (13.3 mg/mL) + 2-fold molar excess of unglycosylated SapB (4.7 mg/mL) in 20 mM citrate pH 6, 150 mM NaCl, and grew against a reservoir containing 16% v/v PEG 500 monomethylether, 8% w/v PEG 20000, 0.1 M bicine/Trizma base pH 8.5, 30 mM sodium nitrate, 30 mM sodium phosphate dibasic and 30 mM ammonium sulfate.

Crystal form (v) (Figure 4D) contained deglycosylated CD1d-H$_6$-β_2m (6.5 mg/mL) + 2-fold molar excess of unglycosylated SapB (2.3 mg/mL) in 100 mM citrate pH 6.0, 150 mM NaCl and grew against a reservoir containing 20% w/v PEG 3350, 0.1 M bis-Tris propane pH 7.5 and 0.2 M di-sodium malonate.

X-ray data collection and molecular replacement

Crystals were cryoprotected in reservoir solution supplemented with 20% v/v glycerol and flash-cooled by plunging into liquid nitrogen. Diffraction data were recorded at Diamond Light Source (DLS) on beamlines I03, I04 and I04-1. Diffraction data were indexed and integrated using the automated data processing pipelines at DLS[46] implementing XIA2 DIALS[47], XIA2 3dii or autoPROC and STARANISO[48] depending on the extent of anisotropic diffraction, then scaled and merged using AIMLESS[49]. Version numbers for crystallography data processing software are detailed in Table 1. The model for molecular replacement was generated using the published structure of CD1d-β_2m bound to lysophosphatidylcholine[50] (PDB ID 3U0P, chains A and B), using phenix.sculptor (Phenix v1.14-3260)[51,52] to remove the lipid ligand from the model and revert the glycosylation site mutations present in this structure. Molecular replacement was performed using phenix.phaser[53] and was

Table 1. Crystallography data processing software.

	Crystal (iii)	Crystal (iv)	Crystal (v)
Processing software	autoPROC (v1.0.5) and STARANISO (v1.10.15)	XIA2 (v0.5.771) 3dii (version January 26, 2018)	XIA2 (v0.5.764) DIALS (v1.12.2)
Scaling software	AIMLESS (v0.7.2)	AIMLESS (v0.7.3)	AIMLESS (v0.7.3)

followed by rigid body refinement using phenix.refine[54]. Molecular replacement into the highly anisotropic data (Crystal form (iii)) was carried out using both the isotropic and anisotropically processed data, resulting in the same solution. Maps were inspected using COOT (v0.8.9)[55]. Structure figures were rendered using PyMOL (v2.1.0, Schrödinger LLC).

SDS-PAGE analysis of crystals
For each crystallisation condition tested, several crystals were harvested from the crystallisation drop and washed by transferring to a drop of reservoir solution to remove uncrystallised protein components. Crystals were then transferred to a second drop of reservoir solution and dissolved in SDS-PAGE loading buffer. Alternatively, large crystals from which data had been collected at the synchrotron were recovered into SDS-PAGE loading buffer from the crystal-mounting loop. Individual crystal components were analysed by SDS-PAGE followed by Coomassie staining.

Results
Purification of CD1d-β_2m complex from a human cell line
Several strategies have been developed previously for the purification of CD1d including refolding from *E. coli* inclusion bodies[56], baculovirus-insect cell expression[50] and mammalian expression systems[57]. An important consideration for CD1d protein expression and purification is the inclusion of the essential partner protein β_2m. In a manner similar to the heavy chain of MHC class I, CD1d non-covalently associates with β_2m and this association is required for maturation of its four glycan chains[58]. In order to obtain high quality, near-native CD1d protein for *in vitro* studies, we chose to co-express human CD1d with β_2m in the mammalian suspension cell line HEK293F as this would confer correct folding, native post-translational modification and full glycosylation of CD1d. Initial trials using polyethylenimine-based transient co-transfection of CD1d and β_2m resulted in very low yields. Thus we used a piggyBac-expression system[41] to establish stable and inducible co-expression of full-length, untagged β_2m with the ectodomain of CD1d possessing a C-terminal hexahistidine tag (H_6) (Figure 1A). Both proteins were expressed with an N-terminal secretion signal sequence targeting synthesis to the endoplasmic reticulum, resulting in protein secretion into the media. This expression strategy results in CD1d molecules that are bound to endogenous human lipids acquired during folding in the endoplasmic reticulum and trafficking through the Golgi apparatus. CD1d-H_6 was purified from conditioned media by nickel affinity chromatography followed by size exclusion chromatography (Figure 1B and C). Untagged β_2m co-purified with CD1d, indicating that both proteins are correctly folded and form a stable complex. Although some CD1d alone was purified, we were able to separate this from CD1d-β_2m following size exclusion (Figure 1C). Using this expression system, we obtained a high yield (1 mg/100 mL media) of very pure CD1d-β_2m protein. The yield was over 10 times higher than that obtained with transient co-transfection in the same cell line.

Purification of SapB
The four saposin proteins (SapA-D) are produced from the proteolytic cleavage of the precursor protein PSAP which normally occurs upon delivery to the lysosome. To produce recombinant SapB alone, the segment of human PSAP corresponding to SapB (Figure 1D) was expressed in *E. coli*. Untagged SapB was purified following a well-established protocol[43] that exploits the heat stability of saposins followed by anion exchange and size exclusion chromatography (Figure 1E and F). Previous structural studies with *E. coli*-expressed SapB identified that it exists as a tight dimer that co-purifies with *E. coli* phosphatidylethanolamine[14].

CD1d binding to SapB is not detectable using *in vitro* interaction assays
Classical pull-down experiments involve the capture and immobilisation onto resin of a tagged bait protein followed by incubation with prey protein. Subsequent wash steps remove unbound protein leaving behind protein complexes for detection. However, as the concentration of free prey protein is reduced at each wash, the equilibrium is pushed towards complex dissociation, meaning this method is not well suited for the capture of weak or transient interactions. Using this approach, no interaction was detectable between immobilised CD1d-β_2m and SapB. Therefore, an alternative approach was adopted to overcome the limitations of prey-depletion by using an *in vitro* equilibrium binding assay (Figure 2A). In this assay, the bait is bound to beads at a range of concentrations and the prey is added at a low, limiting concentration. Following incubation, and no wash steps, the supernatant is separated from the beads and unbound prey is detected using the sensitive protein dye SYPRO Ruby. Monitoring the depletion of prey from the supernatant by the large excess of bait protein, rather than monitoring complex formation directly, represents a more sensitive measure of binding and thus is optimised for weak or transient interactions[59].

Equilibrium binding assays were carried out using CD1d-β_2m as bait at a concentration range of 0-40 μM and with SapB as the prey at 680 nM. Previous *in vitro* studies have identified that SapB can load α-GalCer onto CD1d at a pH range between 5 and 8[33]. Although this exchange appears to be most efficient at pH 6, this pH causes partial dissociation of the CD1d His-tag from the Ni-NTA resin. Therefore, the equilibrium binding assay was performed at pH 7. Previous work, and our preliminary experiments, showed that β_2m dissociates from CD1d in the presence of detergent[60]. However, the gentle detergent digitonin was found to cause minimal disruption of the CD1d-β_2m complex[60] and was used in this assay. Despite the use of this optimised approach, no binding of SapB to CD1d could be detected (Figure 2B). In these conditions, at high CD1d-β_2m concentrations, a small amount of β_2m is detectable in the supernatant due to dissociation from CD1d (Figure 2B). By comparing how little appears to be lost based on the Coomassie-stained bead samples this highlights the sensitivity of this technique and of the SYPRO Ruby stain for protein detection.
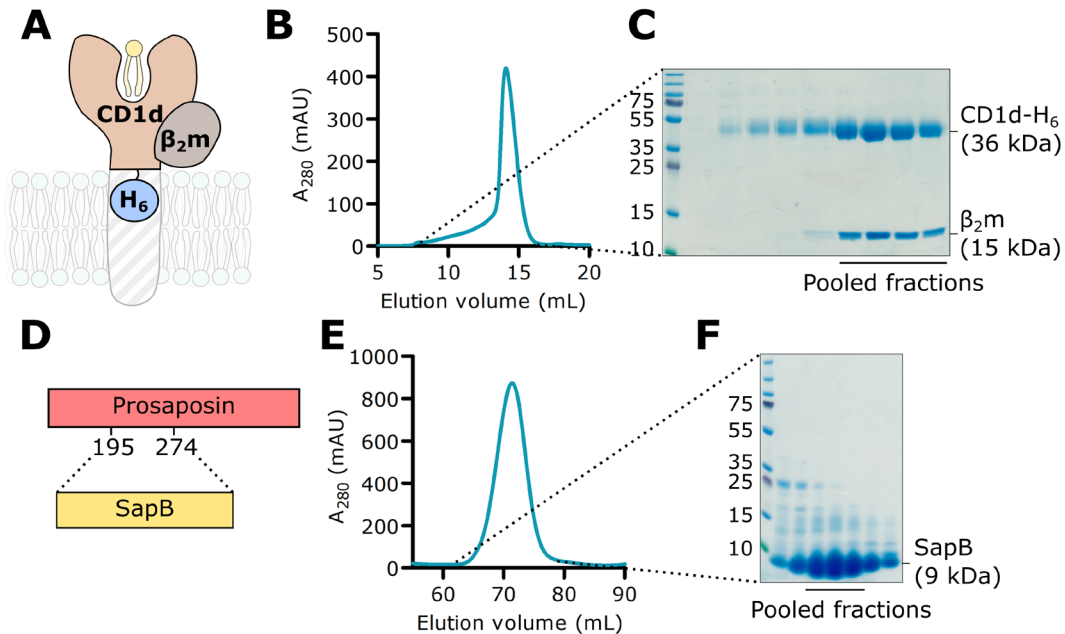
Figure 1. Purification of CD1d-β_2m and SapB. A. A His-tagged construct encoding the extracellular domain of CD1d (CD1d-H$_6$) was co-expressed with untagged full-length β_2m in mammalian cells. **B**. Size exclusion chromatography (SEC) showing co-purification of CD1d-H$_6$ with β_2m. **C**. SDS-PAGE of SEC fractions. The indicated fractions containing β_2m-associated CD1d were used in subsequent experiments. **D**. Untagged SapB (residues 195-274 of the precursor protein PSAP) was expressed in *E. coli*. **E**. SEC of SapB after multi-step purification. **F**. SDS-PAGE of SEC fractions. The indicated fractions were used in subsequent experiments.
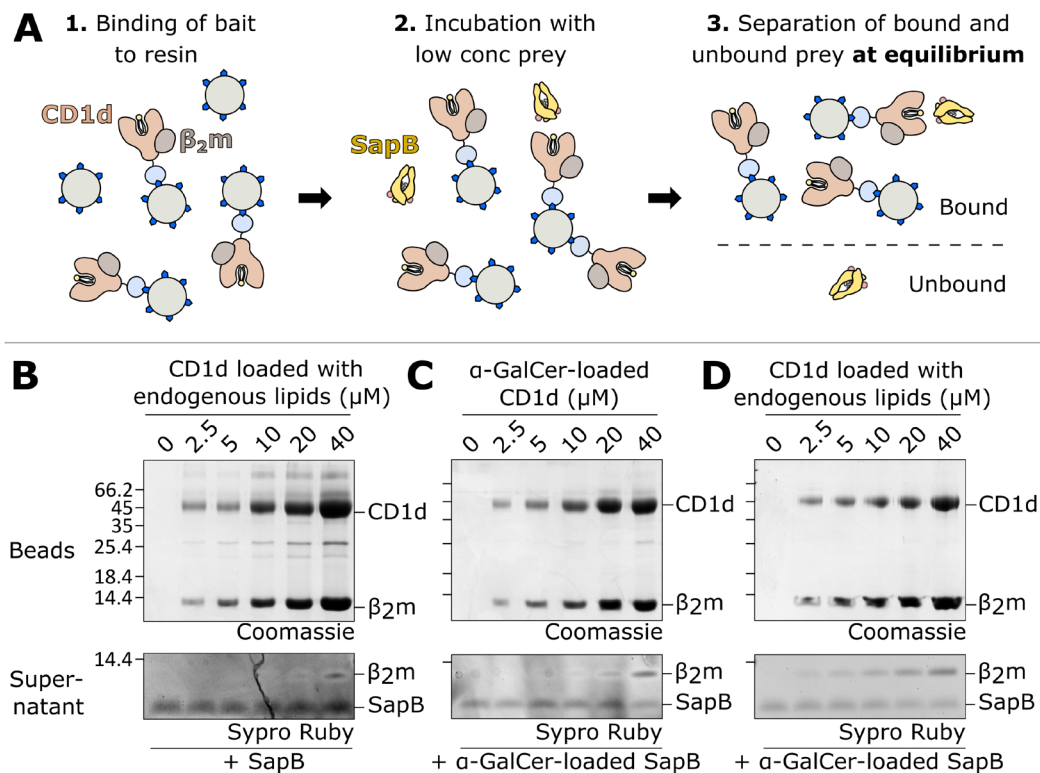

Figure 2. Equilibrium binding assay of CD1d-β_2m and SapB. A. Schematic diagram illustrating the equilibrium binding assay protocol. **B**. Increasing concentrations of CD1d-β_2m were bound to beads and detected by Coomassie-stained SDS-PAGE. After incubation with SapB, unbound SapB was detected in supernatants by SYPRO Ruby-stained SDS-PAGE. The lipids bound to CD1d-β_2m and SapB in this experiment are the endogenous lipids they co-purify with following expression in human cells and *E. coli*, respectively. **C**. As for panel **B** but with CD1d-β_2m and SapB both pre-loaded with the lipid α-GalCer. **D**. As for panel **B** but with only SapB pre-loaded with the lipid α-GalCer.

Previous studies have shown that the ectodomain of CD1d co-purifies with a broad range of cellular lipids following synthesis and trafficking through the secretory pathway, but is likely to be primarily loaded with sphingomyelin[8–10]. SapB co-purifies with *E. coli* phosphatidylethanolamine[14], a lipid species that has also been shown to bind CD1d[61]. Although it seems likely that this lipid composition for SapB and CD1d should be compatible with protein-protein interactions required for lipid exchange, lipid loading onto CD1d has only been formally demonstrated *in vitro* for a few lipids, and in particular α-GalCer[33,34]. Therefore, both proteins were pre-loaded with α-GalCer prior to performing the equilibrium binding assay. However, this variation also did not result in a detectable interaction between SapB and CD1d (Figure 2C). To exclude the possibility that a strong interaction between CD1d and SapB only occurs when SapB exchanges a lower affinity antigen for α-GalCer, we repeated the equilibrium binding assay where SapB was pre-loaded with α-GalCer while CD1d retained the co-purified endogenous lipids (Figure 2D). Again, there was no substantial depletion of SapB from the supernatant in this assay. These results strongly suggest that CD1d and SapB do not directly interact *in vitro*, or that their interaction is extremely weak with a $K_d > 40$ μM.

In vitro cross-linking does not capture an interaction between CD1d and SapB

Cross-linking of proteins using short chemical tethers that react with surface-exposed lysine side-chains can be used to capture transient or weak interactions. Both CD1d and SapB have several surface-exposed lysines, and of particular importance, lysine residues are present near the lipid-binding groove of CD1d where we would predict SapB to bind (Figure 3A and B). Therefore, it is possible that CD1d and SapB interact in a way that is amenable to intermolecular cross-linking of surface lysines by amine-reactive cross-linkers. We used cross-linkers of different lengths to maximise the chances of capturing an interaction: DSSO, with a 10.3 Å spacer arm, and BS(PEG)₅, with a 21.7 Å spacer arm. CD1d-β₂m and SapB were incubated with these cross-linkers either alone or following mixing (Figure 3C). For the CD1d-β₂m samples alone, cross-linking between CD1d and β₂m is clearly evident, as expected. There is also some evidence of additional higher order oligomers, probably due to the large number of surface lysines on both CD1d and β₂m. However, no additional cross-linking products were observed when CD1d-β₂m and SapB were incubated together with the cross-linkers. This indicates that CD1d-β₂m and SapB do not interact together in a conformation that is amenable to cross-linking.

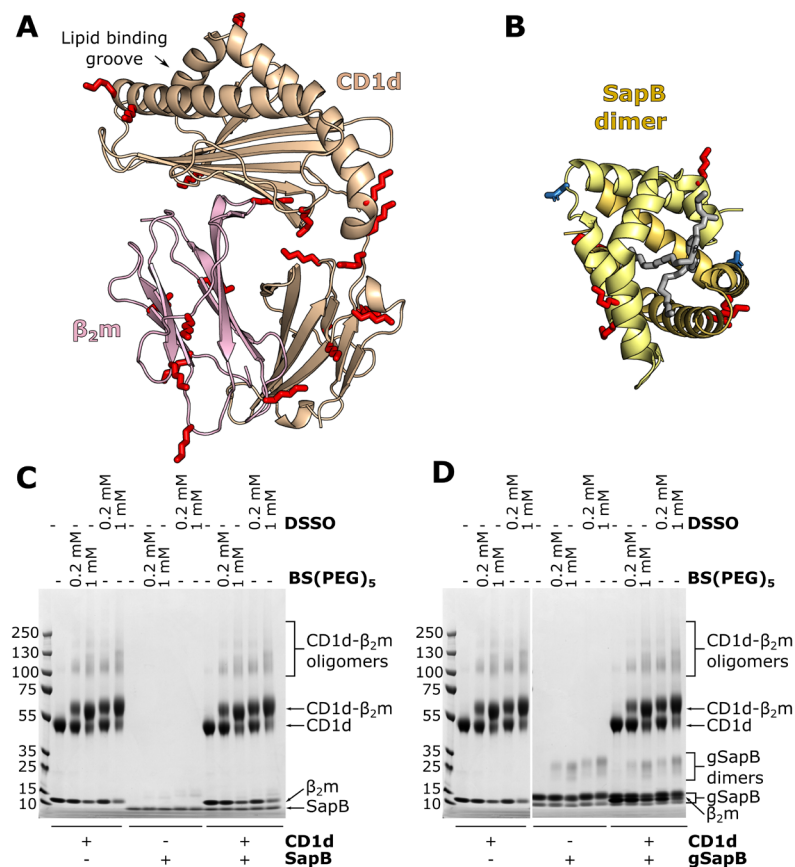**Figure 3. *In vitro* cross-linking of CD1d-β₂m and SapB. A**. Ribbon diagram of the structure of CD1d (beige) and β₂m (pink)(PDB ID 3U0P) with the lipid antigen groove labelled (arrow). Surface-accessible lysine residues available for cross-linking are highlighted (red sticks). **B**. Ribbon diagram of the structure of a SapB dimer (yellow and orange, PDB ID 1N69) with bound lipid (in gray). Lysine residues are highlighted as in panel **A**. The N-linked glycosylation site of SapB is highlighted (blue sticks). **C**. Coomassie-stained SDS-PAGE of CD1d-β₂m and unglycosylated SapB samples following incubation with cross-linkers of different lengths: DSSO (10.3 Å) or BS(PEG)₅ (21.7 Å). **D**. As for panel **C** but using CD1d-β₂m and glycosylated SapB (gSapB).

SapB possesses one N-linked glycosylation site on residue Asn21 (Figure 3B), which remains unglycosylated when expressed in *E. coli*. Although unglycosylated SapB loads lipids onto CD1d[33,34], it is possible that this glycan on SapB may increase its affinity for CD1d. Therefore, we repeated the cross-linking experiment following expression of His-tagged SapB in mammalian HEK293F cells, enabling the purification of glycosylated protein. Following purification, two SapB-H$_6$ species were present, with molecular weights of approximately 10 and 13 kDa, likely corresponding to unglycosylated and glycosylated SapB-H$_6$ (Figure 3D). It was not possible to separate these two SapB species, likely due to SapB dimerization, and so cross-linking experiments were carried out using this mixed sample (Figure 3D). However, we again did not observe formation of any additional cross-linked products when CD1d-β$_2$m was incubated with glycosylated SapB-H$_6$. We note that although the same amount of unglycosylated SapB (Figure 3C) and glycosylated SapB (Figure 3D) were used in cross-linking assays, the Coomassie-stained bands corresponding to glycosylated SapB appear much stronger. This increased staining may be due to the additional histidine residues in the affinity tag increasing the amount of Coomassie reagent binding to this small protein.

CD1d-β$_2$m and SapB do not co-crystallise

An alternative method to capture weak, transient protein-protein interactions is to attempt co-crystallisation. In this experiment both protein components are mixed together at a range of concentrations and different molar ratios, then subjected to crystallisation trials. The benefit of using the sitting-drop vapour diffusion approach is that during the experiment the drop containing protein and precipitant gradually equilibrates with

the reservoir, generally resulting in reduced drop volume and the progressive increase in concentration of the drop components. In this way, the protein components are steadily concentrated together with the aim of capturing an interaction that is otherwise extremely hard to measure using biochemical and biophysical assays[62].

Extensive crystallisation trials containing both CD1d-β$_2$m and SapB were performed, varying the following parameters: (1) protein concentration (6-13 mg/mL CD1d-β$_2$m, 2-6 mg/mL SapB), (2) molar ratio of SapB to CD1d, taking into account the predicted dimeric state of SapB (2:1-3:1 SapB to CD1d); (3) full glycosylation or deglycosylation of protein components; and (4) lipid exchange for α-GalCer. Figure 4A shows an example of the high purity of the protein components that went into crystallisation trials. These experiments yielded several different crystals in a range of conditions, a subset of which are shown in Figure 4B. To determine the composition of these crystals, two approaches were used depending on the quality of the crystals grown. The first approach, which can be used for any protein crystal, involves harvesting and washing the crystals in reservoir solution to remove residual uncrystallised components, then separating the proteins by SDS-PAGE followed by detection using Coomassie staining (Figure 4C, each gel lane corresponds to the above crystal in panel 4B). This revealed that both SapB and CD1d-β$_2$m were capable of forming crystals but in none of the crystals grown did both components crystallise together. The second approach used was to collect diffraction data for any crystals that diffracted to 5 Å resolution or better, then use molecular replacement to confirm the contents of the asymmetric unit (Table 2). Three crystal forms satisfied this criteria, including two that had also
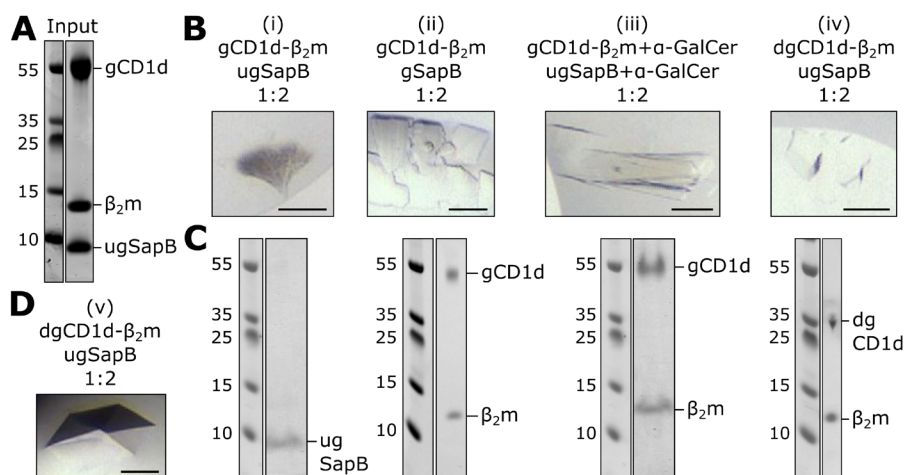

Figure 4. Crystallisation trials of CD1d-β$_2$m and SapB. A. Coomassie-stained SDS-PAGE example of the purified protein sample used in crystallisation trials. **B**. Examples of four crystals (i)–(iv) grown in a range of conditions using different protein compositions. Scale bar represents 100 μm. **C**. Coomassie-stained SDS-PAGE of harvested and washed crystals shown in panel **B**. **D**. Image of the crystal that diffracted to highest resolution as described in Table 2. Scale bar represents 100 μm. Abbreviations: gCD1d-glycosylated CD1d, dgCD1d-deglycosylated CD1d, gSapB-glycosylated SapB, and ugSapB-unglycosylated SapB.

Table 2. Data collection statistics and molecular replacement solutions. For Crystal 4B (iii) statistics have been included for data from a single crystal before (isotropic) and after anisotropic truncation and scaling using STARANISO. Values in parentheses are for the highest-resolution shell.

Data collection	Crystal Fig 4B (iii)		Crystal Fig. 4B (iv)	Crystal Fig. 4D (v)
Beamline	I04		I04-1	I03
Wavelength (Å)	0.9999		0.9159	0.9793
Processing package	autoPROC + STARANISO		XIA2 3dii	XIA2 DIALS
Space group	$C\,2$		$P\,2_1$	$C\,2$
Cell dimensions				
a,b,c (Å)	273.3, 88.0, 127.9		123.8, 122.9, 159.9	186.2, 57.1, 129.2
α,β,γ (°)	90, 114, 90		90, 95, 90	90, 100, 90
	Isotropic	*Anisotropic*		
Resolution (Å)	124.71 – 4.97 (5.05 – 4.97)	124.71 – 4.55 (5.00 – 4.55)	123.27 – 3.49 (3.55 – 3.49)	54.53 – 2.52 (2.56 – 2.52)
R_{merge}	0.438 (2.187)	0.198 (0.507)	0.161 (1.572)	0.072 (2.438)
R_{pim}	0.279 (1.366)	0.127 (0.323)	0.067 (0.663)	0.031 (1.028)
$CC_{1/2}$	0.967 (0.322)	0.987 (0.704)	0.992 (0.714)	0.999 (0.813)
$I/\sigma I$	1.9 (0.5)	3.4 (1.8)	6.9 (1.0)	10.9 (0.8)
Completeness (%)	99.8 (99.8)	e* 80.0 (56.7) s* 39.2 (8.1)	99.8 (99.9)	99.8 (98.0)
Redundancy	3.4 (3.5)	3.4 (3.4)	6.9 (6.6)	6.7 (6.6)
Molecular replacement				
# CD1-β_2m/ASU	4		6	2

*ellipsoidal (e) and spherical (s) completeness are quoted for anisotropic data processing using STARANISO.

been tested using SDS-PAGE (Figure 4B (iii) and (iv) and 4D (v)). These three samples all contained CD1d-β_2m only as confirmed by molecular replacement trials using multiple copies of all potential components as well as manual inspection of maps. In all datasets additional density was observed for unmodelled glycans on CD1d (deglycosylation of CD1d using Endo H leaves a residual acetylated glycosamine), confirming the validity of the molecular replacement solution. For several CD1d molecules, additional unmodelled density near the lipid-binding groove was evident that likely corresponds to partially-ordered lipid components. Further inspection of electron density maps revealed no evidence for the presence of SapB. For most molecules of CD1d in all three different crystal forms the predicted binding site for SapB (over the lipid-binding groove) was occupied by another copy of CD1d. The use of both SDS-PAGE analysis of all grown crystals and molecular replacement solution of higher quality crystals confirmed that, despite extensive efforts with a broad range of CD1d-β_2m/SapB combinations, these do not form a stable, crystallisable complex.

Discussion

Using highly purified components we have been unable to identify a direct interaction between CD1d-β_2m and SapB *in vitro*. Several biochemical and structural approaches were implemented that have the capacity to capture weak and transient interactions, including binding equilibrium assays, protein cross-linking, and co-crystallisation trials. Various factors that may influence the strength or specificity of these interactions were tested, including different pH and buffer systems, exchange of the lipids loaded onto both protein components, and changing the glycosylation state of each protein. None of these variants resulted in the detection of a direct interaction. Our previous work studying saposin interactions with lysosomal hydrolases showed that although these interactions are sensitive to pH and salt concentrations, they were always detectable, and while detergent/lipid was required, neither the nature of the lipid/detergent nor the glycosylation state mattered[19].

Direct protein-protein interactions are crucial for several different lipid transfer pathways. The lipopolysaccharide (LPS) transfer cascade resulting in Toll-like receptor 4 (TLR4) activation involves several lipid transfer steps. LPS binding protein (LBP) extracts LPS and transfers it onto the receptor CD14. CD14 then transfers LPS to the TLR4 co-receptor MD-2. A direct, high affinity (K_d = 5.52 nM) interaction between LBP and CD14 is necessary for lipid transfer, and lipid transfer promotes rapid dissociation of CD14:LPS from LBP. Similarly, a direct interaction between CD14 and the TLR4:MD-2 complex is required for lipid transfer[38]. The transfer of lipids between proteins is also seen in the formation of Apolipoprotein B

(apoB)-containing lipoproteins. Microsomal Triglyceride Transfer protein assists this process by binding to apoB with high affinity (K_d 10-30 nM)[63] and transferring lipids onto apoB through an unknown mechanism. Both functions are required for lipoprotein assembly[39]. As another example, Niemann–Pick C1 (NPC1) and Niemann–Pick C2 (NPC2) proteins collaborate to export cholesterol from the lysosome. Soluble NPC2 binds cholesterol in the lysosomal lumen, interacts with the middle lumenal domain of the multipass transmembrane protein NPC1 and transfers cholesterol to NPC1 via a transfer tunnel linking the cholesterol-binding pockets of both proteins. The interaction between NPC2 and NPC1 (K_d 0.4-2 μM) is required for cholesterol export[40]. In all cases, a high-to-medium affinity direct interaction between proteins engaged in lipid transfer is detectable. In this study, we were unable to detect a direct interaction between CD1d and SapB despite the assays being capable of detecting very weak interactions. Specifically, the equilibrium assay used in this study can detect protein interactions where the dissociation constant is as weak as 40 μM. In the absence of avidity effects, interactions weaker than 40 μM are unlikely to be physiologically relevant. Furthermore, the cross-linking assay can detect short-lived, transient interactions and the co-crystallography technique uses very high concentrations of protein components allowing for the detection of very weak interactions. It therefore seems unlikely that an interaction that is undetectable by these methods could permit direct lipid exchange between SapB and CD1d.

The study of lipid loading of CD1 molecules is technically challenging as biochemical methods often require the inclusion of detergents, which may interfere with lipid solubilisation and binding. Also, the detection of changes to CD1d-lipid complexes is limited by available reagents including specific antibodies and iNKT TCRs. However, the inability to identify a direct interaction between CD1d and SapB raises a number of important questions regarding the role of saposins in lipid antigen presentation.

It is well established that knockout of the saposin precursor protein PSAP results in impaired presentation of lipid antigens by CD1d. Due to the dual role of saposins in lipid loading and lipid processing, the absence of PSAP will not only alter CD1d lipid loading, but will also significantly alter the composition of the lysosomal lipidome. Indeed, the loss of a single saposin results in the cellular accumulation of multiple, different GSLs. For example, loss of SapB alone, in mice or in humans, results in the accumulation of sulfatides, globotriaosylceramide, and lactosylceramide[64,65]. Therefore, in saposin knockout and rescue models, the effects on antigen processing and the changes to local lipid concentrations may have indirect and unpredictable effects on CD1d loading in the lysosome. Similarly, cell-based assays that involve recognition of CD1d-lipid complexes by NKT cells are complicated by the requirement of some glycolipid headgroups to be processed by lysosomal hydrolases[12], a process that is itself dependent upon saposins.

In vitro assays testing the role of different saposins in facilitating lysosomal hydrolase activity identify some of the difficulties in determining specificity of saposin-lipid binding. For example, *in vitro* assays have identified that SapC and SapA are both able to enhance the activity of β-galactosylceramidase (GALC) to promote degradation of the galactosphingolipids[66,67]. However, this does not reflect the specificity of saposins in whole organisms as loss of SapA causes Krabbe disease, similar to that of loss of GALC, while mutations in SapC do not[20,21,23–25]. Why these *in vitro* assays do not recapitulate the specificity of saposins in a whole organism remains unclear but may suggest a non-specific detergent-like effect of saposins when present at relatively high concentrations. It is unclear whether a similar effect may be partially confounding the interpretation of SapB influence on CD1d lipid loading. While *in vitro* studies demonstrating the ability of SapB to enhance CD1d stimulation of iNKT cells or binding to iNKT TCRs are very compelling regarding the importance of SapB in this process, these do represent an indirect way of monitoring how SapB may be involved in lipid exchange[33,34]. In light of our data showing no detectable interaction between CD1d and SapB, the question remains: how can SapB facilitate lipid editing without directly binding CD1d? Modelling of how SapB might facilitate lipid exchange identified a role for SapB in enhancing the kinetics of lipid exchange in a manner similar to that of Tapasin in peptide exchange on MHC class I molecules[34]. This comparison is driven by the crucial roles that Tapasin and SapB play in the binding and exchange of peptides or lipids, respectively, to the antigen-binding grooves of MHC class I or CD1d molecules. In order for Tapasin to carry out this role, it binds directly to MHC class I but as part of a larger complex including additional proteins[2,68]. Although the *in vitro* assays demonstrating the importance of SapB for CD1d lipid presentation did not require other proteins, it is possible that there may be additional factors involved in enhancing the affinity of SapB for CD1d in cells.

Additional factors may influence the efficiency of lipid loading onto CD1d in cells. For example, the relative abundance of different LTPs in the lysosome may influence the lysosomal lipid composition, altering exchange kinetics. Therefore, it may be important that SapA-D exist in equimolar concentrations in the endolysosome, as ensured by their production from a common precursor. If this is the case, studies involving individual saposins or partial PSAP rescues will be difficult to interpret, potentially explaining some experimental inconsistencies. The lysosomal lipidome is not only influenced by the activity of saposins and sphingolipid processing hydrolases but also by the careful balance of other membrane components such as cholesterol and bis(monoacylglycero)phosphate that are crucial for endosomal vesicle formation. Lipid loading of CD1 in endolysosomal compartments is highly complex, requiring the delicate interplay of lipid binding, lipid processing and lipid exchange. For now, the mechanism of transfer of lipids onto CD1 molecules, as well as the molecular determinants of LTP binding specificity, remains unclear.

Data availability

Underlying data

Figshare: Original data used in Figure 1, https://doi.org/10.6084/m9.figshare.8926709[69].

Figshare: Original equilibrium binding assay gels used in Figure 2, https://doi.org/10.6084/m9.figshare.8864384[70].

Figshare: Original cross-linking gels used in Figure 3, https://doi.org/10.6084/m9.figshare.8932856[71].

Figshare: Original gels and images used in Figure 4, https://doi.org/10.6084/m9.figshare.8932898[72].

Apollo: Research data supporting "The lipid transfer protein Saposin B does not directly bind CD1d for lipid antigen loading". https://doi.org/10.17863/CAM.41683[73].

This project contains the following underlying data:

- Original X-ray diffraction datasets, processed diffraction data, molecular replacement solutions for crystals (iii), (iv) and (v)

Data are available under the terms of the Creative Commons Attribution 4.0 International license (CC-BY 4.0).

References

1. Pos W, Sethi DK, Call MJ, *et al.*: **Crystal structure of the HLA-DM-HLA-DR1 complex defines mechanisms for rapid peptide selection.** *Cell.* 2012; **151**(7): 1557–68.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

2. Blees A, Januliene D, Hofmann T, *et al.*: **Structure of the human MHC-I peptide-loading complex.** *Nature.* 2017; **551**(7681): 525–528.
    PubMed Abstract | **Publisher Full Text**

3. Ilca FT, Neerincx A, Hermann C, *et al.*: **TAPBPR mediates peptide dissociation from MHC class I using a leucine lever.** *eLife.* 2018; **7**: pii: e40126.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

4. Layre E, de Jong A, Moody DB: **Human T cells use CD1 and MR1 to recognize lipids and small molecules.** *Curr Opin Chem Biol.* 2014; **23**: 31–8.
    PubMed Abstract | **Publisher Full Text**

5. Moody DB, Cotton RN: **Four pathways of CD1 antigen presentation to T cells.** *Curr Opin Immunol.* 2017; **46**: 127–133.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

6. Brennan PJ, Brigl M, Brenner MB: **Invariant natural killer T cells: an innate activation scheme linked to diverse effector functions.** *Nat Rev Immunol.* 2013; **13**(2): 101–17.
    PubMed Abstract | **Publisher Full Text**

7. Sprong H, van der Sluijs P, van Meer G: **How proteins move lipids and lipids move proteins.** *Nat Rev Mol Cell Biol.* 2001; **2**(7): 504–13.
    PubMed Abstract | **Publisher Full Text**

8. Cox D, Fox L, Tian R, *et al.*: **Determination of cellular lipids bound to human CD1d molecules.** *PLoS One.* 2009; **4**(5): e5325.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

9. Yuan W, Kang SJ, Evans JE, *et al.*: **Natural lipid ligands associated with human CD1d targeted to different subcellular compartments.** *J Immunol.* 2009; **182**(8): 4784–91.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

10. Haig NA, Guan Z, Li D, *et al.*: **Identification of self-lipids presented by CD1c and CD1d proteins.** *J Biol Chem.* 2011; **286**(43): 37692–37701.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

11. Teyton L: **Role of lipid transfer proteins in loading CD1 antigen-presenting molecules.** *J Lipid Res.* 2018; **59**(8): 1367–1373.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

12. Prigozy TI, Naidenko O, Qasba P, *et al.*: **Glycolipid antigen processing for presentation by CD1d molecules.** *Science.* 2001; **291**(5504): 664–7.
    PubMed Abstract | **Publisher Full Text**

13. Darmoise A, Teneberg S, Bouzonville L, *et al.*: **Lysosomal alpha-galactosidase controls the generation of self lipid antigens for natural killer T cells.** *Immunity.* 2010; **33**(2): 216–28.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

14. Ahn VE, Faull KF, Whitelegge JP, *et al.*: **Crystal structure of saposin B reveals a dimeric shell for lipid binding.** *Proc Natl Acad Sci U S A.* 2003; **100**(1): 38–43.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

15. de Alba E, Weiler S, Tjandra N: **Solution structure of human saposin C: pH-dependent interaction with phospholipid vesicles.** *Biochemistry.* 2003; **42**(50): 14729–40.
    PubMed Abstract | **Publisher Full Text**

16. Ahn VE, Leyko P, Alattia JR, *et al.*: **Crystal structures of saposins A and C.** *Protein Sci.* 2006; **15**(8): 1849–57.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

17. Popovic K, Privé GG: **Structures of the human ceramide activator protein saposin D.** *Acta Crystallogr D Biol Crystallogr.* 2008; **64**(Pt 5): 589–94.
    PubMed Abstract | **Publisher Full Text**

18. Popovic K, Holyoake J, Pomès R, *et al.*: **Structure of saposin A lipoprotein discs.** *Proc Natl Acad Sci U S A.* 2012; **109**(8): 2908–12.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

19. Hill CH, Cook GM, Spratley SJ, *et al.*: **The mechanism of glycosphingolipid degradation revealed by a GALC-SapA complex structure.** *Nat Commun.* 2018; **9**(1): 151.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

20. Matsuda J, Vanier MT, Saito Y, *et al.*: **A mutation in the saposin A domain of the sphingolipid activator protein (prosaposin) gene results in a late-onset, chronic form of globoid cell leukodystrophy in the mouse.** *Hum Mol Genet.* 2001; **10**(11): 1191–9.
    PubMed Abstract | **Publisher Full Text**

21. Spiegel R, Bach G, Sury V, *et al.*: **A mutation in the saposin A coding region of the prosaposin gene in an infant presenting as Krabbe disease: first report of saposin A deficiency in humans.** *Mol Genet Metab.* 2005; **84**(2): 160–6.
    PubMed Abstract | **Publisher Full Text**

22. Kuchar L, Ledvinová J, Hrebicek M, *et al.*: **Prosaposin deficiency and saposin B deficiency (activator-deficient metachromatic leukodystrophy): report on two patients detected by analysis of urinary sphingolipids and carrying novel PSAP gene mutations.** *Am J Med Genet A.* 2009; **149A**(4): 613–21.
    PubMed Abstract | **Publisher Full Text** | **Free Full Text**

23. Vaccaro AM, Motta M, Tatti M, *et al.*: **Saposin C mutations in Gaucher disease patients resulting in lysosomal lipid accumulation, saposin C deficiency, but normal prosaposin processing and sorting.** *Hum Mol Genet.* 2010; **19**(15): 2987–97.
    PubMed Abstract | **Publisher Full Text**

24. Motta M, Camerini S, Tatti M, *et al.*: **Gaucher disease due to saposin C deficiency is an inherited lysosomal disease caused by rapidly degraded mutant proteins.** *Hum Mol Genet.* 2014; **23**(21): 5814–26.
    PubMed Abstract | **Publisher Full Text**

25. Kang L, Zhan X, Ye J, *et al.*: **A rare form of Gaucher disease resulting from saposin C deficiency.** *Blood Cells Mol Dis.* 2018; **68**: 60–65.
    PubMed Abstract | **Publisher Full Text**

26. Locatelli-Hoops S, Remmel N, Klingenstein R, *et al.*: **Saposin A mobilizes lipids from low cholesterol and high bis(monoacylglycerol)phosphate-containing membranes: patient variant Saposin A lacks lipid extraction capacity.** *J Biol Chem.* 2006; **281**(43): 32451–60.
    PubMed Abstract | **Publisher Full Text**

27. Remmel N, Locatelli-Hoops S, Breiden B, *et al.*: **Saposin B mobilizes lipids from cholesterol-poor and bis(monoacylglycero)phosphate-rich membranes at

acidic pH. Unglycosylated patient variant saposin B lacks lipid-extraction capacity. *FEBS J.* 2007; **274**(13): 3405–3420.
PubMed Abstract | **Publisher Full Text**

28. Alattia JR, Shaw JE, Yip CM, *et al.*: **Direct visualization of saposin remodelling of lipid bilayers.** *J Mol Biol.* 2006; **362**(5): 943–53.
PubMed Abstract | **Publisher Full Text**

29. Alattia JR, Shaw JE, Yip CM, *et al.*: **Molecular imaging of membrane interfaces reveals mode of beta-glucosidase activation by saposin C.** *Proc Natl Acad Sci U S A.* 2007; **104**(44): 17394–9.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

30. León L, Tatituri RV, Grenha R, *et al.*: **Saposins utilize two strategies for lipid transfer and CD1 antigen presentation.** *Proc Natl Acad Sci U S A.* 2012; **109**(12): 4357–64.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

31. Zhou D, Cantu C 3rd, Sagiv Y, *et al.*: **Editing of CD1d-bound lipid antigens by endosomal lipid transfer proteins.** *Science.* 2004; **303**(5657): 523–7.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

32. Kang SJ, Cresswell P: **Saposins facilitate CD1d-restricted presentation of an exogenous lipid antigen to T cells.** *Nat Immunol.* 2004; **5**(2): 175–81.
PubMed Abstract | **Publisher Full Text**

33. Yuan W, Qi X, Tsang P, *et al.*: **Saposin B is the dominant saposin that facilitates lipid binding to human CD1d molecules.** *Proc Natl Acad Sci U S A.* 2007; **104**(13): 5551–6.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

34. Salio M, Ghadbane H, Dushek O, *et al.*: **Saposins modulate human invariant Natural Killer T cells self-reactivity and facilitate lipid exchange with CD1d molecules during antigen presentation.** *Proc Natl Acad Sci U S A.* 2013; **110**(49): E4753–61.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

35. Schrantz N, Sagiv Y, Liu Y, *et al.*: **The Niemann-Pick type C2 protein loads isoglobotrihexosylceramide onto CD1d molecules and contributes to the thymic selection of NKT cells.** *J Exp Med.* 2007; **204**(4): 841–52.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

36. Winau F, Schwierzeck V, Hurwitz R, *et al.*: **Saposin C is required for lipid presentation by human CD1b.** *Nat Immunol.* 2004; **5**(2): 169–74.
PubMed Abstract | **Publisher Full Text**

37. Wong LH, Gatta AT, Levine TP: **Lipid transfer proteins: the lipid commute via shuttles, bridges and tubes.** *Nat Rev Mol Cell Biol.* 2019; **20**(2): 85–101.
PubMed Abstract | **Publisher Full Text**

38. Ryu JK, Kim SJ, Rah SH, *et al.*: **Reconstruction of LPS Transfer Cascade Reveals Structural Determinants within LBP, CD14, and TLR4-MD2 for Efficient LPS Recognition and Transfer.** *Immunity.* 2017; **46**(1): 38–50.
PubMed Abstract | **Publisher Full Text**

39. Hussain MM, Rava P, Walsh M, *et al.*: **Multiple functions of microsomal triglyceride transfer protein.** *Nutr Metab (Lond).* 2012; **9**: 14.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

40. Li X, Saha P, Li J, *et al.*: **Clues to the mechanism of cholesterol transfer from the structure of NPC1 middle lumenal domain bound to NPC2.** *Proc Natl Acad Sci U S A.* 2016; **113**(36): 10079–84.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

41. Li Z, Michael IP, Zhou D, *et al.*: **Simple *piggyBac* transposon-based mammalian cell expression system for inducible protein production.** *Proc Natl Acad Sci U S A.* 2013; **110**(13): 5004–9.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

42. Aricescu AR, Lu W, Jones EY: **A time- and cost-efficient system for high-level protein production in mammalian cells.** *Acta Crystallogr D Biol Crystallogr.* 2006; **62**(Pt 10): 1243–50.
PubMed Abstract | **Publisher Full Text**

43. Hill CH, Read RJ, Deane JE: **Structure of human saposin A at lysosomal pH.** *Acta Crystallogr F Struct Biol Commun.* 2015; **71**(Pt 7): 895–900.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

44. Pellicci DG, Patel O, Kjer-Nielsen L, *et al.*: **Differential recognition of CD1d-alpha-galactosyl ceramide by the V beta 8.2 and V beta 7 semi-invariant NKT T cell receptors.** *Immunity.* 2009; **31**(1): 47–59.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

45. López-Sagaseta J, Kung JE, Savage PB, *et al.*: **The molecular basis for recognition of CD1d/α-galactosylceramide by a human non-Vα24 T cell receptor.** *PLoS Biol.* 2012; **10**(10): e1001412.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

46. Winter G: ***xia2*: an expert system for macromolecular crystallography data reduction.** *J Appl Crystallogr.* 2010; **43**: 186–190.
Publisher Full Text

47. Winter G, Waterman DG, Parkhurst JM, *et al.*: ***DIALS*: implementation and evaluation of a new integration package.** *Acta Crystallogr D Struct Biol.* 2018; **74**(Pt 2): 85–97.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

48. Tickle IJ, Flensburg C, Keller P, *et al.*: **STARANISO.** Cambridge, United Kingdom: Global Phasing Ltd. 2018.
Reference Source

49. Evans PR, Murshudov GN: **How good are my data and what is the resolution?** *Acta Crystallogr D Biol Crystallogr.* 2013; **69**(Pt 7): 1204–1214.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

50. López-Sagaseta J, Sibener LV, Kung JE, *et al.*: **Lysophospholipid presentation by CD1d and recognition by a human Natural Killer T-cell receptor.** *EMBO J.*

2012; **31**(8): 2047–59.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

51. Adams PD, Afonine PV, Bunkóczi G, *et al.*: ***PHENIX*: a comprehensive Python-based system for macromolecular structure solution.** *Acta Crystallogr D Biol Crystallogr.* 2010; **66**(Pt 2): 213–21.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

52. Bunkóczi G, Read RJ: **Improvement of molecular-replacement models with *Sculptor*.** *Acta Crystallogr D Biol Crystallogr.* 2011; **67**(Pt 4): 303–12.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

53. McCoy AJ, Grosse-Kunstleve RW, Adams PD, *et al.*: ***Phaser* crystallographic software.** *J Appl Crystallogr.* 2007; **40**(Pt 4): 658–674.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

54. Afonine PV, Grosse-Kunstleve RW, Echols N, *et al.*: **Towards automated crystallographic structure refinement with *phenix.refine*.** *Acta Crystallogr D Biol Crystallogr.* 2012; **68**(Pt 4): 352–67.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

55. Emsley P, Lohkamp B, Scott WG, *et al.*: **Features and development of Coot.** *Acta Crystallogr D Biol Crystallogr.* 2010; **66**(Pt 4): 486–501.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

56. Koch M, Stronge VS, Shepherd D, *et al.*: **The crystal structure of human CD1d with and without alpha-galactosylceramide.** *Nat Immunol.* 2005; **6**(8): 819–826.
PubMed Abstract | **Publisher Full Text**

57. Gumperz JE, Roy C, Makowska A, *et al.*: **Murine CD1d-restricted T cell recognition of cellular lipids.** *Immunity.* 2000; **12**(2): 211–21.
PubMed Abstract | **Publisher Full Text**

58. Kim HS, Garcia J, Exley M, *et al.*: **Biochemical characterization of CD1d expression in the absence of beta2-microglobulin.** *J Biol Chem.* 1999; **274**(14): 9289–95.
PubMed Abstract | **Publisher Full Text**

59. Pollard TD: **A guide to simple and informative binding assays.** *Mol Biol Cell.* 2010; **21**(23): 4061–7.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

60. Paduraru C, Spiridon L, Yuan W, *et al.*: **An *N*-linked glycan modulates the interaction between the CD1d heavy chain and and beta 2-microglobulin.** *J Biol Chem.* 2006; **281**(52): 40369–78.
PubMed Abstract | **Publisher Full Text**

61. Brennan PJ, Cheng TY, Pellicci DG, *et al.*: **Structural determination of lipid antigens captured at the CD1d-T-cell receptor interface.** *Proc Natl Acad Sci U S A.* 2017; **114**(31): 8348–8353.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

62. Muenzner J, Traub LM, Kelly BT, *et al.*: **Cellular and viral peptides bind multiple sites on the N-terminal domain of clathrin.** *Traffic.* 2017; **18**(1): 44–57.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

63. Hussain MM, Bakillah A, Jamil H: **Apolipoprotein B binding to microsomal triglyceride transfer protein decreases with increases in length and lipidation: implications in lipoprotein biosynthesis.** *Biochemistry.* 1997; **36**(42): 13060–7.
PubMed Abstract | **Publisher Full Text**

64. Li SC, Kihara H, Serizawa S, *et al.*: **Activator protein required for the enzymatic hydrolysis of cerebroside sulfate. Deficiency in urine of patients affected with cerebroside sulfatase activator deficiency and identity with activators for the enzymatic hydrolysis of GM1 ganglioside and globotriaosylceramide.** *J Biol Chem.* 1985; **260**(3): 1867–71.
PubMed Abstract

65. Sun Y, Witte DP, Ran H, *et al.*: **Neurological deficits and glycosphingolipid accumulation in saposin B deficient mice.** *Hum Mol Genet.* 2008; **17**(15): 2345–56.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

66. Harzer K, Paton BC, Christomanou H, *et al.*: **Saposins (*sap*) A and C activate the degradation of galactosylceramide in living cells.** *FEBS Lett.* 1997; **417**(3): 270–4.
PubMed Abstract | **Publisher Full Text**

67. Harzer K, Hiraiwa M, Paton BC: **Saposins (sap) A and C activate the degradation of galactosylsphingosine.** *FEBS Lett.* 2001; **508**(1): 107–10.
PubMed Abstract | **Publisher Full Text**

68. Dong G, Wearsch PA, Peaper DR, *et al.*: **Insights into MHC class I peptide loading from the structure of the tapasin-ERp57 thiol oxidoreductase heterodimer.** *Immunity.* 2009; **30**(1): 21–32.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

69. Shamin M, Benedyk TH, Graham SC, *et al.*: **Original data used in Figure 1.** *figshare.* Figure. 2019.
http://www.doi.org/10.6084/m9.figshare.8926709.v1

70. Shamin M, Benedyk TH, Graham SC, *et al.*: **Original equilibrium binding assay gels used in Figure 2.** *figshare.* Figure. 2019.
http://www.doi.org/10.6084/m9.figshare.8864384.v1

71. Shamin M, Benedyk TH, Graham SC, *et al.*: **Original cross-linking gels used in Figure 3.** *figshare.* Figure. 2019.
http://www.doi.org/10.6084/m9.figshare.8932856.v1

72. Shamin M, Benedyk TH, Graham SC, *et al.*: **Original gels and images used in Figure 4.** *figshare.* Figure. 2019.
http://www.doi.org/10.6084/m9.figshare.8932898.v1

73. Deane J, Graham S, Shamin M, *et al.*: **Research data supporting "The lipid transfer protein Saposin B does not directly bind CD1d for lipid antigen loading".** [Dataset]. 2019.
http://www.doi.org/10.17863/CAM.41683

Open Peer Review

Current Peer Review Status: ✓ ✓ ✓

Version 2

Reviewer Report 25 October 2019

https://doi.org/10.21956/wellcomeopenres.16966.r36814

✓   **Mariolina Salio** (iD)

Radcliffe Department of Medicine, Medical Research Council human Immunology Unit, Medical Research Council Weatherall Institute of Molecular Medicine, University of Oxford, Oxford, UK

I am satisfied with the revised version and the response to my queries.

Competing Interests: No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 21 October 2019

https://doi.org/10.21956/wellcomeopenres.16966.r36816

✓   **Tim P. Levine** (iD)

Institute of Ophthalmology, University College London, London, UK

All required changes made, as described in the Authors' Rebuttal.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Lipid transfer

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 21 October 2019

✔

Weiming Yuan 🔵

Department of Molecular Microbiology and Immunology, Keck School of Medicine, University of Southern California, Los Angeles, CA, 90033, USA

The authors have addressed my concerns and comments.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Innate immunology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Version 1

Reviewer Report 30 September 2019

?

Mariolina Salio 🔵

Radcliffe Department of Medicine, Medical Research Council human Immunology Unit, Medical Research Council Weatherall Institute of Molecular Medicine, University of Oxford, Oxford, UK

Shamin and colleagues investigate whether the LTP Saposin B directly binds to CD1d molecules for lipid antigen loading. It is known from the literature - well quoted in the manuscript - that Saposin B is the main regulator of CD1d-lipid antigen presentation to iNKT cells but to date it is not clear whether the two proteins directly interact.

Using highly purified proteins, glycosylayed and not, and through different biochemical methods (in vitro equilibrium binding assay, in vitro cross linking and crystallization trials) the authors conclude there is no direct binding between CD1d and Saposin B.

The group led by JE Deane has expertise in the field of GSL metabolism, and has used similar methods to prove interactions of Saposin A with GALC, including careful evaluation of the role of pH, presence or

absence of lipids, influence of NaCl on electrostatic interactions. To this regard, however, it is not clear if the authors have tried the equilibrium binding assay of unloaded CD1d-b2m with aGalCer loaded Saposin B as additional control in Figure 2. This could be an important discriminator in the ability of the two proteins to interact.

Although a negative result is always difficult to interpret (and publish), the authors discuss the limitations of their in vitro results, as well as that of previous assumptions stemming from knock out models where the lysosomal lipidome is severely altered. Overall, the results are in agreement with the fundamental distinct mode of action of Saposin C (which has been shown to interact with CD1b and CD1c) and Saposin B. Future studies looking at the ligandome of CD1d associated proteins in the lysosome may shed light on perhaps a larger loading complex which includes Saposin B.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Not applicable

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Cellular Immunology, innate/adaptive immunity

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 14 Oct 2019
Maria Shamin, University of Cambridge, Cambridge, UK

Thank you for your thoughtful comments and constructive feedback.

It is not clear if the authors have tried the equilibrium binding assay of unloaded CD1d-b2m with aGalCer loaded Saposin B as additional control in Figure 2. This could be an important discriminator in the ability of the two proteins to interact.
This important concern is similar to that raised by reviewer 1. We have addressed this concern by performing an additional equilibrium binding assay to test the binding of α-GalCer loaded SapB to CD1d loaded with endogenous lipids (Fig. 2D). Although this does not represent an "unloaded

CD1d-β2m", as mentioned in this comment, this experiment includes the endogenous lipid that co-purifies with CD1d following purification from human cells and therefore closely-resembles the state of CD1d that would be expected to occur in cells. As mentioned in response to reviewer 2, the relevance of an "empty" or "unloaded" CD1d for these assays is questionable as CD1d purified from insect or mammalian cells always appears to have lipids bound.

Competing Interests: No competing interests were disclosed.

Reviewer Report 16 September 2019

? Tim P. Levine iD

Institute of Ophthalmology, University College London, London, UK

This work sets out to show if saposins bind directly to CD1, which is relevant to the mechanism lying behind lipid loading into CD1, which is known to require saposins. Multiple biochemical techniques, some highly demanding, were performed with purified proteins and with great attention to detail and very clear controls.

My major point about this work is that I could not tell which, if any, experiments also included relevant lipid, particularly pre-loaded into saposin. Either key sentences in the MS should be rewritten to avoid that impression (if it is wrong), or the MS should clearly include the caveat that some aspects of the physiological situation were not reproduced in the binding experiments. On that basis, it has not been addressed if prolonged interaction only occurs when one of the proteins is occupied by lipid. This might even be asymmetric so that prolonged interaction requires lipid in Saposin, but CD1 must be empty.

The rationale for this work is explained in 2 sentences of the final paragraph of the Introduction: "…several references in the literature [about] an inability to measure a direct interaction between saposins and human CD1d [3 refs]. Unfortunately, these reports do not show any data or detail the approaches used to monitor binding and the implication is that these interactions exist but are weak and very transitory."

This rationale is not explained as clearly as it might be. In the 1st sentence, do the authors mean that the 3 refs were written to indicate that the lipid binding proteins must be able to bind each other even when lipid is absent to have a productive relationship for lipid handover? The different models should be described more, and the limits to the data mentioned in the 2nd sentence should be outlined. In addition, the Introduction and Discussion should both describe (in brief and extensive terms, repsectively) what is known for other examples of lipid handover: NPC1/NPV2 MPT/ApoB LBP/CD14 CD14/MD2. Also in discussion of tapasin, describe if the relationship parallels the one envisaged here. Finally, is there handover of peptide from another binding protein to MHC?

The estimated maximum level of Kd that these techniques would find is 40 μM (Fig 2B). The authors should discuss the physiological relevance of an interaction weaker than that. They should also discuss how proximity labelling (BioID, APEX) might find that.

State that SapB used might lack PTM required for binding in Fig 2, although this was tested in Fig 3.

State whether conditions in Fig 2C were shown to permit transfer of lipid. Ideally, this should be shown for a parallel experiment under the same conditions.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Partly

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Not applicable

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Lipid transfer.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 14 Oct 2019

Maria Shamin, University of Cambridge, Cambridge, UK

Thank you for your thoughtful comments and constructive feedback. In-line responses to your queries are included below.

My major point about this work is that I could not tell which, if any, experiments also included relevant lipid, particularly pre-loaded into saposin. Either key sentences in the MS should be rewritten to avoid that impression (if it is wrong), or the MS should clearly include the caveat that some aspects of the physiological situation were not reproduced in the binding experiments. Most experiments were carried out with SapB and CD1d-β2m loaded with the lipids they co-purified with following protein expression. Based on previous studies, these are likely to be *E.coli* phosphatidylethanolamine for SapB and endogenous human lipids that bind during folding in the endoplasmic reticulum and trafficking through the Golgi apparatus for CD1d-β2m (primarily sphingomyelin). As phosphatidylethanolamine is a lipid species that has been shown previously to bind CD1d then the proteins *as purified* are not necessarily in a non-physiologically relevant lipid-bound state. However, we accept that in light of no detectable interaction this is a crucial

factor to be clear about in the text. To ensure that the lipids used in each experiment is clear, we have modified the relevant sections of the main text and figures (also see next comment).

On that basis, it has not been addressed if prolonged interaction only occurs when one of the proteins is occupied by lipid. This might even be asymmetric so that prolonged interaction requires lipid in Saposin, but CD1 must be empty.

We agree with the reviewer that the lipid-bound state of the protein components may be a crucial factor in the affinity and on/off-rates of their potential interaction. An experiment to try and address this, suggested by reviewer 1, is now included where the SapB has been exchanged to bind α-GalCer and the CD1d used with endogenous lipids, similar to those that would be bound upon delivery to the endocytic compartments where exchange should occur. This did not result in significant depletion of SapB in equilibrium binding assays (Fig. 2D) suggesting that if the lipid-bound state of these components is a driving factor in the interaction it is sufficiently complex to be outside the scope of this study. Regarding the reviewer's statement that CD1d "must be empty", it is unclear that CD1d actually ever exists in a truly empty form as it appears to always co-purify, from insect or mammalian cells, with lipids bound.

The rationale for this work is explained in 2 sentences of the final paragraph of the Introduction. This rationale is not explained as clearly as it might be. In the 1st sentence, do the authors mean that the 3 refs were written to indicate that the lipid binding proteins must be able to bind each other even when lipid is absent to have a productive relationship for lipid handover?

Statements in the referenced papers are not specific about what conditions the individual proteins might be in regarding lipid content for an interaction to occur. Despite this, all references agree that Saposins are crucial for lipid loading of CD1. In the review by Teyton 2018, he states "We have not been able to reliably measure an interaction between any mouse or human CD1 molecules and the four Saps…". In both Yuan 2007 and Salio 2013 they reference previous work identifying interactions between CD1b and/or CD1c with Saposin C but both state that they have been unable to identify direct interactions of saposins with CD1d despite these papers being specifically focused on the role of CD1d and SapB in lipid loading. As the referenced papers are not specific enough in their statements to address the reviewers points we do not feel we can substantially re-write this statement. The lack of detail in the published statements were part of the motivation for our own studies and the range of techniques and conditions we tested.

The different models should be described more, and the limits to the data mentioned in the 2nd sentence should be outlined.

As above, we do not feel we can provide more detail as there were no models proposed and no data provided in the references. We have however, extended the first part of the last paragraph of the Introduction based on this reviewer's next comment to try and clarify that a direct interaction was expected for this process.

In addition, the Introduction and Discussion should both describe (in brief and extensive terms, repsecively) what is known for other examples of lipid handover: NPC1/NPV2 MPT/ApoB LBP/CD14 CD14/MD2.

We thank the reviewer for highlighting these additional protein complexes involved in lipid handover and agree that this is an important addition as it helps put the current work in perspective regarding the requirement, in these other systems, for direct protein-protein interactions for lipid transfer. This is especially compelling as the affinities described for these interactions would have been clearly detectable in the assays used here. We have rewritten the final paragraph of the introduction to cite these examples of lipid handover that involve a direct interaction between

proteins involved in lipid transfer. We have also added a substantial paragraph to the discussion where we discuss the mechanisms of lipid transfer between these proteins and the requirement for medium-to-strong, direct interactions between proteins engaged in lipid transfer.

Also in discussion of tapasin, describe if the relationship parallels the one envisaged here. Finally, is there handover of peptide from another binding protein to MHC?
The original comparison of saposin function to tapasin function was made by Salio *et al.* in their 2013 paper. The parallels envisaged between these systems are the requirement for a direct protein-protein interaction (MHC I to Tapasin versus CD1d to SapB) and the functional outcome of this interaction being a change to the antigen content of the binding groove (MHC I-peptide versus CD1d-lipid). Tapasin has been shown to bind directly to MHC I and functions to load and optimize the peptide binding to MHC I. There are clearly potential differences between these systems particularly as the relevant antigens have different solubility and thus peptides do not require "transfer proteins". We have added a sentence to the discussion describing more clearly the potential parallels between these systems. However, we feel that any further speculation at this stage is unwarranted.

The estimated maximum level of Kd that these techniques would find is 40 µM (Fig 2B). The authors should discuss the physiological relevance of an interaction weaker than that.
We thank the reviewer for this point and how it relates also to the additional protein-protein interactions mentioned above involved in lipid transfer. The published affinities for these interactions range from 5 nM to 2 µM thus readily detectable using the techniques adopted in our study. An interaction weaker than 40 µM falls outside what would be considered a physiologically relevant interaction affinity in the absence of a highly-multivalent interaction, which we do not expect for SapB and CD1d. We have now added additional text to the discussion explicitly stating this point.

They should also discuss how proximity labelling (BioID, APEX) might find that.
Although BioID and APEX are excellent techniques for detecting transient and weak protein-protein interactions in cells, these techniques are not yet available for the analysis of interactions within the endolysosome due to the low pH of these compartments that significantly reduce the efficacy of the biotinylation reaction. We would be very excited to implement these sorts of techniques when they become available.

State that SapB used might lack PTM required for binding in Fig 2, although this was tested in Fig 3.
The reviewer is correct that the SapB used in Fig 2 is not glycosylated. However, previous *in vitro* lipid loading experiments (Salio 2013; Yuan 2007) did not use glycosylated SapB, indicating that this PTM is not necessary for function. Our experiment using glycosylated SapB in Fig. 3 was performed in the hope that this may increase the affinity to detectable levels, rather than be required for it. We have ensured this point is now clearer in the text.

State whether conditions in Fig 2C were shown to permit transfer of lipid. Ideally, this should be shown for a parallel experiment under the same conditions.
The conditions used in our binding experiments fall within the range of different conditions used in previous studies with SapB and CD1d. The pH and salt concentration chosen for this assay were based on previous studies, particularly Yuan 2007. For technical reasons we also included 0.05% digitonin. However, we note that the SPR experiment performed by Salio 2013 also included detergent, 0.005% surfactant P20.

Reviewer Report 29 August 2019

? **Weiming Yuan** (iD)

Department of Molecular Microbiology and Immunology, Keck School of Medicine, University of Southern California, Los Angeles, CA, 90033, USA

Saposin B has been reported to mediate the lipid loading to CD1d in lysosomal compartments. This report employed several sensitive analytical methods to dissect whether saposin B directly interacts with CD1d/beta2m to deliver the lipid antigens to CD1d. The authors have extensively explored different experimental conditions to analyze the potential interactions with equilibrium binding assay, chemical cross-linking and co-crystallization methods. None of these assays detected direct saposin B-CD1d/beta2m interaction. The authors concluded that saposin B does not directly bind CD1d lipid loading.

While the authors' studies are particularly thorough and extensive, the reviewer still has reservation to make a statement that this work could establish "comprehensively" that the role of saposin B in lipid loading does not involve direct interaction with CD1d. As the authors mentioned that the "*in vivo*" condition may be understandably different from the *in vitro* experimental conditions the authors have extensively tried. For example, as the authors pointed out, in lysosomes, there are multiple saposins present at possibly higher local concentrations, the potential "loading complex" may requires additional proteineous factors, etc. Therefore, while all results strongly suggested there might not be direct interaction, it is still hard to conclusively state there is none.

The additional factor is the pH in experimental condition may still affect the potential interaction even though it may not be critical for saposin and other lipid hydrolases.

Other comments:
1. The amount of cross-linked saposin/CD1d may be lower than detection limit in Commassie blue staing. The authors may consider using western blotting to increase the detection sensitivity.

2. In equilibrium binding assay with a-GalCer, the lipid exchange/editing can be imagined as unloading of "endogenous" lipids in CD1d (co-purified from bacteria or mammalian cells) and replacing with a-GalCer. It is unknown if both saposin and CD1d loaded with the same a-GalCer lipid, whether this editing and saposin/CD1d interaction would occur. As antigen editing would be stronger affinity antigen replacing the lower affinity antigen. It is strongly suggested that the same experiment in Fig. 2C to be repeated with purified CD1d (no a-GalCer) with a-GalCer-loaded saposin B.

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Innate immunology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 14 Oct 2019
Maria Shamin, University of Cambridge, Cambridge, UK

Thank you for your thoughtful comments and constructive feedback. In-line responses to your queries are included below.

While the authors' studies are particularly thorough and extensive, the reviewer still has reservation to make a statement that this work could establish "comprehensively" that the role of saposin B in lipid loading does not involve direct interaction with CD1d. As the authors mentioned that the "in vivo" condition may be understandably different from the in vitro experimental conditions the authors have extensively tried. For example, as the authors pointed out, in lysosomes, there are multiple saposins present at possibly higher local concentrations, the potential "loading complex" may requires additional proteineous factors, etc. Therefore, while all results strongly suggested there might not be direct interaction, it is still hard to conclusively state there is none.
We acknowledge that the lack of a detectable interaction does not necessarily mean that there is no interaction. We have therefore removed the word "comprehensively" from the abstract so that the conclusion now reads: "This work strongly indicates that the role of SapB in lipid loading does not involve direct binding to CD1d."

The additional factor is the pH in experimental condition may still affect the potential interaction even though it may not be critical for saposin and other lipid hydrolases.
The equilibrium binding assays and cross-linking experiments were performed at pH 7. As described in the text, this is a pH previously demonstrated to be able to facilitate SapB loading of lipids onto CD1d. Although this may not represent the most optimal pH for the interaction it was a

necessary compromise that supported both the technical requirements of our assays and a pH at which an interaction should have been observable.

The amount of cross-linked saposin/CD1d may be lower than detection limit in Commassie blue staining. The authors may consider using western blotting to increase the detection sensitivity. Although we agree that Western blot would have the capacity to visualize weaker bands following cross-linking, there is one primary reason we have not used this approach here. If the interaction between SapB and CD1d is so weak that, even in the presence of high concentrations of purified proteins and crosslinker, the proportion forming a complex must be detected by Western blot then to us it seems likely this interaction is too weak for further structural analysis and unlikely to be of physiological relevance (in agreement with our equilibrium binding analysis).

In equilibrium binding assay with a-GalCer, the lipid exchange/editing can be imagined as unloading of "endogenous" lipids in CD1d (co-purified from bacteria or mammalian cells) and replacing with a-GalCer. It is unknown if both saposin and CD1d loaded with the same a-GalCer lipid, whether this editing and saposin/CD1d interaction would occur. As antigen editing would be stronger affinity antigen replacing the lower affinity antigen. It is strongly suggested that the same experiment in Fig. 2C to be repeated with purified CD1d (no a-GalCer) with a-GalCer-loaded saposin B.
We thank the reviewer for this suggestion and have now performed this additional experiment. We have repeated the equilibrium binding assay with SapB pre-loaded with α-GalCer, and CD1d loaded with the endogenous lipids with which it co-purifies following expression in a human cell line. In agreement with our other results, this alternate lipid loading of the protein components did not result in depletion of SapB from the supernatant even in the presence of 40 µM CD1d-β2m. As this additional experiment addresses an important point regarding relevant lipid loading (mentioned also by the other reviewers), we have updated the manuscript to include this new equilibrium binding assay in Fig.2, panel D.

Competing Interests: No competing interests were disclosed.