Elucidation and Chemical Modulation of Sulfolipid-1 Biosynthesis in Mycobacterium tuberculosis*

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Keywords:

Background: Sulfolipid-1 is a Mycobacterium tuberculosis outer membrane lipid whose biosynthesis is not fully understood.

Results: Chp1 catalyzes two acyl transfer reactions to form sulfolipid-1. Sap modulates sulfolipid-1 levels and transmembrane transport.

Conclusion: The activities of Chp1 and Sap complete the sulfolipid-1 pathway.

Significance: Lipid biosynthesis and transport are coupled at the membrane interface by multiple proteins that may regulate substrate specificity and flux.

SUMMARY

Mycobacterium tuberculosis (Mtb) possesses unique cell-surface lipids that have been implicated in virulence. One of the most abundant is sulfolipid-1 (SL-1), a tetraacyl-sulfotrehalose glycolipid. Although the early steps in SL-1 biosynthesis are known, the machinery underlying the final acylation reactions is not understood. We provide genetic and biochemical evidence for the activities of two proteins, Chp1 and Sap (corresponding to gene loci rv3822 and rv3821) that complete this pathway. The membrane-associated acyltransferase Chp1 accepts a synthetic diacyl sulfolipid and transfers an acyl group regioselectively from one donor substrate molecule to a second acceptor molecule in two successive reactions to yield a tetraacylated product. Chp1 is fully active in vitro, but in Mtb its function is potentiated by the previously identified sulfolipid transporter MmpL8. We also show that the integral membrane protein Sap and MmpL8 are both essential for sulfolipid transport. Finally, the lipase inhibitor tetrahydrolipstatin disrupts Chp1 activity in Mtb, suggesting an avenue for perturbing SL-1 biosynthesis in vivo. These data complete the SL-1 biosynthetic pathway and corroborate a model in which lipid biosynthesis and transmembrane transport are coupled at the membrane-cytosol interface through the activity of multiple proteins, possibly as a macromolecular complex.

Mycobacterium tuberculosis (Mtb), the causative agent of tuberculosis, is characterized by a complex cell wall that contributes to its pathogenesis and inherent resistance to therapeutics. The cell wall encompasses multiple layers exterior to the cytosolic membrane and comprises not only peptidoglycan, but also arabinogalactan polysaccharide layers and an extremely hydrophobic bilayer known as the mycobacterial outer membrane. Abundant Mtb-specific surface lipids such as sulfatides, acyltrehaloses and dimycocerosates are noncovalently assembled in the mycobacterial outer
membrane and have been implicated in virulence and host immune responses (1-4). Sulfolipid-1 (SL-1), the most abundant sulfatide, is unique to pathogenic mycobacteria (Fig. 1). Levels of this tetraacylated glycolipid have been positively correlated with strain virulence, but despite a half-century of research into this connection, the biological functions of SL-1 have remained elusive.

Various studies have implicated SL-1 in the inhibition of mitochondrial oxidative phosphorylation, alteration of phagosome-lysosome fusion, and stimulation as well as suppression of cytokine and reactive oxygen species production in host leukocytes (5-12). However, Mtb gene disruption strains lacking fully elaborated SL-1 do not appear to have consistent phenotypes or phenotypes distinguishable from wild-type Mtb in animal models of infection (13-17). In contrast, the diacyl sulfolipid SL-1278, a biosynthetic precursor of SL-1, is a well-documented active metabolite (Fig. 1). SL1278 was found to bind to the MHC-like lipid receptor CD1b and to stimulate the cytokines IFN-gamma and IL-2 in CD8+ T-cells from donors positive for the tuberculin skin test (18). Subsequent work using synthetic analogs of SL1278 showed that the ability of SL-1278 to elicit a CD1-restricted T-cell response is dependent on the length of the fatty acid acyl chains, as well as the presence and number of methyl-branched substituents on the acyl chains (19).

Elucidating the biosynthetic pathway of SL-1 is a key aspect in understanding how Mtb regulates SL-1 and its precursors as a potential mechanism for host immune modulation. Many of the initial steps in SL-1 biosynthesis have been defined; in addition, SL-1 biosynthesis appears to be coupled to lipid transport across the cytosolic membrane (15-25). However, the machinery underlying the final biosynthetic steps is still not understood. The complete elucidation of SL-1 biosynthesis could provide additional avenues for targeted disruption of Mtb sulfolipids and further means of dissecting their biological roles.

SL-1 comprises a trehalose-2-sulfate (T2S) core elaborated with four acyl groups: a straight-chain fatty acid (palmitate or stearate) and three multiply methyl-branched (hydroxy)phthioceranoic acids (Fig. 1). The sulfotransferase Stf0 initiates SL-1 biosynthesis by sulfating the abundant disaccharide trehalose to form T2S. The acyltransferase PapA2 then catalyzes the esterification of T2S at the 2' position to generate a monoacylated intermediate, SL659 (15). The polyketide synthase Pks2 synthesizes multiply methyl-branched (hydroxy)phthioceranoyl chains using an activated fatty acid starter unit provided by the fatty acid AMP ligase FadD23 (also known as FAAL23) (20,21). PapA1 transfers the product of Pks2 to the 3' position of SL659, yielding the diacylated SL1278 (15). Additional acylations of the 6 and 6' positions of SL-1278 are required to produce fully elaborated SL-1. These final steps are chemically similar to the reaction catalyzed by PapA1, but there is no in vitro evidence that PapA1 is capable of this activity.

Intriguingly, the lipid transporter MmpL8 has been implicated in SL-1 formation. MmpL8 belongs to the resistance-nodulation-division (RND) permease protein family and is hypothesized to transport either SL-1 or SL1278 from the cytosolic leaflet to the periplasmic leaflet of the cytosolic membrane (18,19). The Mtb ΔmmpL8 gene disruption mutant accumulates the diacyl precursor SL-1278 in the cell membrane, rather than the predicted SL-1, implying that MmpL8 is required for biosynthesis as well as transport (18,19). However, no member of the RND permease family has been shown to have enzymatic activity, nor does MmpL8 contain any known conserved catalytic domains (22).

In addition to the genes described above, the SL-1 biosynthetic locus encompasses a putative operon with two ORFs, rv3821 and rv3822, both of which are annotated as conserved hypothetical proteins that we have named Sap and Chp1, respectively (Fig. 1). In this work we demonstrate that the final steps in SL-1 biosynthesis and SL-1 transport require Sap and Chp1 in addition to MmpL8. Lipid analysis of Mtb gene disruption strains revealed that Sap, Chp1 and MmpL8 are all necessary for Mtb to produce wild-type levels of SL-1. Chp1 and MmpL8 are essential for SL-1 biosynthesis, whereas Sap and MmpL8 are required for sulfolipid transport. In vitro, Chp1 was specifically modified by an activity-based fluorophosphonate probe, identifying Chp1 as a serine hydrolase superfamily member. Chp1 can also use a fully synthetic diacyl sulfolipid analogue as both an acyl donor and acceptor in two
successive, regioselective reactions to form a tetraacylated sulfolipid. Using the combined activities of Chp1, PapA1 and PapA2, all four sulfolipid acylation reactions were reconstituted in a one-pot synthesis. Finally, in Mtb the clinically approved lipase inhibitor THL inhibits the activity of Chp1, but not PapA1 or PapA2. These data complete the SL-1 biosynthetic pathway and corroborate a model in which SL-1 biosynthesis and transmembrane transport are coupled through the activity of multiple proteins at the membrane-cytosol interface.

EXPERIMENTAL PROCEDURES

Reagents and chemicals- Trehalose-2-sulfate (T2S) and the sulfolipid-1 model compound 6,6'-di-O-(2-methylarachidoyl)-3'-O-(2-methylstearoyl)-2'-O-palmitoyl-trehalose-2-O-sulfate (SL-A) were synthesized as described (23,24). The synthesis and characterization of 2-O-palmitoyl-3-O-stearoyl-α,α-D-trehalose (T2S-PS) and the construction of Chp1 heterologous expression vectors are detailed in the supplemental Experimental Procedures.

Bacterial strains and growth media- M. tuberculosis Erdman strain (ATCC 35801) and Mycobacterium smegmatis mc²155 (ATCC 70084) were grown at 37 °C. The growth medium was 7H9 (liquid) or 7H11 (solid) with 0.5% glycerol and 0.05% Tween-80 plus 0.5% glucose or 10% albumin-dextrose-catalase for M. smegmatis and plus 10% oleate-albumin-glucose or 10% albumin-dextrose-catalase for Mtb. For selective media, antibiotic concentrations were 100 μg/mL kanamycin or 50 μg/mL hygromycin for E. coli and 20 μg/mL kanamycin or 50 μg/mL hygromycin for mycobacteria.

Sequence homology analysis and structure prediction - Amino acid sequences for Sap (Rv3821) and Chp1 (Rv3822) were obtained from Tuberculist (http://tuberculist.epfl.ch/) (25). Transmembrane helices were predicted by the TMHMM Hidden Markov model (http://www.cbs.dtu.dk/services/TMHMM/). The Chp1 sequence was also submitted to Phyre for protein fold and structure prediction (http://www.sbg.bio.ic.ac.uk/~phyre/) (26).

Construction of gene disruption mutants- The Δsap and Δchp1 mutant strains were created by homologous recombination using specialized phage transduction (27). These mutants replaced 429 bp of sap (aa 27-171) and 862 bp of chp1 (aa 44-331) with a hygromycin resistance cassette. Recombinant clones were confirmed by PCR (supplemental Fig. S7). Strains were complemented with integrating plasmids encoding the target gene with a native promoter (upstream 1kb of the first gene in the putative operon).

Lipid extraction and mass spectrometry analysis- Mtb strains were grown for 3-5 days to late-log phase. Cultures were diluted in Tween-free medium to OD₆₀₀ of 0.25-0.3 and grown for two days. Cells were harvested and extracted in 1 mL of hexanes per 50 mL of culture. The upper organic phase (“surface lipid” fraction) was removed and added to an equal volume of 1:1 chloroform/methanol. The remaining cell pellet and aqueous phase were extracted in 4 mL of 1:1 chloroform/methanol and incubated at room temperature overnight. Cell debris was pelleted by centrifugation and the supernatant (“cell pellet” fraction) was decanted. All extractions were repeated in at least three independent experiments. The triacylated sulfolipid SL-1₈₆₈ was partially purified from wild-type H37Rv cells in an adapted protocol (see supplemental Experimental Procedures) (14).

High-resolution FT-ICR MS and MSⁿ data were obtained on an Apex II FT-ICR mass spectrometer (Bruker Daltonics) as previously described (28) with the following modifications. Two sets of ESI source tuning parameters were used to acquire mass spectra: For the mass range of m/z 300-1000, the capillary voltage was set to 4.5 kV, the capillary exit voltage was -300 V, the skimmer 1 voltage was -20 V, and the skimmer 2 voltage was set to -7 V. For the mass range of m/z 1000-3000, the skimmer 2 voltage was lowered to ≈ -1 to -3 V.

Additional MSⁿ spectra were obtained on a LTQ linear ion-trap mass spectrometer equipped with an cryospray ionization source (ThermoFinnigan), operating in the negative ion mode. Ions were introduced into the ion source via direct injection at a rate of 5-10 μl/min. Collision-induced dissociation was used for MSⁿ experiments. The precursor ions were isolated with an isolation width of 1–3 Da, the ions were activated with a 26% normalized collision energy for 100 ms, and the qₑ value was maintained at 0.250.

Chp1 subcellular localization by fractionation and immunoblot- M. smegmatis expressing full-length Chp1 with a C-terminal 3xFLAG epitope tag
was grown to late-log phase (OD_{600} of 1-1.5) and fractionated by sonication and differential centrifugation to generate cytosol-, membrane- and cell wall-enriched fractions as described previously and in the supplemental Experimental Procedures (29). Protein concentrations were determined by bicinchoninic acid protein assay, and 5 μg of protein from each fraction were separated by SDS-PAGE. For the anti-MspA blot, samples were extracted with 0.6% octylthioglucoside as described (30) and 310 ng of each subcellular fraction were separated by SDS-PAGE. Blots were probed with anti-KatG (Colorado State University), anti-FLAG M2, anti-GroEL2 (Abcam ab20519) and anti-MspA (31) antibodies and visualized by chemiluminescence.

**Enzyme activity of Chp1-alkaline phosphatase (AP) and Chp1-β-galactosidase (βGal) fusions**- Chp1-AP and Chp1-βGal fusion constructs were electroporated into M. smegmatis, and βGal and AP activity were determined using the substrates 2-nitrophenyl β-D-galactopyranoside and 4-nitrophenylphosphate essentially as reported (35,36). Activity is reported in Miller units (rxn OD_{420}/(culture OD_{600} x Vs x min), where Vs = volume of original culture used in the reaction). Control vectors encoding a secretion signal and secreted AP were a kind gift of Miriam Braunstein (University of North Carolina, Chapel Hill).

**Expression and purification of Chp1-cat domain in E. coli**- HM-Chp1-cat, which is the putative catalytic domain of Chp1 fused to an N-terminal 6xHis tag and maltose binding protein (32), was expressed in E. coli BL21(DE3). Following a 4-hr induction with 1 mM IPTG at 37 °C, cells were lysed in 50 mM sodium phosphate pH 7.2, 10% glycerol (buffer A), and the clarified crude lysate was incubated in batch with 10 mL of amylase resin and washed with 100 mL buffer A. Bound protein was eluted in buffer A plus 10 mM maltose, and fractions containing the His-MBP-Chp1-cat fusion protein were pooled, dialyzed and incubated overnight at 4 °C with TEV protease. Cleaved MBP and other impurities were removed by incubation with amylose resin. The flow-through containing purified Chp1-cat protein was concentrated and stored at -80 °C.

In vitro **sulfolipid biosynthetic reactions**- PapA2 and PapA1 were expressed and purified as described (15). For reconstitution of SL-1 analogue biosynthesis, reactions contained 1 μM each of PapA2, PapA1 and Chp1-cat, 50 μM palmitoyl-CoA, and 1 mM T2S in 100 μL of reaction buffer (100 mM sodium phosphate pH 7.2, 1 mM DTT, 10% glycerol). To test reactivity with T2S-PS, Chp1-cat was incubated at 1 μM with 0.1 mM T2S-PS in 100 μL of reaction buffer. Competition reactions also included either 0.1 mM palmitoyl-CoA or 0.1 mM SL-A. Reactions were incubated at RT for 12-16 hrs. Reactions were extracted with an equal volume of 1:1 chloroform/methanol. The organic phase was co-spotted with an equal volume of 10 mg/mL 2-(4'-hydroxybenzeneazo)benzoic acid suspended in 1:1 water:ethanol. Spots were analyzed by matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry in negative mode using a 20k V accelerating voltage and 110 ns extraction delay with 500 shots per spectrum (QB3/Chemistry Mass Spectrometry Facility, University of California, Berkeley). For MS^n analysis (performed as above), 100 μL of each reaction in 100 mM ammonium bicarbonate pH 7.2 were lyophilized and dissolved in methanol prior to analysis.

**35S and 14C metabolic labeling and lipid analysis by thin-layer chromatography**- Mtb strains were grown to late-log phase. For 35S labeling, cells were resuspended at OD_{600} ~1 in 10 mL of phosphate buffered saline with 1% acetate and 100 μCi of 35S-sulfate. For 14C labeling, 5 μCi of 14C-propionic acid were added directly to 10 mL of culture at OD_{600} ~1. After overnight incubation, cell pellets were extracted sequentially in hexanes and 1:1 chloroform/methanol as described above. An equal volume of extracts resuspended in 1/10 or 1/20 the original extraction volume was spotted on silica plates (HPTLC Silica Gel 60, EMD Chemicals) and developed in 60:12:1 chloroform/methanol/water followed by phosphorimaging. For tetrahydrolipstatin (THL) treatment experiments, THL in DMSO was added to 10-mL cultures at 0, 10, 20, and 40 μg/mL for 6 hrs followed by the addition of 5 μCi of 14C-propionic acid with further incubation, extraction, and analysis as above. The lipid phthiocerol dimycocerosate was used as a loading control and resolved in 90:10 petroleum ether/hexanes.
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RESULTS AND DISCUSSION

Bioinformatic analysis of Sap and Chp1-
The *rv3821* locus encodes a 237-aa integral membrane protein homologous to the *M. smegmatis* Gap protein, which is required for glycopeptidolipid transport to the cell surface (33). Since *rv3821* may be analogously involved in SL-1 transport, we refer to the protein encoded by *rv3821* as Sap (sulfolipid-1 addressing protein). Sap has six predicted transmembrane helices with a hydrophilic domain between helices 3 and 4 (aa 93-134) that is highly variable among identified Gap-like proteins and has been hypothesized to be involved in substrate recognition (Fig. 2) (33). Sap shares 30% sequence identity with *M. smegmatis* Gap (MSMEG_0403); more distant homologues in Mtb include Rv1517, which is encoded by a locus linked to lipooligosaccharide biosynthesis in *Mycobacterium marinum*, and Rv3481c, whose gene is in the same operon as a putative triacylglycerol synthase. Sap also belongs to the LysE protein superfamily (Pfam ID PF01810), whose members have been implicated in small-molecule transport in bacteria. For example, LysE from *Corynebacterium glutamicum*, which belongs to the same taxonomic suborder as Mtb, exports L-lysine and has two homologues in Mtb (Rv0488 and Rv1986) (34). Other LysE superfamily members are associated with antibiotic resistance and metal ion transport. These analyses support the hypothesis that Gap-like proteins are involved in the export of metabolites across the cell membrane, and that Sap specifically may be involved in SL-1 transmembrane transport.

The *rv3822* locus encodes a 404-aa protein with a predicted N-terminal transmembrane helix (aa 46-64). The C-terminal domain (aa 104-325) has predicted α/β-hydrolase secondary structure that is conserved among certain members of the Mtb PE and PPE protein families, but the native functions of these proteins are unknown (35,36). The closest homologue of Rv3822 is Rv1184c, which shares the conserved C-terminal domain and is associated with the polyacetyltrehalose biosynthetic locus. Rv3822 is more distantly related to Mtb proteins known as the cutinase-like proteins (CLPs) (Fig. 2), which have been shown to have phospholipase, esterase and thioesterase activities on a variety of model substrates (37-39). One of the CLPs, Rv3802c, is associated with the mycolic acid biosynthetic gene locus and displays hydrolitic activity similar to that of other CLPs, but its possible role in mycolic acid biosynthesis has not been elucidated (37). Due to its similarity to CLPs, we refer to Rv3822 as a cutinase-like hydrolase protein (Chp1). From an *in silico* structural analysis, we identified a putative catalytic triad Ser156-Asp232-His255 in Chp1 based on the alignment of these residues with the known active site of a fungal acetylxylan esterase from *Penicillium purpurogenum* (36,40). Based on these analyses, we hypothesized that Chp1 is a membrane-anchored acyltransferase involved in SL-1 biosynthesis.

*Initial characterization of the roles of Sap and Chp1 in mycobacterial sulfolipid biosynthesis*- To test our hypothesis that Sap and Chp1 function in SL-1 biosynthesis, we compared the lipid profiles of Mtb Erdman wild-type cells and the gene disruption strains Δ*stf0*, Δ*sap*, Δ*chp1* and Δ*mmpL8*. Cells were grown in the presence of 14C-propionate, which preferentially labels methyl-branched lipids, and the cell pellet lipid extracts were analyzed by thin-layer chromatography. SL-1 was detected in wild-type cells, but not in Δ*mmpL8* cells, which accumulated SL1278 as previously observed (Fig. 3) (18,19). The Δ*chp1* strain displayed a similar phenotype to Δ*mmpL8*. Intriguingly, Δ*sap* not only accumulated SL1278, but also produced SL-1, albeit at reduced levels. The complementation of Δ*chp1* and Δ*sap* with their corresponding genes restored the ability of these strains to synthesize SL-1. Thus, the reduced amount of SL-1 produced by the Δ*sap* mutant is not due to a downstream effect of the tagged gene deletion on *chp1* transcription. Metabolic labeling with 35S-sulfate to detect sulfated lipids yielded analogous results and further confirmed the identity of SL-1 and SL1278; neither metabolite was observed in Δ*stf0*, which does not produce sulfated trehalose and therefore lacks sulfated glycolipids (see supplemental Fig. 1) (16).

These results were corroborated by high-resolution mass spectrometry analysis of the surface lipid and cell pellet lipid fractions, which were obtained by extracting cells with hexanes and 1:1 chloroform/methanol, respectively (Fig. 4, supplemental Fig. 2). Uniquely and unexpectedly, SL1278 was found in Δ*chp1* in the surface lipid...
fraction as well as the cell pellet fraction. Both this SL-1278 transport defect and SL-1 biosynthesis were restored by complementation with wild-type chp1, confirming that the presence of SL-1278 in the surface lipid fraction is not due to a non-specific loss of membrane integrity in Δchp1. The presence of SL-1278 in the surface lipid fraction in Δchp1, but not in either Δsap or ΔmmpL8, suggests that both Sap and MmpL8 are necessary for sulfolipid transport.

Biochemical characterization of Chp1 function. To test our hypothesis that Chp1 is membrane-anchored, we determined its subcellular location by fractionation of M. smegmatis cells expressing full-length Chp1. As predicted, Chp1 was found in the cytosolic membrane- and cell wall-enriched fractions (Fig. 5A). Based on the hypothesis that Chp1 is most likely associated with the cytosolic membrane, we determined the enzymatic activity of a set of Chp1 fusion constructs attached to either β-galactosidase (βGal), which is folded and active only in the cytosol, or to alkaline phosphatase (AP), which is active only in the oxidizing environment of the periplasm (36,45). Fusions of βGal or AP to the C-terminus of full-length Chp1 or the Chp1 putative transmembrane helix (aa 1-71) were expressed in M. smegmatis and the cells were assayed for enzymatic activity. In all cases, activity above background was detected only when Chp1 was fused to β-Gal (Fig. 5B). Similar results were obtained by qualitative examination of growth on agar containing chromogenic substrate (supplemental Fig. 3). These data suggest that Chp1 is membrane-associated and oriented with the C-terminal catalytic domain in the cytosol (Fig. 2).

We next expressed and purified from E. coli the conserved C-terminal catalytic domain of Chp1 (Chp1-cat, aa 65-404) and sought to characterize its enzymatic activity in biochemical assays. We first tested for covalent labeling by a fluorescent fluorophosphonate activity-based probe (TAMRA-FP), which selectively modifies the catalytic residue of serine hydrolase superfamily members (41). Chp1-cat was effectively labeled with TAMRA-FP when properly folded though not when denatured by heat, and mutation of the putative catalytic Ser156 to Ala abrogated reactivity, confirming the assignment of Chp1 as a serine hydrolase (supplemental Experimental Procedures and Figure S4). To test Chp1-cat activity on sulfolipids, we synthesized the diacyl sulfolipid trehalose-2-sulfate-2'-palmitate-3'-stearate (T2S-PS) as a SL-1278 analogue. Surprisingly, when Chp1-cat was incubated with T2S-PS, products of lipid acyl transfer were detected in the reaction mixture by MALDI-MS, even in the absence of any acyl-CoA donor (Fig. 6A). The higher molecular weight components at m/z 1192 and 1458 were consistent with one and two additions of stearate to T2S-PS to form T2S-PS₂ and T2S-PS₃. These products indicate that Chp1 can use T2S-PS as both an acyl donor and acceptor. The observed products imply that Chp1 catalyzes the regiospecific transfer of a fatty acyl group, in this case stearate, from the 3' position of an acceptor molecule to the 6- or 6'-position of an acceptor molecule. By this mechanism, T2S-P (i.e., the monoacylated SL-1 precursor SL₆₅₉) should be generated as a by-product, and indeed this species is also observed in the mass spectrum. Palmitoyl-CoA did not successfully compete with T2S-PS as an acyl donor, as the products of palmitate addition to T2S-PS were not detected (supplemental Fig. 5A). Chp1-cat also did not appear to use SL-A, a tetraacylated analogue of SL-1, as an acyl donor to T2S-PS, but was capable of hydrolyzing SL-A (supplemental Fig. 5B,C) (24).

Tandem MS (MSⁿ) fragmentation of the T2S-PS₃ ion at m/z 1192 revealed a mix of regioisomers in which the additional stearoyl group was attached to either glucose monomer of T2S (Fig. 6B). SL₁₈₆₅, a triacylated-T2S species (trehalose-2-sulfate-3'-palmitate-4',6'-bisphthioceranoate) purified from wild-type H37Rv Mtb was found by MSⁿ analysis to comprise an analogous mixture of regiosomers (supplemental Fig. 6). Based on these data, we postulate that Chp1 catalyzes acyl transfer to either glucose monomer of the acceptor molecule, and this lack of regioselectivity with respect to the acceptor substrate is physiologically relevant.

Finally, we reconstituted the biosynthesis of SL-1 in a one-pot reaction by combining the acyltransferases PapA2 and PapA1 and Chp1-cat with palmitoyl-CoA as the acyl donor and T2S as the acceptor substrate. The product mixture included all of the products expected from a series of acyl transfer reactions, including the mono-, di-, tri-, and tetraacylated species (Fig. 6D). In the absence of Chp1, only the mono- and diacylated species were detected, as observed previously (15).
Chp1 inhibition by tetrahydrolipstatin (THL) in Mtb - Because Chp1 is a serine hydrolase-type enzyme that recognizes a hydrophobic substrate, we hypothesized that it may be inhibited by THL, a clinically approved lipase inhibitor. More commonly known as Orlistat (Xenical; Roche), THL is a lipophilic lactone active against gastric lipase and is approved for the treatment of obesity. THL has been shown to have bactericidal effects on some mycobacterial species. More specifically, THL inhibits general TAG lipase activity in M. bovis BCG as well as the in vitro activity of the CLP family member Rv3802c and the extracellular lipase Rv0183 (37,42-45). In this study, Mtb treated with THL and labeled with 14C-propionate showed a dose-dependent decrease in SL-1 production with a concomitant accumulation of SL1278 (Fig. 7). SL-1 synthesis was not completely suppressed even at THL concentrations close to the MIC of 50 μg/mL, consistent with the hypothesis that THL has multiple targets that contribute to its bactericidal activity. These results support our prediction that the lipophilic lactone THL preferentially inhibits Chp1 over the SL-1 acyltransferases PapA1 and PapA2 due to its higher affinity for Chp1 and/or its preferential partitioning into lipid membranes where Chp1 resides.

Conclusions- Based on the in vitro data presented here, the SL-1 biosynthetic pathway appears complete: Stf0 sulfates trehalose to generate T2S, which is then acylated once by PapA2, once by PapA1 using fatty acids from Pks2, and twice by Chp1. However, the lipid profiles of the ΔmmpL8 and Δsap mutants contradict this linear scheme. Following formation of the SL1278 precursor, SL-1 biosynthesis in Mtb is also dependent on the transport-associated membrane protein MmpL8 and Sap (Rv3821). Indeed, although ΔmmpL8, Δsap and Δchp1 all accumulate SL1278, only in Δchp1 is SL1278 detected in the surface lipid fraction, implying that MmpL and Sap together mediate sulfolipid transport. However, while MmpL8 is essential for SL-1 formation, Sap appears to modulate flux through the pathway, similar to MmpS4-mediated modulation of glycopeptidolipid levels in M. smegmatis (46).

The accumulation of SL1278 in ΔmmpL8 and Δsap is consistent with two models for the coupling of biosynthesis and transport (Fig. 8) (13,14). In the “sequential” model, MmpL8 transports SL1278, which is then processed to SL-1 in the periplasm. (We here assume that MmpL8 acts solely as a lipid flippase; the question of how SL-1 is transported from the periplasm to its ultimate location in the mycobacterial outer membrane will not be discussed further.) However, this model contradicts our Chp1 topology results and also requires retrograde transport of SL659 byproducts for re-entry into the SL-1 pathway (Fig. 8).

The data presented here and elsewhere more strongly support the “scaffolding” model, in which MmpL8 facilitates biosynthesis and then transports the final SL-1 product across the cytosolic membrane. MmpL8 could couple lipid biosynthesis and transport by acting as a scaffold that nucleates a macromolecular complex of cytosolic PapAs and Pks2 and, based on this study, membrane-associated Chp1. The scaffolding concept has a precedent in the Mtb phthiocerol dimycocerosate lipid biosynthetic pathway, in which the transporter MmpL7 and the biosynthetic enzyme PpsE were shown to interact in a yeast two-hybrid assay (47). In the SL-1 pathway, the close association of related enzymes could facilitate recycling of the Chp1 side product SL659 back into the biosynthetic pathway and thereby drive the Chp1 reaction forward. Importantly, a recent high-resolution structural analysis of lipids extracted from ΔmmpL8 revealed unexpected triacylated sulfolipids, suggesting that Chp1 is active in the absence of MmpL8, although at reduced levels (48).

Sap could be an additional component of the proposed scaffold. While Sap is not absolutely essential for SL-1 biosynthesis, it appears to potentiate SL-1 levels and may confer specificity for sulfolipids over structurally similar glycolipids such as trehalose monomycolate and polyacyltrehalose. In this role Sap may be functionally analogous to small integral membrane proteins that are substrate-specific components in bacterial vitamin transport (49). Close association between membrane-associated Chp1 and an MmpL8/Sap complex could aid transport of SL-1 away from Chp1. This action would prevent reverse hydrolysis by Chp1, an activity at low levels in vitro (Figure S5C).

Chp1 catalysis of two successive acyl transfers is similar to the activity of the polyacyltrehalose enzyme PapA3, which esterifies trehalose with palmitic and mycolipenic acid (50). However, unlike the PapA enzymes, Chp1 rather does not use an
activated thioester donor such as an acyl-CoA, but rather catalyzes regioselective transesterification between two substrate molecules. This mechanism has precedent in Mtb with the antigen 85 complex (Ag85A, B, and C), a group of cell-wall mycolyltransferases that synthesize trehalose dimycolate from two molecules of trehalose monomycolate (51). In comparison, the activity of Chp1 is more complex, with a combination of specificity and promiscuity that raises intriguing questions about how it achieves substrate recognition and chemical specificity. On the one hand, Chp1 is selective for diacyl over monoacyl sulfolipids and specific for the donor 3'-T2S position, yet it can accommodate two different triacyl regioisomers and catalyze ester formation at two chemically non-equivalent positions. As has been noted previously, the SL-1 and polyacyltrehalose biosynthetic loci are structurally similar (50). Indeed, the closest homologue of Chp1 is Chp2, encoded by rv1184c in the polyacyltrehalose locus (43% sequence identity), and preliminary results indicate that Chp2 is also essential for polyacyltrehalose biosynthesis (J. C. Seeliger, unpublished data).

These data thus define a class of mechanistically similar glycolipid acyltransferases that comprises the Ag85 complex, Chp1 and possibly Chp2. Other members may include eight Mtb PE-PPE proteins that are the closest homologues of Chp1 and Chp2 (35). Although the PE/PPE protein family constitutes about 10% of the Mtb genome, only Rv3097c (PE_PGRS63, or LipY) has assigned enzymatic activity as a cell-wall associated TAG lipase (28,62,63). Whether our new insights into Chp1 acyltransferase activity will aid the functional assignment of these conserved proteins—and whether they can be targeted as a group by inhibitory molecules like THL—awaits further investigation.

REFERENCES

2. Gangadharam, P. R. J., Cohn, M. L., and Middlebrook, G. (1963) Tubercle 44(4), 452-455

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FOOTNOTES

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FIGURE LEGENDS

**FIGURE 1.** Genes of unknown function in the sulfolipid-1 locus may be involved in biosynthesis. Genes associated with SL-1 biosynthesis are clustered in the Mtb genome, but one putative operon contains two genes of unknown function, *sap* (*rv3821*) and *chp1* (*rv3822*). After sulfation of trehalose by Stf0, trehalose-2-sulfate is successively esterified by PapA2 and PapA1. MmpL8 participates in the final two esterifications by an unknown mechanism and is essential for sulfolipid transport; Chp1 and Sap may also be involved.

**FIGURE 2.** Sap and Chp1 are membrane-associated proteins, and Chp1 is related to the Mtb cutinase-like proteins. (top) A member of the Gap protein family, Sap is an integral membrane protein with six transmembrane helices and a hydrophilic domain (aa 93-134). Chp1 has a single predicted N-terminal transmembrane helix followed by a conserved C-terminal PE-PPE domain with an α/β-hydrolase fold. The domain structures and membrane orientations shown were predicted by the TMHMM algorithm. (bottom) The Chp1 putative catalytic serine (black box) was identified by combined sequence/structure alignment with *P. purpurogenum* AXE II. In both Chp1 and the related Chp2, the sequence surrounding
Complete sulfolipid-1 biosynthesis in Mycobacterium tuberculosis

this serine shares some similarity with the conserved cutinase motif (residues in bold). In contrast, the Mtb CLPs have an identifiable, albeit modified cutinase motif (38).

**FIGURE 3.** Chp1 is essential for SL-1 biosynthesis and Sap modulates SL-1 levels. Mtb wild type, Δsap, Δchp1, ΔmmpL8 and corresponding complemented strains were metabolically labeled with 14C-propionate. Cell pellet extracts were analyzed by TLC and phosphorimaging. SL-1 was observed at reduced levels in Δsap and not at all in Δchp1 and ΔmmpL8, and all three strains accumulated SL1278. The wild-type lipid profile was restored by complementation for all strains.

**FIGURE 4.** Δchp1 transports SL-1278 to the cell surface. ESI-FT-ICR MS analysis of lipid extracts from Mtb wild type, Δsap, Δchp1, ΔmmpL8 showed that the three knockout strains lack SL-1 and accumulate SL1278. (To aid comparison, the m/z 2460 ion belonging to the SL-1 series is marked with a cross, and the m/z 1277.9, 1278.9, and 1279.9 ions belonging to the SL-1278 series are marked with asterisks to distinguish them from other isobaric compounds in the lipid extracts). In addition, SL1278 was found in the surface lipid fraction only in Δchp1, and both SL-1 production and the SL-1278 transport phenotype were restored by complementation with chp1.

**FIGURE 5.** Chp1 localizes to the cell membrane with the catalytic domain in the cytosol. (A) Immunoblot on subcellular fractions of *M. smegmatis* expressing Chp1 with a C-terminal 3xFLAG tag shows Chp1 enriched in the cell membrane and cell wall. KatG and MspA are markers for the cytosol- and cell wall-enriched fractions, respectively. (B) In *M. smegmatis* strains expressing full-length Chp1 or the Chp1 N-terminal domain with C-terminal fusions to AP (light gray bars) and βGal (dark gray bars), enzymatic activity is observed only from βGal fusions. *M. smegmatis* strains transformed with empty vector, or AP or βGal with or without an N-terminal secretion signal served as negative and positive controls. Turnover of colorimetric substrates is expressed in Miller units.

**FIGURE 6.** Chp1 uses diacyl-T2S as an acyl donor and acceptor. (A) MALDI-MS analysis revealed higher-molecular weight reaction products when Chp1-cat was incubated with T2S-PS. Observed ions at m/z 659.1, 1192.4, and 1458.4 are consistent with the formation of the designated sulfolipid species. Starred ions indicate a minor T2S-P2 contaminant in the T2S-PS stock, as well as the corresponding T2S-P2S and T2S-PS2 product ions following stearate addition from T2S-PS. (B) Reaction scheme for Chp1 activity on T2S-PS. (C) MS² and subsequent MS³ (inset) analysis of the m/z 1192 ion showing fragmentation peaks consistent with stearate on either the glucose or acyl-sulfoglucose monomers (6 and 6’ positions of T2S, respectively). (D) Incubation of PapA2, PapA1, and Chp1 with T2S and palmitoyl-CoA yields ions at m/z 897.4, 1135.4, and 1374.4 consistent with acylation products T2S-P2, T2S-P3, and T2S-P4.

**FIGURE 7.** THL treatment specifically inhibits the conversion of SL-1278 to SL-1. Lipid extracts from Mtb treated with different concentrations of THL for 6 h followed by 14C-propionate labeling reveal the dose-dependent, but incomplete, inhibition of SL-1 and the accumulation of SL1278 by TLC and phosphorimaging. Lower panel shows phthiocerol dimydocerosate loading control.

**FIGURE 8.** Proposed model for SL-1 biosynthesis and transmembrane transport. The data are most consistent with a model in which Chp1 completes SL-1 biosynthesis in the cytosolic leaflet and MmpL8 and Sap transport SL-1 across the membrane. The membrane localization of Chp1 and the coupling of biosynthesis and transport via MmpL8 suggest that the SL-1 machinery may form a macromolecular complex to facilitate function. The mechanisms by which SL-1 is transported to the mycobacterial outer membrane are unknown. (Note that in this figure, the hydroxyphthioceranoic groups on SL-1 are truncated.)
Figure 1
Complete sulfolipid-1 biosynthesis in Mycobacterium tuberculosis

Figure 2

![Diagram of Sap and Chp1 with protein sequences and motifs](image-url)

- **Sap** and **Chp1** are shown with their predicted TM helix and catalytic domain.
- **P. purpurigenum** esterase (AXE II) is also depicted.
- **Cutinase 1 motif** is highlighted with sequences for Rv3822, Chp1, Rv1184c, Chp2, P. purpurigenum esterase, and Mtb Clp consensus.
- Color codes indicate sequence similarity: red (90-100%), orange (80-90%), yellow (50-80%).
- * derived from ProSite ID PS00155
Figure 3
Complete sulfolipid-1 biosynthesis in Mycobacterium tuberculosis

Figure 4

<table>
<thead>
<tr>
<th>Surface lipids</th>
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<tr>
<td>ΔmmpL8</td>
<td></td>
</tr>
<tr>
<td>Δsap</td>
<td></td>
</tr>
<tr>
<td>Δchp1</td>
<td></td>
</tr>
<tr>
<td>Δchp1::chp1</td>
<td></td>
</tr>
</tbody>
</table>

2400  2425  2450  2475  2500  2525  2550  2575  2600
1278  1280  m/z
Complete sulfolipid-1 biosynthesis in Mycobacterium tuberculosis

Figure 5

(a) Western blot analysis of α-FLAG, α-KatG, and α-MspA for vector and Chp1-FLAG constructs under different conditions (C, M, W).

(b) Graph showing galactosidase and phosphatase activities for different constructs: vector, cytosolic control, secreted control, Chp1, Nterm Chp1. Bar graphs indicate Miller units for each condition.
Figure 7

Complete sulfolipid-1 biosynthesis in Mycobacterium tuberculosis
Elucidation and Chemical Modulation of Sulfolipid-1 Biosynthesis in *Mycobacterium tuberculosis*

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