Structural enzymological studies of the long chain fatty acyl-CoA synthetase FadD5 from the *mce1* operon of *Mycobacterium tuberculosis*

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Abstract

The cell wall of *Mycobacterium tuberculosis* (Mtb), the causative agent of tuberculosis, is rich in complex lipids. During intracellular stage, Mtb depends on lipids for its survival. Mammalian cell-entry (Mce) 1 complex encoded by the *mce1* operon is a mycolic/fatty acid importer. *mce1* operon also encodes a putative fatty acyl-CoA synthetase (FadD5; Rv0166), potentially responsible for the activation of fatty acids imported through the Mce1 complex by conjugating them to Coenzyme A. Here we report that FadD5 is associated to membrane although it can be purified as a soluble dimeric protein. ATP and CoA binding influence FadD5's stability and conformation. Enzymatic studies with fatty acids of varying chain lengths show that FadD5 prefers long chain fatty acids as substrates. X-ray crystallographic studies on FadD5 and its variant reveal that the C-terminal domain (~100 residues) is cleaved off during crystallization. Noteworthy, deletion of this domain renders FadD5 completely inactive. SAXS studies, however, confirm the presence of full length FadD5 as a dimer in solution. Further structural analysis and comparisons with homologs provide insights on the possible mode of membrane association and fatty acyl tail binding.

Keywords: *Mycobacterium tuberculosis*, mce operon, FadD5, FACS, FAAL.

1. Introduction

Tuberculosis (TB) is an alarming global health issue and millions of new cases are being reported every year with more than a million deaths every year [1]. *Mycobacterium tuberculosis* (Mtb), the causative agent of TB, demonstrates remarkable metabolic versatility due to its unique fatty acid metabolism system. Mtb possesses a large number of genes involved in fatty acid metabolism. Among the lipid metabolizing genes, 34 genes are designated as *fadD*s [2] which code for acyl activating enzymes (AAE). Sequence alignment and a phylogenetic tree, shows two subgroups of FadDs, namely, fatty acyl-AMP ligase (FAAL) (EC 6.2.1.20) and the fatty acyl-CoA synthetase (FACSs) (EC 6.2.1.3) [3]. FAALs activate fatty acids by converting them to acyl-adenylates and transfer them to modular enzymes such as polyketide synthases for chain extension or biosynthesis of lipidic metabolites. Most frequently, genes coding for FAAL are present adjacent to genes coding for polyketide synthases [4-6]. FACSs, on the other hand, activate fatty acids by conjugating them to coenzyme A (CoA) [7]. The addition of CoA to the fatty acids is the first step needed for further processing of fatty acids by other pathways such as β-oxidation. FACS converts fatty acid to fatty acyl-CoA in a two-step reaction. One distinguishing difference from FAAL to FACS is the presence of ~20 amino acid insertion motif in FAAL [4]. Structural studies have been conducted for FadDs from Mtb, such as FadD10, FadD13, FadD23, FadD28 and FadD32 in the unliganded form or in the presence of different ligands and also with only the N-terminal domain [3, 7-10].

FadDs contain the conserved AAE fold with two domain structure with a large N-terminal domain and a smaller C-terminal domain. The substrate binding pocket is located between the two domains [4]. In FACS, during catalysis, C-terminal domain moves from adenylate to thiolation conformation which is known as domain alternation [11, 12]. One of the key characteristics of long chain FACS enzymes is their membrane bound nature which is important for anchoring large substrates [9, 13].

Function of *mce1* operon has been studied extensively and the structural studies have been conducted on individual Mce proteins as well as full Mce1 complex [14-16]. Interestingly, *mce1* loci has a gene *fadD5*, a putative FACS which is co-transcribed with the other genes in the *mce1* operon [17]. Previous studies showed that mice infected with *fadD5* mutant survived significantly longer than those infected with the wild type Mtb [18] suggesting that FadD5 is a potential drug target. This study also showed that *fadD5* mutant grows slower in minimal media supplemented with mycolic acid compared to other long chain fatty acid as a sole carbon source [18] suggesting FadD5 being involved in mycolic acid recycling during infection. Moreover,

mce1 operon mutant also shows an accumulation of mycolic acid in its cell wall which also suggests that Mce1 complex is a mycolic acid ABC transporter [15]. Interestingly, whenever *E.coli fadD* was complemented with Mtb *fadD*5, it was unable to utilize long chain fatty acid as a sole carbon source, demonstrating the uniqueness of FadD5 which indicate its different function or substrate specificity [18]. Though FadD5 has been studied *in vivo* no structural and enzymatic studies have been carried out so far.

Considering the importance of FadD5 involved in activating the lipids transported by the Mce1 complex, this study is about the structural and functional characterization of FadD5. Biophysical studies suggested that although FadD5 is stable as a soluble dimeric enzyme, it is also associated to membrane. Interestingly, the C-terminal domain was cleaved off during crystallization. Enzymatic studies demonstrated its FACS activity with chain length of up to 24. Structural and modelling studies provide insights on the possible mode of fatty acyl tail binding. Overall, the studies provide insight on the structural and enzymatic properties of FadD5, an important enzyme for the utilization/recycling of lipids imported by the Mce1 complex.

2. Materials and methods

2.1 Sequence analysis

The sequence similarity was analyzed by the Basic Local Alignment Search Tool (BLAST) program from the NCBI, USA server against protein data bank [19]. MycoBrowser portal (http://mycobrowser.epfl.ch) was used as a source to get gene and protein information of Mtb [20]. Multiple sequence alignment was performed by the T-Coffee program on EMBL-EBI website [21] and sequence alignment was visualized with ESPript3 [22].

2.2 Cloning and expression of fadD5

fadD5 was PCR amplified and cloned into MCS-1 of pETDuet-1 vector using a restriction-based cloning approach using EcoRI and HindIII restriction enzymes resulting in a clone coding for His_6 tag at the N-terminus. The genomic DNA of Mtb H37Rv (purchased from ATCC) was used as the template. A deletion construct coding for $FadD5_{1-448}$ was prepared, truncating the region coding for the C-terminal domain. All the constructs made were confirmed by DNA sequencing. The constructed vector pETDuet-*fadD5* and pETDuet-$fadD5_{1-448}$ was transformed into chemically competent *E. coli* BL21 cells. Overnight-grown cultures were added into new LB media and grown at 30 °C until the OD_{600} reached 0.6 and expression of *fadD5* was induced by adding 0.1 mM isopropyl β-D-thiogalactopyranoside (IPTG) at 20 °C.

2.3 Purification of FadD5

The cells expressing FadD5 and $FadD5_{1-448}$ were harvested by centrifugation at 4000 g for 20 mins at 4 ºC. The harvested bacterial pellet was resuspended in lysis buffer (20 mM HEPES pH 7.5, 500 mM NaCl, 5 mM $MgCl_2$, 5 mM Imidazole, 1 mM β-mercaptoethanol (BME)) with one EDTA-free protease inhibitor tablet, lysozyme, DNase and RNase. The cells were lysed using a French press and the soluble fraction was collected by centrifuging for 40 min at 16000 g at 4 °C. Then, FadD5 was purified by immobilized metal affinity chromatography (IMAC) by washing with the lysis buffer and eluted with a buffer containing 400 mM imidazole. The eluted protein was concentrated and injected into Superdex 200 10/300 (Cytiva) size-exclusion chromatography (SEC) column pre-equilibrated with 20 mM HEPES buffer containing 500 mM NaCl, 5 mM $MgCl_2$, 1 mM BME at pH 7.5. The peak fractions were collected, concentrated, flash-frozen in aliquots and stored at −70 °C for further use. The fractions were analyzed by 12% SDS-PAGE and the identity of the protein was confirmed by peptide mass finger printing analysis.

2.4 Membrane association studies of FadD5

For membrane association studies, FadD5 and $FadD5_{1-448}$ expressed cells were lysed using a French press and cell debris were removed by centrifugation at 6000 g. From the resulting supernatant, membrane fraction was isolated by ultracentrifugation at 45000 g for 1 h at 4 °C. The pellet was washed twice by resuspending in a buffer containing 20 mM HEPES, 500 mM NaCl, 5 mM $MgCl_2$, 1 mM BME at pH 7.5 and membrane fraction was isolated by centrifugation again. The membrane was solubilized in the membrane extraction buffer containing 10 mM DDM. FadD5 was purified from the solubilized fraction as mentioned earlier and analyzed by SDS-PAGE and peptide mass fingerprinting analysis.

2.5 Blue native PAGE (BN-PAGE)

Approximately 40 µg of protein was loaded onto 4-15% mini-PROTEAN TGX precast gel (BIORAD) and run for 2-3 hours at 20 mA at 4 ºC using Tris-glycine buffer as anode buffer and Tris-glycine supplemented with 0.02% Coomassie G-250 as the cathode buffer. Bovine serum albumin (BSA) was used as a control. The gel was then destained overnight in water and the bands were analyzed.

2.6 Multi-angle laser light scattering (MALLS)

60 µl (1 mg ml^{-1}) of purified FadD5 or its variant was injected into a Superdex 200 Increase 10/300 GL column (GE Healthcare) pre-equilibrated with protein buffer coupled to a Shimadzu HPLC/FPLC system, a refractive index (RI) detector (Wyatt Technologies), a UV detector and a MALLS device

(Wyatt Mini DAWN Treos instrument, Wyatt Technologies). The molecular weight of the protein was calculated (UV and RI signals were used as the source of concentration) for the eluted peaks using *ASTRA* 7.0 software (Wyatt Technologies).

2.7 Circular dichroism (CD) spectroscopy

Protein was diluted in water to a final protein concentration of 0.1 mg ml^{-1}. The buffer was also diluted in a similar way to use as the blank. The final buffer composition was 2 mM HEPES, pH 7.5, 50 mM NaCl, 0.1 mM BME. CD spectroscopy data were collected in a Chirascan CD spectrometer (Applied Photophysics, Leatherhead, UK) between 280 and 190 nm at 22 °C in a 0.1 cm path-length quartz cuvette. *Chirascan Pro-Data Viewer* (Applied Photophysics) and *CDNN* software (http://www.xn--gerald-bhm-lcb.de/download/cdnn) were used to process and deconvolute the collected CD data to calculate the secondary structure composition. The direct CD measurements (θ; mdeg) were converted into mean residue molar ellipticity ($[\theta]_{MR}$) by Pro-Data Viewer. Thermal unfolding was recorded between 190 and 280 nm from 22 to 92 °C at a rate of 1 °C per min using a Peltier temperature control TC125 (Quantum Northwest, Liberty Lake, WA). Thermal melting temperature (T_m) was calculated using *Global3* software (Applied Photophysics) using the global fit analysis protocol by fitting the data to a one-transition model.

2.8 Nano differential scanning fluorimetry (nanoDSF)

A label-free fluorescence-based approach was used for thermal stability analysis of FadD5 through nanoDSF, using Prometheus NT.48 (NanoTemper Technologies, Germany). 10 µl of the purified protein alone or mixed with 2 mM ATP or 2 mM CoA was loaded into standard glass capillaries for nanoDSF. The fluorescence signal resulting from the thermal unfolding of the protein was measured at 330 nm and 350 nm (F350/F330) by heating the sample from 20 °C to 90 °C by a thermal ramping rate of 1 °C per min. The fluorescence intensity ratio and its first derivatives were calculated with the PR.ThermalControl (NanoTemper Technologies, Germany). The data was further analyzed with MoltenProt (https://spc.embl-hamburg.de/app/moltenprot).

2.9 Enzyme activity assay

FadD5 activity was measured by monitoring the first half of the reaction through the measurement of inorganic phosphate (Pi) produced from the hydrolysis of inorganic pyrophsophate (PPi) resulting from the enzyme catalyzed reaction [23, 24]. The amount of Pi was quantified using a colorimetric Malachite Green phosphate assay kit (Sigma) at 630 nm. The standard 100 µl reaction contained 50 mM HEPES, pH 7.5, 5 mM $MgCl_2$, 1 mM BME, 0.001% Brij-35, 0.5 mM ATP, 0.5 mM CoA, 0.3 U pyrophosphatase, 100 µM fatty acids. The reaction was started by adding 0.5 µg of purified protein

and continued for 30 min at RT. Then the reaction was stopped by incubating the reaction mix at 80 ºC in a water bath for 5 min. Then the reaction was diluted with 400 µl of 50 mM HEPES, pH 7.5 buffer. Then 80 µl of the sample was mixed with 20 µl of color developing reagent according to the manufacturer's recommendation and waited for 30 min for color development. Then the absorbance was recorded in a Tecan Spark plate reader (Tecan, Switzerland). Reaction without protein/substrate was used as a blank. Then the amount of Pi released was calculated from the calibration curve plotted with a known concentration of Pi according to the manufacturer's instruction. All the experiments were done in triplicates.

2.10 Liquid chromatography–mass spectrometry (LCMS) experiment to detect the product formation by FadD5

Standard reaction without CoA was considered as the first half of reaction and addition of CoA was considered as the full reaction. The control reactions were carried out without the enzyme. LCMS was used to detect the formation of C12-AMP and C12-CoA from C12 in a two-step reaction. The standard reaction mix was diluted 500-fold and analysed by LCMS on a Q Exactive system linked to an Aquity UPLC system equipped with ACQUITY UPLC® BEH C18 1.7 µm (2.1 mm x 100 mm) column (Waters Acquity). The column was eluted at 0.3 ml min^{-1} with a gradient of 10 mM ammonium acetate (solvent A) and acetonitrile (solvent B) with the following gradient points: 1 min 99% A, 9 min 10% A, 1 min 99% A. Mass spectra were recorded in negative ion mode from m/z 300 to 1500 at resolution of 70000 for up to 200 msec per scan and automatic gain control target at $3x10^6$. Data were analyzed by the Qual browser option of XCalibur (Thermo Fisher).

2.11 Small-angle X-ray scattering (SAXS)

SAXS data were collected at B21 beamline at Diamond Light Source, UK in batch-mode. Measurements were collected for FadD5 at 4 mg ml^{-1} and in the presence of 2 mM ATP or 2 mM CoA, with an appropriate buffer as blank. 20 frames/conditions were collected. ScÅtter and PRIMUS software [25, 26] were used for the initial data processing. The buffer scattering was subtracted from the protein scattering using ScÅtter and the subtracted data was rebinned. The radius of gyration (R_g), forward scattering I(0), interatomic distance distribution function P(r), maximum particle distance (D_{max}) and porod volume (V_p) were calculated by *ScÅtter* and *PRIMUS*. Molecular weight was calculated using the calculated porod volume and *SAXSmow* [27].

2.12 Crystallization studies

FadD5 and its variants were crystalized in TTP plates using the sitting drop vapor diffusion method using an alternative reservoir approach [28] using Mosquito robot (SPT Labtech). MIADSplus

commercial screen (Molecular dimensions) was used as the reservoir solution. Freshly purified, FadD5 or its variants were mixed with 5 mM CoA and 1 mM ATP to a final concentration of 18 mg ml^{-1} and mixed with 0.1 M Sodium formate, 20 % w/v SOKALAN CP 45 (crystalizing solution) in 1:3 ratio at room temperature. Crystal appearance was monitored by IceBear [29]. Crystals appear in 1-5 days. The crystalizing solution was mixed with 25% glycerol (v/v) for cryo-protection and flash-frozen in liquid nitrogen for diffraction studies. For binding studies, cryoprotectant solution was supplemented with ATP and CoA.

2.13 Data collection, structure determination and structure refinement

X-ray crystallographic data from the crystals of FadD5 and its variants were collected from Diamond Light Source (UK). Data reduction and scaling of the collected data was done by *XDS* [30] and *AIMLESS* [31] or the auto processed data from different data processing software available at Diamond Light Source, such as *fast_dp* [32], *xia 2* [33] were used for further processing. Molecular replacement was done using *Expert MR-PHASER* of *CCP4i2* package [34] using FadD13 structure (PDB id: 3R44) as the search model. The model building was performed with *COOT* [35] and the refinement was done by *REFMAC* from *CCP4i2* [34] or using *Phenix* [36]. The images of the structures were generated, visualized and compared using *PyMOL* (https://www.pymol.org) or *UCSF Chimera* [37].

3 Results and discussion

3.1 Sequence analysis shows the conserved motifs of FadD5

Mtb FadD5 (Uniprot id: O07411, Mycobrowser id: Rv0166) consists of 554 amino acids with a calculated molecular mass of ~60 kDa. The recombinant MtFadD5 has an additional 16 amino acids with a total calculated molecular mass of ~62 kDa. Sequence comparison with other FadD homologs shows the presence of the conserved motifs, A1 to A10 and signature motifs in FadD5 as described in previous studies (Fig S1) [38, 39]. Important motifs identified in FadD5 are listed here. i) 27 amino acids long signature motif/FACS motif, responsible for fatty acid binding (^{407}GGWFHSGDLVRMDSDGYVWVVDRKKDM^{433}). ii) Linker (L) motif responsible for various closed conformations of the C-terminal domain, displays a consensus sequence "Asp-Arg-Xaa-Lys" in all long chain FACSs, while the short chain and medium chain FACSs, the consensus motif sequence is "Gly-Arg-Xaa-Asp" [40, 41]. Sequence analysis suggests that FadD5's L motif is Asp428-Arg429-Xaa-Lys431 (^{428}DRKKDM^{433}) as observed in other long chain FACS that connect N- and C-terminal domains. iii) P-loop (^{187}IMYTSGTTGRPKGA^{202}) is responsible for binding phosphate of ATP. iv) A motif (^{328}LAAFGQTE^{335}) for the binding of adenine ring of

ATP/AMP. P-loop and A motif collectively also known as ATP/AMP-binding signature motif [42, 43] (Fig S1). Gate (G) motif (^{232}VPLFHIAG^{239}) keeps the enzyme in the closed conformation required for catalysis and interact with the fatty acyl chain. G motif plays a role in determining the specific functions, activities and substrate length preferences in FadDs. Firefly luciferase's G motif contains Phe247 [44], potentially the gating residue for its catalytic activity. Similarly, the gating residue in TtLC-FACS is Trp234 [38]. The gating residue is thought to change conformation to accommodate longer fatty acyl chains. However, interestingly in FadD5, the corresponding residue is less bulky Ile240. Similarly, the gating residue in FadD13 is Leu226 [9] which is also known to bind very long acyl chains.

3.2 FadD5 and FadD5$_{1-448}$ are dimer in solution and are peripheral membrane proteins

FACS exists as monomers as well as dimers whereas FAALs mostly function as monomers [8, 9, 38]. The FadD5 and FadD5$_{1-448,}$ expressed in *E. coli* were purified from the soluble fraction using IMAC followed by SEC which shows that FadD5 and FadD5$_{1-448}$ elute at a retention volume of ~13.5 ml and ~14.5 ml respectively, in a 24 ml Superdex 200 10/300 column (Fig. 1A). Blue-native PAGE analysis shows a predominant band of FadD5 close to the dimeric band of BSA corresponding to a molecular mass of 132 kDa suggesting that FadD5 is purified as a homodimer in solution (theoretical molecular mass of 124 kDa) (Fig. 1B). The dimeric nature of FadD5 was further confirmed by SEC-MALLS experiment according to which the calculated molecular mass of FadD5 was ~115 kDa. Similarly, the molecular mass of FadD5$_{1-448}$ as calculated by SEC-MALLS is ~96 kDa which is close to the theoretical dimeric molecular mass of ~101 kDa. Further, the molar mass distribution of the peaks corresponding to FadD5 and FadD5$_{1-448}$ show that they are monodispersed in solution (Fig. S2).

Although we have purified FadD5 as a soluble protein without the use of any detergents, predictions from MemType2 [45] and PPM web server [46] suggested FadD5 to be a peripheral membrane protein. Purification from the membrane fraction of cells expressing FadD5 and analysis with SDS-PAGE clearly showed the presence of FadD5. This confirmed that FadD5 can be associated to membrane although it is stable as a soluble protein. Moreover, a similar study with FadD5$_{1-448}$ variant showed that the N-terminal domain is associated to the membrane (Fig. 1A).

3.3 ATP increases the stability of FadD5

CD spectroscopy analysis shows that the purified protein is well folded (Fig. S3A). Melting temperature analysis shows that it has a T_m of 43 ºC (Fig. S3B). Further, the T_m of FadD5 calculated

from nanoDSF is 44 ºC in close agreement to that calculated by CD. Thermal stability of FadD5 has increased by 3 ºC to 47 ºC in the presence of ATP. However, the addition of CoA to FadD5 did not change T_m (Fig. S4A). The aggregation onset temperature (T_{agg}) calculated from the inflection points (IPs)/T_m from the nanoDSF data also suggests that ATP has delayed thermal aggregation (Fig. S4B).

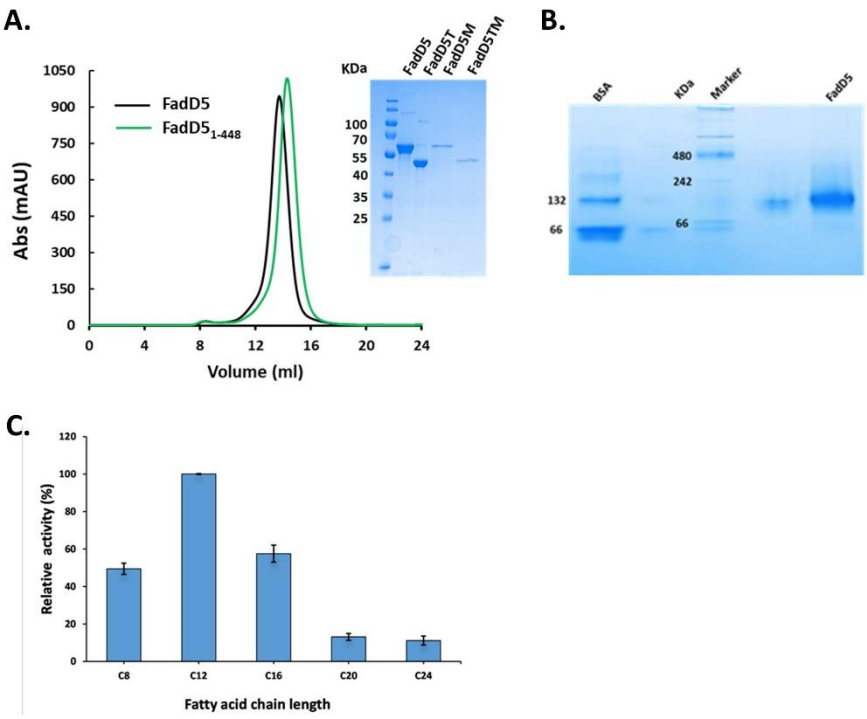

Fig 1: A. SEC profile and SDS-PAGE analysis of FadD5 and FadD5$_{1-448}$ from the soluble as well as membrane fraction solubilized using DDM. FD5=FadD5, T=Truncated, M=Membrane fraction. **B.** Blue-native-PAGE analysis for FadD5. **C.** Relative specific activity of FadD5 measured using fatty acids of different chain length from C8 to C24. The activity of FadD5 towards C12 was defined as 100%.

3.4 FadD5 is a FACS with preference for long chain fatty acids

The sequence analysis already suggested that FadD5 is a FACS with substrate specificity for very long acyl chains. Therefore, enzyme activity of FadD5 was tested with fatty acid substrates with varying acyl chain lengths; C8, C12, C16, C20 and C24 (Fig.1C). While all the tested substrates showed measurable activity, specific activity calculation showed that lauric acid (C12) has the highest specific activity followed by palmitic acid (C16). Further detailed enzyme kinetic studies were performed with C12 and C16 fatty acids. These studies revealed that C16 has a lower K_m value compared to C12. However, C12 has higher k_{cat} value than C16 (Table 1). N-

terminal domain alone did not show any activity confirming that the C-terminal domain is important to bind the substrate as also demonstrated recently in FadD23 [47].

Substrate	Specific activity (pmol $mg^{-1}min^{-1}$)	K_m (μM)	Vmax (pmol/min)	k_{cat} (min^{-1})	k_{cat}/K_m (M^{-1} S^{-1})
C12	2.92 ± 0.11	102 ± 8.55	1646 ± 109.3	0.20 ± 0.013	32.85 ± 1.05
C16	1.60 ± 0.07	89.83 ± 9.71	774.9 ± 23.95	0.096 ± 0.002	17.79 ± 1.35

Table 1: Specific activities and Michaelis-Menten kinetic constants of FadD5 towards C12 and C16 substrate

To further confirm the FACS activity of FadD5 the formation of the final product was tested through LCMS assays. We have used lauric acid (C12) as the substrate for this test. In the presence of ATP and CoA, FadD5 converts C12 into C12-AMP in the first half of the reaction and then to C12-CoA in the second half of the reaction. The reaction was monitored by following the accurate mass of C12-AMP $C_{22}H_{36}N_5O_8P$ (529.2228 Da) and C12-CoA $C_{33}H_{58}N_7O_{17}P_3S$ (949.2765 Da) by selected ion chromatography (SIC). In the control sample, no signal was detected, while the half reaction has a peak for C12-AMP and the full reaction shows both compounds C12-AMP and C12-CoA. The peaks indicated with peak 1 (RT 5.48) corresponds to m/z 528.2228 while peak 2 (RT 5.7) represents m/z 948.2765. The corresponding mass spectra are shown in Fig. S5. Therefore, through enzyme activity assays, we have demonstrated that FadD5 has activity with C12 to C16 fatty acids, providing evidence for its ability to metabolize long chain fatty acids. Tests with C20 and C24 could not be performed further due to solubility issues. It will indeed be interesting to see if FadD5 shows higher catalytic efficiency for these substrates.

3.5 FadD5 crystallizes with the C-terminal domain cleaved off

FadD5 was crystallized in sitting drop vapor diffusion method. Interestingly, FadD5 crystals appeared only when the drop contained a particular lot of condition B1 of the Midas plus screen whereas the reservoir solution could be entirely different. This approach is known as 'alternate reservoir' method [28]. The crystals obtained diffracted to about 2.8 Å resolution. The crystals belonged to the space group $P4_12_12$ with two molecules in the asymmetric unit based on the solvent content analysis. The closest available structural homolog, Mtb FadD13, was used for molecular replacement. Structurally, like other adenylate-forming enzyme family proteins, each monomer of FadD5 is composed of two domains, a larger N-terminal domain (residues 1-427) and a smaller C-terminal domain (residues 434-554) linked by a flexible linker (^{428}DRKKDM^{433}). Individual domain searches (N- and C-terminal domains) resulted in a solution in which the two

N-terminal subunits could be placed with an expected 2-fold symmetry as observed in other FadDs. Despite multiple trials, no solutions were obtained where the C-terminal domain could be placed confidently. However, the N-terminal domain could be built and refined to a final R-free and R of 0.23 and 0.20, respectively. N-terminal 1-19 residues did not show any density, most likely due to the disordered nature of this region. The determined structure of FadD5 is shown in Fig. 2. Crystals obtained were in unliganded form even after incubating the protein with CoA, ATP or CoA+ATP during crystallization. The detailed statistics of data collection and refinement are provided in Table 2.

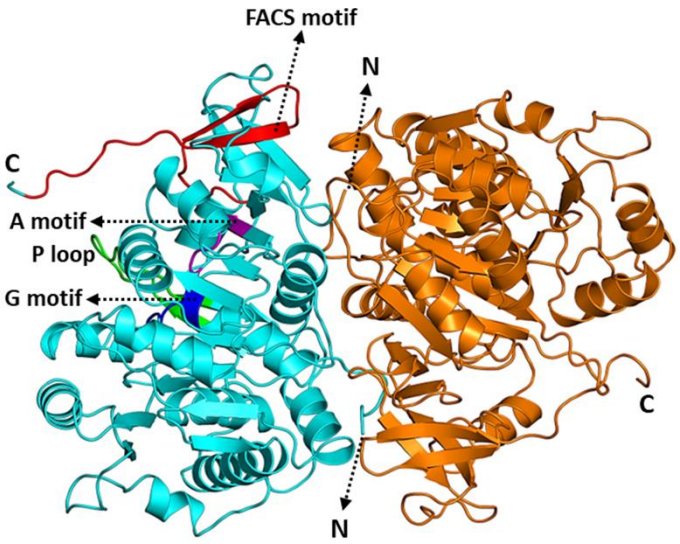

Fig 2: Cartoon representation of the solved crystal structure of FadD5 (amino acids 20-435) with 2 molecules in the asymmetric unit. Chain A in cyan and Chain B in orange. FACS motif in red, A motif in magenta, P loop in green, G motif in blue.

To understand why the C-terminal domain is missing, we further designed a construct for only the N-terminal domain ($FadD5_{1-448}$; as described in the previous sections). Interestingly, $FadD5_{1-448}$ crystallized under the same conditions, same space group and with the same crystal packing (Table 2). Furthermore, analysis of the crystal packing of the N-terminal domains suggested that there is no space available for the C-terminal domain to be placed in the asymmetric unit/unit cell (Fig. S6). This strongly suggests that the full length FadD5 undergoes proteolytic cleavage for reasons not yet known and the resulting N-terminal domain is crystalized. Noteworthy, the crystals do appear within 3 days. Therefore, we believe that the cleavage of C-terminal domain is mainly a crystallization artefact. Interestingly, the cleavage of C-terminal domain during crystallization is also reported for other Mtb FadDs, namely, FadD13 and FadD28 [4, 48].

Dataset	FadD5	$FadD5_{1-448}$
Crystallization		
Protein Buffer	20 mM HEPES, pH-7.5; 500 mM NaCl,1 mM BME	
Crystallization solution	0.1 M Sodium formate, 20 % w/v SOKALAN CP 45	
Protein concentration	18 mg ml^{-1}	
Cryo protectant	25% glycerol + Crystallization solution	
Temperature (°K)	295	
Data Collection		
Beamline	Diamond Light source Beamline I04	
Detector	DECTRIS EIGER X 16M	
Wavelength (Å)	0.9795	
Temperature (°K)	100	
Data Processing		
Space group	$P\ 4_1\ 2_1\ 2$	$P\ 4_1\ 2_1\ 2$
Unit cell parameters		
a, b, c (Å)	120.91 120.91 247.91	121.67 121.67 249.87
α, β, γ (°)	90 90 90	90 90 90
Processing software	XDS, AIMLESS	xia 2, AIMLESS
Resolution range (Å)	86.56–2.80 (2.90–2.80)	60.84–2.47 (2.56–2.47)
$CC_{1/2}$	0.99 (0.39)	0.99 (0.33)
R_{merge} (%)	0.13 (2.32)	0.03 (0.97)
R_{meas} (%)	0.14 (2.48)	0.04 (1.38)
R_{pim} (%)	0.05 (0.86)	0.03 (0.97)
I/sigma I	10.7 (1.0)	12.5 (0.3)
Completeness	99.7 (100.0)	97.88 (84.03)
Multiplicity	7.5 (7.8)	1.9 (1.9)
No of reflections	344933 (34862)	128204 (8654)
No of unique reflections	45898 (4454)	67795 (4491)
Wilson B-factor	79.89	73.04
Refinement Statistics		
Resolution	86.56–2.80	60.84–2.47
Rwork (%)	20.52	19.79
Rfree (%)	23.84	22.24
No of Atoms	6331	6255
Proteins	6248	6196
Water	53	35
ligands	30	24

Average B factor (Å^2)		
Macromolecules	76.96	80.91
ligands	79.90	100.31
Water	63.73	73.99
RMS deviation		
RMS bond (Å)	0.002	0.003
RMS angle (°)	0.49	0.64
Ramachandran plot		
favoured	95.42	97.79
allowed	4.46	2.21
outliers	0.12	0
PDB id	8R2Q	8R2R

Table 2: Data collection and refinement statistics of FadD5

FadD5 dimer interface is through their N-terminal domain with an interface area of 1818 Å^2. A total of 19 amino acids from each monomer are involved to form the dimer through intermolecular hydrogen bond formation. The dimeric interface complex formation significance (CSS) score of 0.725 and the solvation energy gain on complex formation (ΔiG) is calculated to be –20.2 kcal/mol. The overall of fold of N terminal domain of FadD5 is conserved as in other FACS. The solved crystal structure of FadD5 (N-terminal domain; residues 20-435) superposes with the N-terminal domain of FadD13 (PDB id: 3r44), *T. thermophilus* FACS (TtLC-FACS; PDB id: 1ult), *N. tabacum* (Nt4CL2; PDB id: 5bsm) with RMSD values of 2.0, 2.3 and 2.3 Å, respectively, as calculated by the SSM superpose [49] option in *COOT* [35].

3.6 C-terminal domain movement and SAXS studies on FadD5

One limitation of this study is that we could not get the structure of full-length FadD5. Although the overall fold of N- and C- terminal domains are conserved between various FACS, the relative position of C-terminal domain with respect to N-terminal domain is very different in different FACS (Fig. S7). The N- and C-terminal domains are linked by a flexible linker and the C-terminal domain moves as a rigid body and takes different conformation either in acyl-adenylate/open conformation or acyl-CoA-forming (thio)/closed conformation with respect to the N-terminal domain based on the bound ligand [38, 50, 51]. For example, in plant 4-coumarate CoA ligase (Nt4CL2) C-terminal domain rotates as much as 140° from the adenylate conformation upon binding to CoA [11]. It happens due to the displacement of core motif A10 away from the active site and exposed to solvents, leading to a new set of residues stabilizing the bound nucleotide. Additionally, this change was accompanied by a more closed P loop structure facilitated by the

insertion of the A8 loop [51]. In the absence of the full-length crystal structure of FadD5, we utilized *in silico* methods to reconstruct the C-terminal domain and generate the full-length FadD5 structure. The predicted model from AlphaFold server [52] was already in adenylate conformation. Monomeric AlphaFold predicted structure was superposed to the crystal structure dimer to generate full length FadD5 dimer in adenylate conformation. In addition, the AlphaFold predicted structure of C-terminal domain (residues 430-554) was superposed on other FACS enzyme TtLC-FACS (PDB id: 1ult, 1v25 and 1v26), FadD13 (PDB id: 3r44), and NtCL2 (PDB id: 5bsr) to generate full length FadD5 models with different C-terminal domain conformations. In the figure we show two conformations of C-terminal domain to highlight the possible C-terminal domain movement (Fig. 3) [51].

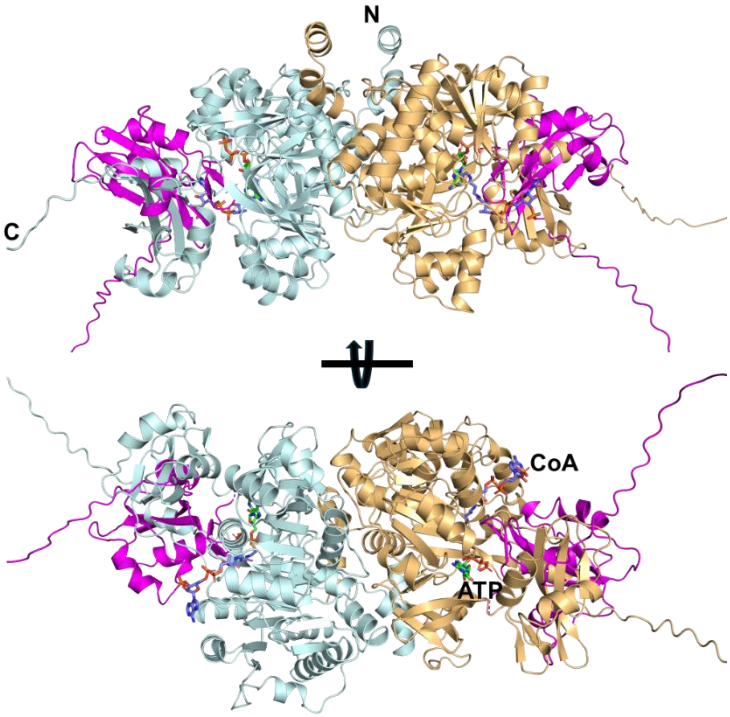

Fig 3: Cartoon representation of the modelled FadD5 dimer based on AlphaFold predicted structure. The two monomers are shown in light cyan and light orange. A different conformation of C-terminal domain modelled based on PDB id 5bsr is shown in magenta cartoon. Modelled ATP and CoA based on structural superposition is shown in green and blue sticks, respectively showing the possible binding sites in FadD5.

In addition to the missing C-terminal domain in the crystal structure, obtaining ligand-bound complex structures through co-crystallization or soaking were unsuccessful, despite extensive efforts, most likely due to the absence of the C-terminal domain in the crystals. Therefore, to

further understand whether FadD5 stays as a full-length stable dimer in solution and to identify if there are any C-terminal domain movements due to the binding of ligands, we performed SAXS studies on FadD5 in the unliganded form as well as in the presence of ATP or CoA. The dimensionless Kratky plot analysis suggests that FadD5 is well folded (Fig. 4) with an R_g of 35.5 Å and D_{max} of 123 Å. The calculated molecular weights were close to the expected molecular mass of FadD5 dimer (Table 3). Different models of FadD5 were fitted against these SAXS scattering profiles using FoXS. The solved structure of FadD5 containing only the dimer of N-terminal domain or the full-length monomer (AlphaFold predicted structure) does not fit very well with the experimental curve with the respective χ^2 values of 39 and 87. However, full length FadD5 dimer models fitted well to the SAXS data (Table 3) suggesting that FadD5 exists in its full-length and dimeric form confirming that C-terminal cleavage is only a crystallization artefact. Among the tested models, FadD5 models based on AlphaFold, FadD13 (PDB id: 3r44), and TtLC-FACS (PDB id: 1ult) fitted better while the other models showed a downward bump near 0.13 q $Å^{-1}$. It should be noted that each of these good fitting models still have C-terminal domain in slightly different conformations. The R_g, D_{max} and the molecular mass calculated for FadD5 in the presence of ATP or CoA were very similar to that of the unliganded FadD5 (Table 3). Also, as in the case of unliganded form, FadD5 dimer models based on AlphaFold, FadD13 (PDB id: 3r44), and TtLC-FACS (PDB id: 1ult) fitted better to the SAXS data of FadD5 in the presence of ATP. Among these three, the best fit was observed for the model with the C-domain conformation as in TtLC-FACS (PDB id: 1ult). Similarly, for FadD5 SAXS data collected in the presence of CoA, the fit was better for the model with C-domain conformation as in TtLC-FACS (PDB id: 1ult). Even for this fit, the C2 value as defined in FoXS [53] is 3.9. For other models, the C2 values were 4 or higher, indicating overfitting. It is possible that the conformation for FadD5 C-terminal domain is different from those in the tested models in the presence of CoA. Higher resolution data is indeed needed to ascertain this.

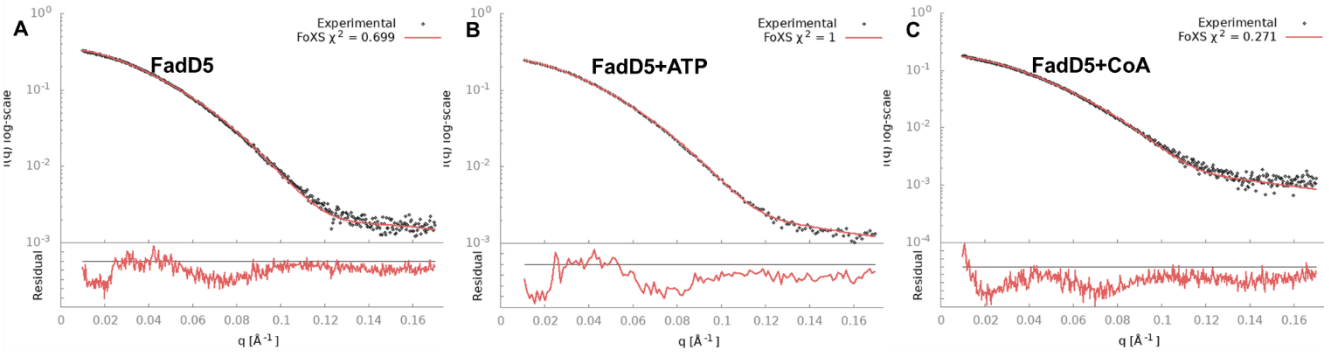

Fig 4: SAXS curves for FadD5 collected in **A.** unliganded form **B.** in the presence of ATP and **C.** in the presence of CoA. The fit of the structural models (**A.** FadD5 dimer based on AlphaFold predicted structure; **B** and **C.** FadD5 dimer based on PDB id 1ult) to the experimental scattering curve is shown in red. The residuals are plotted at the bottom of the curve.

Table 3. Rg and Dmax for Apo-, ATP- and CoA-bound FadD5 were calculated from scatter program and the molecular mass of was estimated with the Porod invariant (Qp) method

Parameter	FadD5			+ ATP			+ CoA		
Buffer	20 mM HEPES, pH-7.5; 500 mM NaCl, 1 mM BME.			20 mM HEPES, pH-7.5; 500 mM NaCl, 1 mM BME, 2mM ATP			20 mM HEPES, pH-7.5; 500 mM NaCl, 1 mM BME, 2mM CoA.		
Protein concentration (mg ml^{-1})	4			4			4		
Method	Batch			Batch			Batch		
Data Collection									
Beamline	B21, Diamond Light Source, UK								
Wavelength (Å)	0.9537								
Detector	EigerX 4M (Dectris)								
R_g (Å)	35.5			35.4			36.1		
D_{max} (Å)	123			121			120		
Mw (kDa)	138			129			127		
Curve Fitting	$\chi^{2,}$	C1	C2	$\chi^{2,}$	C1	C2	$\chi^{2,}$	C1	C2
FadD5 N-terminal domain dimer (pdb id: 8R2Q)	39.12	1.05	> 4.00	70.15	1.05	> 4.00	16.32	1.05	> 4.00
FadD5 monomer (AlphaFold)	87.62	1.05	> 4.00	149.53	1.05	> 4.00	28.29	1.05	> 4.00
FadD5 dimer based on									
AlphaFold	0.70	1.04	1.83	1.10	1.02	2.46	0.36	1.01	> 4.00
1ult	0.76	1.04	1.32	1.00	1.03	1.42	0.27	0.99	3.91
3r44	0.64	1.04	1.49	0.87	1.03	1.63	0.29	1.00	4.00
1v25	0.62	1.04	1.88	0.93	1.03	1.89	0.49	1.00	4.00
1v26	0.62	1.04	1.96	0.98	1.03	1.94	0.54	1.00	4.00
5bsr	0.61	1.01	3.98	0.98	1.00	> 4.00	0.55	1.01	4.00

3.7 ATP and CoA binding sites of FadD5

ATP molecule was modelled by the superposition of ATP bound structure of Nt4CL2 (PDB id: 5bsm) [51] onto FadD5 in adenylate conformation and residues within 5 Å radius of the modelled ATP have been identified to understand important residues interacting with ATP molecule (Fig S8). When compared, we found that the adenosine molecule is enveloped by the core motif A5/A motif, denoted as ^{346}AAFGQTE^{352}. Notably, Glu352 is highly conserved, but variations are observed in Ala346, where Gln299 is present in FadD13 and Gln331 in Nt4CL2. Additionally, Phe348 is substituted by Tyr301 and Tyr333 in FadD13 and Nt4CL2, respectively. The P-loop, also known as motif A3, engages with the ATP molecule through the highly conserved sequence ^{203}IMYTSGTTGRPKGA^{216}. Lys535, situated in core motif A10 and being the sole residue from the C-terminal domain, plays a crucial role in the adenylation reaction [51]. Mutations affecting His252 and Thr351, corresponding to His237 (core motif A4) and Thr336 (core motif A5), have been shown to impair activity in previous studies [51] (Fig. S9). CoA molecule was modelled on to FadD5 by the superposition of CoA bound structure of Nt4CL2 (PDB id: 5bsr) [51]. Residues ^{247}GVPXXHIAG^{255} belong to the G motif and Trp485 and Arg515 are from the C-terminal domain of FadD5. Comparison of residues interacting with CoA in FadD5 and Nt4CL2 suggests that FadD5 has smaller residues. For example, residues Gly247, Val248, Ala254, Gly255, Ala276, Gly453, Glu455, and Arg515 in FadD5 correspond to Val232, Leu233, Tyr239, Ser240, Lys260, Lys443, Phe445, and Phe506 in Nt4CL2.

3.8 Fatty acyl tail binding pocket of FadD5

In TtLC-FACS, Trp234 has been described as a gating residue that opens the fatty acid binding tunnel followed by ATP binding. However, interestingly, the corresponding Tyr234 is replaced with Ile240 in FadD5 suggesting that no gating is required for the binding of long chain substrates to FadD5. Structural analysis suggests that Ile240 in FadD5 is pointing away from the proposed fatty acid binding tunnel. Further comparison of the modelled structure of FadD5 with the myristoyl-AMP bound structure of TtLC-FACS (PDB id: 1v26) [38] reveals a putative fatty acid binding pocket in FadD5 (Fig 5A). Analysis of this pocket (Fig 5A) suggest that it could accommodate substrates slightly longer than C14. The acyl binding pocket is approaching the dimer interface and therefore may interfere with the binding of very long acyl chains. In TtLC-FACS, the longer tails are proposed to be accommodated through a tunnel facing the space between the dimer. FadD13 has been proposed to be in an equilibrium of monomer and dimer while the dimer stays in the solution and the monomer binds to the membrane thus accommodating very long chain fatty acyl tails [9]. Interestingly, our data also suggests that FadD5 can be associated to

membrane. However, the oligomeric state of the membrane bound form is not known. Moreover, a comparison of the predicted membrane binding region of FadD13 (Fig. 5B) with the corresponding region of FadD5 suggests that the surface properties of FadD5 are different (Fig 5C). As FadD5 is associated with *mce1* operon and likely processes the lipids imported through the Mce1 complex, it might act differently when compared to FadD13 for membrane association. Interestingly, FadD5 has an extended N-terminal region which is disordered in the crystal structure. However, structure prediction from AlphaFold [52] suggests this region to be composed of a helix with a few positively charged residues and predominantly hydrophobic surface. It is possible that this region may have a role in membrane association. Interestingly, our studies also show that the N-terminal domain of FadD5 has the ability to associate to membrane. Further studies are indeed needed to shed light on whether FadD5 is associated to membrane as a monomer or as dimer and via the N-terminal helix.

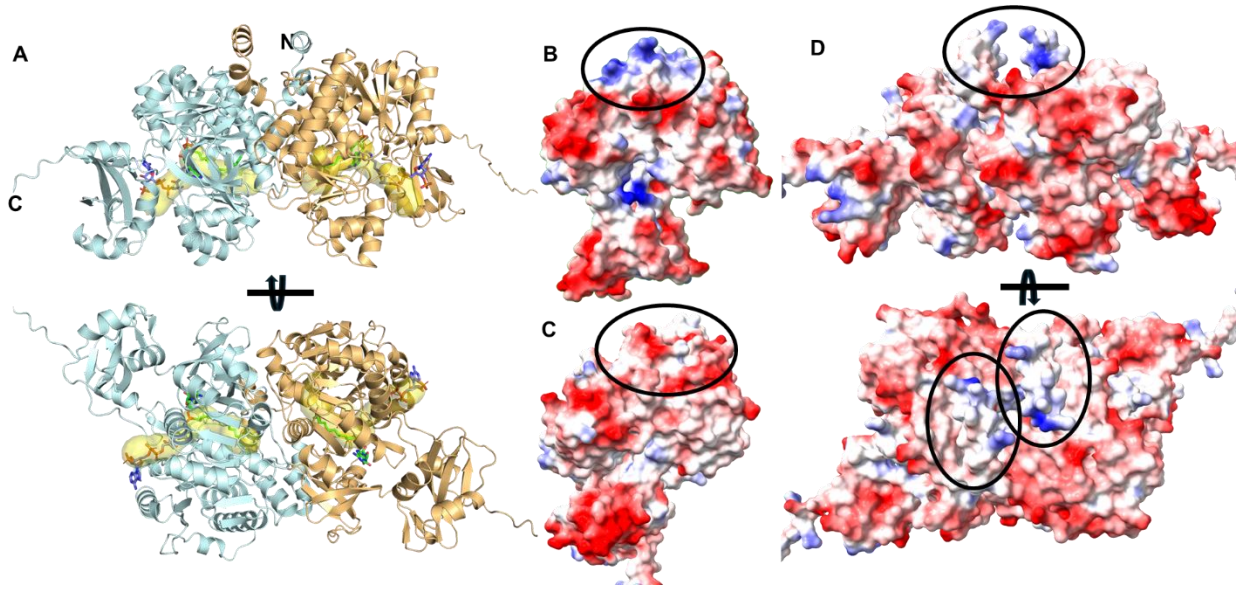

Fig 5: A. Predicted binding pocket for fatty acyl tail based on structural superposition with PDB id 1v26. The CoA and myristoyl AMP are shown in blue and green sticks. The predicted binding pocket from Mol2 analysis [54] is shown in surface representation in yellow. B. Electrostatic surface potential for FadD13 monomer. The potential membrane binding site as proposed by Lundgren et al [55] is highlighted in black. C. Electrostatic surface potential of FadD5. The surface corresponding to that highlighted in B is highlighted in black showing different charge distribution in FadD5. D. Electrostatic surface potential of FadD5 dimer based on AlphaFold predicted structure. The N-terminal helix is highlighted in black oval in both the orientations.

4. Concluding remarks

Mtb demonstrates remarkable metabolic versatility due to its unique fatty acid metabolism system. It possesses a large amount of fatty acid metabolism genes, including FACSs and FAALs, pivotal in activating fatty acids for metabolic pathways. FadD5 is a FACS and a crucial enzyme in Mtb's survival, plays a role in mycolic acid recycling and is a central player in the *mce1* operon's function, possibly as a mycolic acid transporter. This study on FadD5 suggests that it likely acts as a peripheral membrane protein, which is crucial for anchoring longer fatty acyl substrates. Predictive tools and experimental evidence support this membrane association. FadD5 has a dimeric arrangement in its active soluble form and the C-terminal domain is crucial for its activity. ATP and CoA binding influence FadD5's stability and conformation. The closed conformation is stabilized by ATP and helps guide fatty acids through the binding tunnel, essential for substrate specificity. Our study has confirmed the involvement of FadD5 in the conversion of fatty acids to fatty acyl-CoA. Although the full-length crystal structure and the structural flexibility between N- and C-terminal domains still remain unknown, full-length structural modelling along with ligand-based modelling and solution structure studies provides insights on to the possible mode of fatty acyl tail binding.

Abbreviations: Mtb-Mycobacterium tuberculosis; MCE- mammalian cell entry; FACS- Fatty acyl-CoA synthetase, FAAL- fatty acyl-AMP ligase.

Data availability statement: All data generated in this study are included in this article.

Supplementary Material: Supplementary data is included as a separate file:

CRediT authorship contribution statement: Mohammad Asadur Rahman: Writing–original draft, Conceptualization, Methodology, Formal analysis, Investigation, Visualization. **Subhadra Dalwani:** Methodology, Formal analysis, Visualization. **Rajaram Venkatesan**: Writing–review & editing, Supervision, Funding acquisition, Conceptualization.

Declaration of competing interest: The authors declare that they have no conflict of interest.

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Consent for publication: Not applicable.

5. References

[1] WHO, Global Tuberculosis Report, 2021, (2021).

[2] J.C. Camus, M.J. Pryor, C. Medigue, S.T. Cole, Re-annotation of the genome sequence of Mycobacterium tuberculosis H37Rv, Microbiology (Reading) 148(Pt 10) (2002) 2967-2973.

[3] Z. Liu, T.R. Ioerger, F. Wang, J.C. Sacchettini, Structures of *Mycobacterium tuberculosis* FadD10 protein reveal a new type of adenylate-forming enzyme, J Biol Chem 288(25) (2013) 18473-18483.

[4] P. Arora, A. Goyal, V.T. Natarajan, E. Rajakumara, P. Verma, R. Gupta, M. Yousuf, O.A. Trivedi, D. Mohanty, A. Tyagi, R. Sankaranarayanan, R.S. Gokhale, Mechanistic and functional insights into fatty acid activation in *Mycobacterium tuberculosis*, Nature Chemical Biology 5(3) (2009) 166-73.

[5] O.A. Trivedi, P. Arora, V. Sridharan, R. Tickoo, D. Mohanty, R.S. Gokhale, Enzymic activation and transfer of fatty acids as acyl-adenylates in mycobacteria, Nature 428(6981) (2004) 441-5.

[6] S. Gavalda, M. Leger, B. van der Rest, A. Stella, F. Bardou, H. Montrozier, C. Chalut, O. Burlet-Schiltz, H. Marrakchi, M. Daffe, A. Quemard, The Pks13/FadD32 crosstalk for the biosynthesis of mycolic acids in *Mycobacterium tuberculosis*, Journal of Biological Chemistry 284(29) (2009) 19255-64.

[7] M.L. Kuhn, E. Alexander, G. Minasov, H.J. Page, Z. Warwrzak, L. Shuvalova, K.J. Flores, D.J. Wilson, C. Shi, C.C. Aldrich, W.F. Anderson, Structure of the Essential Mtb FadD32 Enzyme: A Promising Drug Target for Treating Tuberculosis, ACS Infect Dis 2(8) (2016) 579-591.

[8] W. Li, S. Gu, J. Fleming, L. Bi, Crystal structure of FadD32, an enzyme essential for mycolic acid biosynthesis in mycobacteria, Scientific Reports 5(1) (2015) 15493.

[9] C.S. Andersson, C.A. Lundgren, A. Magnusdottir, C. Ge, A. Wieslander, D. Martinez Molina, M. Hogbom, The *Mycobacterium tuberculosis* very-long-chain fatty acyl-CoA synthetase: structural basis for housing lipid substrates longer than the enzyme, Structure 20(6) (2012) 1062-70.

[10] A. Goyal, M. Yousuf, E. Rajakumara, P. Arora, R.S. Gokhale, R. Sankaranarayanan, Crystallization and preliminary X-ray crystallographic studies of the N-terminal domain of FadD28, a fatty-acyl AMP ligase from Mycobacterium tuberculosis, Acta Crystallogr Sect F Struct Biol Cryst Commun 62(Pt 4) (2006) 350-2.

[11] A.S. Reger, R. Wu, D. Dunaway-Mariano, A.M. Gulick, Structural characterization of a 140 degrees domain movement in the two-step reaction catalyzed by 4-chlorobenzoate:CoA ligase, Biochemistry 47(31) (2008) 8016-25.

[12] A.S. Reger, J.M. Carney, A.M. Gulick, Biochemical and crystallographic analysis of substrate binding and conformational changes in acetyl-CoA synthetase, Biochemistry 46(22) (2007) 6536-46.

[13] P.A. Watkins, Very-long-chain acyl-CoA synthetases, Journal of Biological Chemistry 283(4) (2008) 1773-7.

[14] P. Asthana, D. Singh, J.S. Pedersen, M.J. Hynonen, R. Sulu, A.V. Murthy, M. Laitaoja, J. Janis, L.W. Riley, R. Venkatesan, Structural insights into the substrate-binding proteins Mce1A and Mce4A from Mycobacterium tuberculosis, IUCrJ 8(Pt 5) (2021) 757-774.

[15] S.A. Cantrell, M.D. Leavell, O. Marjanovic, A.T. Iavarone, J.A. Leary, L.W. Riley, Free mycolic acid accumulation in the cell wall of the mce1 operon mutant strain of *Mycobacterium tuberculosis*, Journal of Microbiology 51(5) (2013) 619-626.

[16] S. Arruda, G. Bomfim, R. Knights, T. Huima-Byron, L.W. Riley, Cloning of an M. tuberculosis DNA fragment associated with entry and survival inside cells, Science 261(5127) (1993) 1454-7.

[17] N. Casali, A.M. White, L.W. Riley, Regulation of the *Mycobacterium tuberculosis* mce1 operon, J Bacteriol 188(2) (2006) 441-9.

[18] K.Y. Dunphy, R.H. Senaratne, M. Masuzawa, L.V. Kendall, L.W. Riley, Attenuation of *Mycobacterium tuberculosis* functionally disrupted in a fatty acyl-coenzyme A synthetase gene fadD5, J Infect Dis 201(8) (2010) 1232-1239.

[19] S.F. Altschul, W. Gish, W. Miller, E.W. Myers, D.J. Lipman, Basic local alignment search tool, J Mol Biol 215(3) (1990) 403-10.

[20] A. Kapopoulou, J.M. Lew, S.T. Cole, The MycoBrowser portal: a comprehensive and manually annotated resource for mycobacterial genomes, Tuberculosis 91(1) (2011) 8-13.

[21] F. Madeira, M. Pearce, A.R.N. Tivey, P. Basutkar, J. Lee, O. Edbali, N. Madhusoodanan, A. Kolesnikov, R. Lopez, Search and sequence analysis tools services from EMBL-EBI in 2022, Nucleic Acids Research 50(W1) (2022) W276-W279.

[22] X. Robert, P. Gouet, Deciphering key features in protein structures with the new ENDscript server, Nucleic Acids Research 42(Web Server issue) (2014) W320-4.

[23] S. Galandrin, V. Guillet, R.S. Rane, M. Leger, R. N, N. Eynard, K. Das, T.S. Balganesh, L. Mourey, M. Daffe, H. Marrakchi, Assay development for identifying inhibitors of the mycobacterial FadD32 activity, Journal of Biomolecular Screening 18(5) (2013) 576-87.

[24] R.H. Upson, R.P. Haugland, M.N. Malekzadeh, R.P. Haugland, A spectrophotometric method to measure enzymatic activity in reactions that generate inorganic pyrophosphate, Analytical Biochemistry 243(1) (1996) 41-5.
[25] P.V. Konarev, V.V. Volkov, A.V. Sokolova, M.H.J. Koch, D.I. Svergun, PRIMUS: a Windows PC-based system for small-angle scattering data analysis, Journal of Applied Crystallography 36(5) (2003) 1277-1282.
[26] S. Förster, L. Apostol, W. Bras, Scatter: software for the analysis of nano- and mesoscale small-angle scattering, Journal of Applied Crystallography 43(3) (2010) 639-646.
[27] V. Piiadov, E. Ares de Araújo, M. Oliveira Neto, A.F. Craievich, I. Polikarpov, SAXSMoW 2.0: Online calculator of the molecular weight of proteins in dilute solution from experimental SAXS data measured on a relative scale, Protein Science 28(2) (2019) 454-463.
[28] J. Newman, Expanding screening space through the use of alternative reservoirs in vapor-diffusion experiments, Acta Crystallographica Section D 61(4) (2005) 490-493.
[29] E. Daniel, M.M. Maksimainen, N. Smith, V. Ratas, E. Biterova, S.N. Murthy, M.T. Rahman, T.R. Kiema, S. Sridhar, G. Cordara, S. Dalwani, R. Venkatesan, J. Prilusky, O. Dym, L. Lehtio, M.K. Koski, A.W. Ashton, J.L. Sussman, R.K. Wierenga, IceBear: an intuitive and versatile web application for research-data tracking from crystallization experiment to PDB deposition, Acta Crystallographica Section D 77(Pt 2) (2021) 151-163.
[30] W. Kabsch, Xds, Acta Crystallographica Section D 66(Pt 2) (2010) 125-32.
[31] P.R. Evans, G.N. Murshudov, How good are my data and what is the resolution?, Acta Crystallographica Section D 69(Pt 7) (2013) 1204-14.
[32] G. Winter, K.E. McAuley, Automated data collection for macromolecular crystallography, Methods 55(1) (2011) 81-93.
[33] G. Winter, xia2: an expert system for macromolecular crystallography data reduction, Journal of Applied Crystallography 43(1) (2010) 186-190.
[34] L. Potterton, J. Agirre, C. Ballard, K. Cowtan, E. Dodson, P.R. Evans, H.T. Jenkins, R. Keegan, E. Krissinel, K. Stevenson, A. Lebedev, S.J. McNicholas, R.A. Nicholls, M. Noble, N.S. Pannu, C. Roth, G. Sheldrick, P. Skubak, J. Turkenburg, V. Uski, F. von Delft, D. Waterman, K. Wilson, M. Winn, M. Wojdyr, CCP4i2: the new graphical user interface to the CCP4 program suite, Acta Crystallographica Section D 74(Pt 2) (2018) 68-84.
[35] P. Emsley, B. Lohkamp, W.G. Scott, K. Cowtan, Features and development of Coot, Acta Crystallographica Section D 66(Pt 4) (2010) 486-501.
[36] D. Liebschner, P.V. Afonine, M.L. Baker, G. Bunkóczi, V.B. Chen, T.I. Croll, B. Hintze, L.W. Hung, S. Jain, A.J. McCoy, N.W. Moriarty, R.D. Oeffner, B.K. Poon, M.G. Prisant, R.J. Read, J.S. Richardson, D.C. Richardson, M.D. Sammito, O.V. Sobolev, D.H. Stockwell, T.C. Terwilliger, A.G. Urzhumtsev, L.L. Videau, C.J. Williams, P.D. Adams, Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix, Acta Crystallographica Section D 75(Pt 10) (2019) 861-877.
[37] E.F. Pettersen, T.D. Goddard, C.C. Huang, G.S. Couch, D.M. Greenblatt, E.C. Meng, T.E. Ferrin, UCSF Chimera--a visualization system for exploratory research and analysis, Journal of Computational Chemistry 25(13) (2004) 1605-12.
[38] Y. Hisanaga, H. Ago, N. Nakagawa, K. Hamada, K. Ida, M. Yamamoto, T. Hori, Y. Arii, M. Sugahara, S. Kuramitsu, S. Yokoyama, M. Miyano, Structural basis of the substrate-specific two-step catalysis of long chain fatty acyl-CoA synthetase dimer, Journal of Biological Chemistry 279(30) (2004) 31717-26.
[39] G. Khare, V. Gupta, R.K. Gupta, R. Gupta, R. Bhat, A.K. Tyagi, Dissecting the role of critical residues and substrate preference of a Fatty Acyl-CoA Synthetase (FadD13) of *Mycobacterium tuberculosis*, PLoS One 4(12) (2009) e8387-e8387.
[40] G. Jogl, L. Tong, Crystal structure of yeast acetyl-coenzyme A synthetase in complex with AMP, Biochemistry 43(6) (2004) 1425-31.
[41] A.M. Gulick, V.J. Starai, A.R. Horswill, K.M. Homick, J.C. Escalante-Semerena, The 1.75 A crystal structure of acetyl-CoA synthetase bound to adenosine-5'-propylphosphate and coenzyme A, Biochemistry 42(10) (2003) 2866-73.
[42] J.D. Weimar, C.C. DiRusso, R. Delio, P.N. Black, Functional role of fatty acyl-coenzyme A synthetase in the transmembrane movement and activation of exogenous long-chain fatty acids. Amino acid residues within the ATP/AMP signature motif of *Escherichia coli* FadD are required for enzyme activity and fatty acid transport, Journal of Biological Chemistry 277(33) (2002) 29369-76.
[43] P.C. Babbitt, G.L. Kenyon, B.M. Martin, H. Charest, M. Slyvestre, J.D. Scholten, K.H. Chang, P.H. Liang, D. Dunaway-Mariano, Ancestry of the 4-chlorobenzoate dehalogenase: analysis of amino acid sequence identities among families of acyl:adenyl ligases, enoyl-CoA hydratases/isomerases, and acyl-CoA thioesterases, Biochemistry 31(24) (1992) 5594-604.
[44] Y. Oba, K. Iida, S. Inouye, Functional conversion of fatty acyl-CoA synthetase to firefly luciferase by site-directed mutagenesis: a key substitution responsible for luminescence activity, FEBS Letters 583(12) (2009) 2004-8.

[45] K.C. Chou, H.B. Shen, MemType-2L: a web server for predicting membrane proteins and their types by incorporating evolution information through Pse-PSSM, Biochemical and Biophysical Research Communications 360(2) (2007) 339-45.
[46] M.A. Lomize, I.D. Pogozheva, H. Joo, H.I. Mosberg, A.L. Lomize, OPM database and PPM web server: resources for positioning of proteins in membranes, Nucleic Acids Research 40(Database issue) (2012) D370-6.
[47] M. Yan, L. Cao, L. Zhao, W. Zhou, X. Liu, W. Zhang, Z. Rao, The Key Roles of *Mycobacterium tuberculosis* FadD23 C-terminal Domain in Catalytic Mechanisms, Front Microbiol 14 (2023) 1090534.
[48] A. Goyal, P. Verma, M. Anandhakrishnan, R.S. Gokhale, R. Sankaranarayanan, Molecular basis of the functional divergence of fatty acyl-AMP ligase biosynthetic enzymes of *Mycobacterium tuberculosis*, Journal of Molecular Biology 416(2) (2012) 221-38.
[49] E. Krissinel, K. Henrick, Secondary-structure matching (SSM), a new tool for fast protein structure alignment in three dimensions, Acta Crystallographica Section D 60(Pt 12 Pt 1) (2004) 2256-68.
[50] A.M. Gulick, Conformational dynamics in the Acyl-CoA synthetases, adenylation domains of non-ribosomal peptide synthetases, and firefly luciferase, ACS Chemical Biology 4(10) (2009) 811-27.
[51] Z. Li, S.K. Nair, Structural Basis for Specificity and Flexibility in a Plant 4-Coumarate:CoA Ligase, Structure 23(11) (2015) 2032-42.
[52] J. Jumper, R. Evans, A. Pritzel, T. Green, M. Figurnov, O. Ronneberger, K. Tunyasuvunakool, R. Bates, A. Zidek, A. Potapenko, A. Bridgland, C. Meyer, S.A.A. Kohl, A.J. Ballard, A. Cowie, B. Romera-Paredes, S. Nikolov, R. Jain, J. Adler, T. Back, S. Petersen, D. Reiman, E. Clancy, M. Zielinski, M. Steinegger, M. Pacholska, T. Berghammer, S. Bodenstein, D. Silver, O. Vinyals, A.W. Senior, K. Kavukcuoglu, P. Kohli, D. Hassabis, Highly accurate protein structure prediction with AlphaFold, Nature 596(7873) (2021) 583-589.
[53] D. Schneidman-Duhovny, M. Hammel, A. Sali, FoXS: a web server for rapid computation and fitting of SAXS profiles, Nucleic Acids Res 38(Web Server issue) (2010) W540-4.
[54] L. Pravda, D. Sehnal, D. Toušek, V. Navrátilová, V. Bazgier, K. Berka, R. Svobodová Vařeková, J. Koča, M. Otyepka, MOLEonline: a web-based tool for analyzing channels, tunnels and pores (2018 update), Nucleic Acids Research 46(W1) (2018) W368-W373.
[55] C.A.K. Lundgren, M. Lerche, C. Norling, M. Hogbom, Solution and Membrane Interaction Dynamics of *Mycobacterium tuberculosis* Fatty Acyl-CoA Synthetase FadD13, Biochemistry 60(19) (2021) 1520-1532.