Cryo-EM snapshots of mycobacterial arabinosyltransferase complex EmbB2-AcpM2

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Cryo-EM snapshots of mycobacterial arabinosyltransferase complex EmbB2-AcpM2

Lu Zhang1, Yao Zhao2,3,4, Ruogu Gao4,6, Jun Li2, Xiuna Yang2, Yan Gao6, Wei Zhao1, Sudagar S. Gurcha7, Natacha Veerapen7, Sarah M. Batt7, Kajelle Kaur Besra7, Wenqing Xu2, Lijun Bi5, Xian’en Zhang6, Luke W. Guddat8, Haitao Yang2, Quan Wang2,5, Gurdyal S. Besra7, Zihe Rao1,2,5,6

1 State Key Laboratory of Medicinal Chemical Biology, College of Life Sciences and College of Pharmacy, Nankai University, Tianjin 300353, China
2 Shanghai Institute for Advanced Immunochemical Studies and School of Life Science and Technology, ShanghaiTech University, Shanghai 201210, China
3 CAS Center for Excellence in Molecular Cell Science, Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences (CAS), Shanghai 200031, China
4 University of Chinese Academy of Sciences, Beijing 100101, China
5 National Laboratory of Biomacromolecules and Key Laboratory of RNA Biology, CAS Center for Excellence in Biomacromolecules, Institute of Biophysics, CAS, Beijing 100084, China
6 Laboratory of Structural Biology, Tsinghua University, Beijing 100084, China
7 School of Biosciences, Institute of Microbiology and Infection, University of Birmingham, Birmingham B15 2TT, UK

Correspondence: wangq@ibp.ac.cn (Q. Wang), G.Besra@bham.ac.uk (G. S. Besra), raozh@tsinghua.edu.cn (Z. Rao)

ABSTRACT

Inhibition of Mycobacterium tuberculosis (Mtb) cell wall assembly is an established strategy for anti-TB chemotherapy. Arabinosyltransferase EmbB, which catalyzes the transfer of arabinose from the donor decaprenyl-phosphate-arabinose (DPA) to its arabinosyl acceptor is an essential enzyme for Mtb cell wall synthesis. Analysis of drug resistance mutations suggests that EmbB is the main target of the front-line anti-TB drug, ethambutol. Herein, we report the cryo-EM structures of Mycobacterium smegmatis EmbB in its “resting state” and DPA-bound “active state”. EmbB is a fifteen-transmembrane-spanning protein, assembled as a dimer. Each protomer has an associated acyl-carrier-protein (AcpM) on their cytoplasmic surface. Conformational changes upon DPA binding indicate an asymmetric movement within the EmbB dimer during catalysis. Functional studies have identified critical residues in substrate recognition and catalysis, and demonstrated that ethambutol inhibits transferase activity of EmbB by competing with DPA. The structures represent the first step directed towards a rational approach for anti-TB drug discovery.

KEYWORDS Mycobacterium tuberculosis, EmbB, cryo-EM, ethambutol, cell wall synthesis, arabinogalactan, arabinosyltransferase, acyl-carrier-protein, drug discovery

INTRODUCTION

Tuberculosis (TB) caused by Mycobacterium tuberculosis (Mtb) is, worldwide, the leading cause of human fatalities due to any infectious disease (WHO, 2018). Of great concern is the emergence of multi-drug-resistant (MDR)-TB and extensively drug-resistant (XDR)-TB, which has further exacerbated the global burden of TB and at the same time continues to lead to a reduction in clinical recovery rates (WHO, 2018). Ethambutol (EMB) is one of the five front-line drugs used to treat TB and is particularly important in MDR-chemotherapy regime (Alliance, 2008). It exhibits its mode of action by inhibiting the biosynthesis of arabinogalactan (AG)
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embC mutations within the tance to ethambutol has been shown to be caused by has remained unresolved (Mikusova et al., 1995). Resi- et al., 2015). However, the molecular basis for this inhibition (Takayama and Kilburn, 1989; Mikusova et al., 1995; Lee et al., 2005), a key component of the cell wall mycoly- arabinogalactan-peptidoglycan (mAGP) complex (Jankute et al., 2015). However, the molecular basis for this inhibition has remained unresolved (Mikusova et al., 1995). Resis- tance to ethambutol has been shown to be caused by mutations within the embCAB operon (embC, embA, and embB) that encode membrane-associated arabinosyltransferases, amongst which EmbB has been identified as the primary target (Safi et al., 2008; Sun et al., 2018). Functional studies have shown that all the Emb proteins play key roles in cell wall synthesis. Specifically, EmbA and EmbB partici- pate in arabinosylation of AG, which is linked via covalent attachment to the outer mycolic acids layer and the inner peptidoglycan layer, ultimately forming the cell wall core (Escuyer et al., 2001), thus acting as a natural barrier sur- rounding the cell membrane (Fig. 1A). On the other hand, EmbC is involved in the formation of lipoarabinomannan (LAM), a glycolipid which may modulate the host immune response during Mtb infection (Goude et al., 2008).

The embB gene has been shown to be essential for the survival of Mtb in culture (Sassetti et al., 2003), whereas a Mycobacterium smegmatis (Msm) embB-knockout strain was shown to be viable but possessed profound morphological alterations upon gene inactivation (Escuyer et al., 2001). Furthermore, EmbB has been shown to play a key role in forming the characteristic terminal hexarabinofuranosyl motif (Fig. 1A) of AG, which is the template for mycolylation (Escuyer et al., 2001; Jankute et al., 2015). Together with the other Emb proteins (EmbA and EmbC), EmbB belongs to the glycosyltransferase C (GT-C) super-family (Berg et al., 2007; Lairson et al., 2008), whose structures comprises an N-terminal transmembrane domain and a C-terminal soluble domain located on the periplasmic side of the membrane (Berg et al., 2007). However, the Emb proteins show no overall sequence similarity to any other GT-C members or any other proteins beyond mycobacteria or related genera (Berg et al., 2005). The lipid donor utilized by EmbB is decaprenyl-phosphate-arabinose (DPA), which is the only proven arabinose donor for mycobacterial species (Lee et al., 1997). In a very recent study three dimensional structures of Mtb and Msm EmbA-EmbB heterodimer complexes and Msm EmbC2 homodimer complex were determined (Zhang et al., 2020). Nevertheless, embA knockout Msm (斜体) strain can survive, indicating EmbB protein can work alone in cell (Escuyer et al., 2001). However, other fashions of the Emb-containing assembly, i.e. (斜体), EmbB as an individual protein has not been reported.

Here, we have characterized EmbB in terms of its structure, catalytic mechanism and its inhibition by ethambutol. We present the cryo-EM structures of a full-length Msm EmbB in two distinct conformations, which we refer to as the “resting” and donor-bound “active” states at 3.6 Å and 3.5 Å resolution, respectively. EmbB is observed as a dimer along with an acyl-carrier-protein (AcpM) associated with each protomer, thus forming a heterotetrameric EmbB2-AcpM2 complex. We show that ethambutol inhibits the enzymatic activity of the EmbB2-AcpM2 complex and structurally iden- tify the site that is most susceptible to ethambutol resistance based on isolates from clinical studies.

Figure 1. Arabinosyltransferase activity of EmbB and inhibition by ethambutol. (A) Schematic representation of the components and assembly of the mycobacterial membrane and cell wall. EmbB catalyzes the addition of an arabinose residue in an α(1→3) linkage from DPA resulting in the precursor for a subsequent extension by AftB, further resulting in the characteristic terminal branching hexamotif found in AG. (B) Arabinosyltransferase activity measured using di-arabinoside NV6. The [14C] labeled arabinose transferred from DP[14C]A to the product was con...
**RESULTS AND DISCUSSION**

**Enzyme purification, characterization and structure determination**

To gain insights into the structure and function of EmbB, we screened several mycobacterial orthologues to assess protein yield and purity. From these studies, we identified *Msm* EmbB (MSMEG_6389) as the ideal candidate for investigation. *Msm* EmbB, whose sequence is 69.6% identical to *Mtbb* EmbB (Rv_3795) was cloned into the pMV261 vector containing a 10× His tag fusion at its C-terminus. *Msm* EmbB protein was subjected to overexpression (Snapper et al., 1990). Detergent purified followed by amphipoll exchanged EmbB protein (Fig. S1A–C) was then subjected to cryo-EM analysis.

The natural acceptor of EmbB remains to be defined, but cell-free arabinosyltransferase activity could be measured using a diarabinoside, NV6, as an acceptor analog (Fig. 1B). An EmbB arabinosyltransferase assay was used to determine the transfer of $[^{14}C]$-arabinose from DP$[^{14}C]A$ to NV6. The resulting product, NV12, was identified by autoradiographic thin-layer chromatography (TLC) (Fig. 1B). NV12 had a similar retardation factor to a synthetic tri-arabinoside. The related NV13 containing a 10× His tag fusion at its C-terminus. NV12 catalyzed by EmbB, which is presumably an $\alpha$-1,3-linkage based on previous studies (Escuyer et al., 2001). Not surprisingly, EmbB arabinosyltransferase activity is inhibited by ethambutol (Fig. 1B). Given NV6 allows three potential glycosylation sites at 2-OH, 3-OH and 5-OH on the terminal non-reducing arabinose, we sought to use a chemical biology approach to further characterize the $[^{14}C]$-arabinose containing NV12 product. The related NV13 acceptor, where the 3-OH position of the terminal arabinose unit of NV6 is blocked by an azide group was used in subsequent cell-free experiments for purified EmbB, EmbC, and the abundant AftB activity from *Msm* membranes (Lee et al., 1997). Not surprisingly, EmbB arabinosyltransferase activity is inhibited by ethambutol (Fig. 1B). Given NV6 allows three potential glycosylation sites at 2-OH, 3-OH and 5-OH on the terminal non-reducing arabinose, we sought to use a chemical biology approach to further characterize the $[^{14}C]$-arabinose containing NV12 product. The related NV13 acceptor, where the 3-OH position of the terminal arabinose unit of NV6 is blocked by an azide group was used in subsequent cell-free experiments for purified EmbB, EmbC, and the abundant AftB activity from *Msm* membranes (Lee et al., 1997), to determine the resulting new glycosidic linkage in NV12 catalyzed by EmbB, which is presumably an $\alpha$(1→3)-linkage based on previous studies (Escuyer et al., 2001). The azide group in NV13 prevented glycosylation by EmbB but allowed purified EmbC to catalyze an ethambutol-sensitive $\alpha$(1→5)-linkage (NV15), and an ethambutol-resistant AftB $\beta$(1→2)-linkage (NV14) (Fig. S1E). In addition, 2D heteronuclear single quantum correlation (HSQC) NMR experiments using purified AG from wild type *Msm* and the *Msm* embB knockout strain were consistent with the above cell-free arabinosyltransferase data and showed that the cell wall from the knockout strain lacked the terminal linkage of arabinose unit by virtue of the absence of the characteristic 2-α-Araf-3 NMR signal (Fig. S1F).

Purified, amphipoll exchanged EmbB appeared as homogeneous and dispersed particles in negative staining EM and when embedded in vitreous ice (Fig. S2A). 2D class averages revealed a dimeric assembly of EmbB (Fig. S2B) with two attachments on the cytoplasmic side, subsequently identified by silver staining (Fig. S1C) and mass-spectrometry (Fig. S1D) as the endogenous acyl-carrier-protein AcpM (MSMEG_4326). Two major classes generated by 3D classification were selected and subjected to individual refinements, ultimately yielding two different reconstructions at 3.5 Å and 3.6 Å overall resolution (Fig. S2C-F). The quality of both maps allowed us to build, de novo, two near-atomic models of EmbB that include most of the residues (Tables S1 and S2), while AcpM could be docked and refined using a homologous structure (PDB: 1KLP (Wong et al., 2002)). Additional features in the cryo-EM map could be accounted for by the donor substrate, DPA, whose presence was confirmed by mass spectrometry (Fig. S1G). This feature shows DPA is bound in its expected binding cavity in the asymmetric EmbB dimer, and the potential by-product, decaprenyl phosphate (DP) bound to regions that are likely in the transmembrane domain of EmbB.

**Two distinct states of EmbB$_2$-AcpM$_2$ complex**

The EmbB$_2$-AcpM$_2$ complex is captured in two states, one with C2-symmetry and the other that is asymmetric (Fig. 2A). In both reconstructions, each EmbB protomer is associated with an AcpM on its cytoplasmic side (Fig. 2A), resulting in a hetetrotetrameric assembly. Given their differences in composition and conformation, the two states are referred to as the asymmetric “donor-bound” active state and the symmetric “resting” state (Fig. 2A). The symmetry refers not only to the asymmetric binding of DPA, but also to the asymmetry of the enzyme dimer assembly (see below). The EmbB protomers in the two states share common structural features which include two periplasmic domains (PDs) and 15 transmembrane helices (TMH) arranged into an approximately crescent-shaped bundle (Fig. 2B–E). The PDs comprise a PD$_N$ located between TMH1 and TMH2 and a PD$_C$ at the C-terminus (Fig. 2B and 2C). PD$_C$ features a jelly-roll-fold subdomain coordinated with a Ca$^{2+}$ ion, similar to the previously reported crystal structure of the C-terminal soluble domain of EmbC from *Mtbb* (Alderwick et al., 2011), and a mixed α/β fold subdomain, whose interactions with both the TM domain and PD$_N$ are observed here in the intact EmbB structure (Figs. 2C, S3B and S3C). PD$_N$ also adopts a jelly-roll-fold and interacts with the C-terminal tail of PD$_C$ by forming a three-stranded β-sheet (Figs. 2B, 2C and S3C), which may help to stabilize the entire PD. Not surprisingly, this overall folding represented by EmbB$_2$-AcpM$_2$ complex agrees well with that of the previously reported Emb proteins (Zhang et al., 2020).

The two EmbB$_2$-AcpM$_2$ complexes show significant differences in their subunit organizations (Fig. 2A, and 2D–G). Most significantly, the two EmbB protomers in the DPA bound complex are asymmetrically associated. Relative to the DPA-bound protomer, the other EmbB protomer is translated by ~16 Å along the dimer interface, and in the plane of the membrane (Fig. 2D and Movie S1). This change in subunit organization dramatically alters the dimer
interface, in which, for instance, the distance between the pair of TMH11 at the interface has halved, resulting in a more compact active site (Fig. 2E). While this asymmetric movement is induced, the expected steric clashes in the periplasmic domains of the two EmbB protomers are resolved by rearrangements of the PLs and PDs within the unbound protomer (Fig. 2F, 2G, and Movie S1).

**DPA binding in the active complex**

In the “active” complex, a semi-confined gulf is formed in the membrane space that is surrounded by TMH1, TMH7-9 and TMH11 from the DPA-bound EmbB protomer and TMH10, TMH13, and TMH14 from the other protomer (Figs. 2E, 3A and 3B). Once the nearby side-chains were assigned
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I469TMH9 in the membrane space, with the end of the tail the arabinose moiety forms hydrogen bonds with E313 PL2. The whole of the DPA is reasonable to build a DPA into this region (Fig. 3A and 3B). The last seven prenyl groups of DPA extend to the other half of the hydrophobic groove via extensive hydrophobic interactions, and mutations within this hydrophilic cavity result in severe loss of the arabinosyltransferase activity (Figs. S5A and 5B). When a triple-alanine mutant (R249, R253, and R454) of EmbB that abolished its interaction with AcpM was transformed into the Msm embB knockout strain, this activity was reduced by the induced disorder-to-helix transition of α6 at the dimer interface. Considering that the bound DPA is the major composition difference between the two states, it is reasonable to speculate that the dramatic structural rearrangement of the enzyme complex in the active state occurs upon DPA binding, and is mediated by the induced disorder-to-helix transition of α6 at the dimer interface. This kind of concerted disorder-to-helix transition of a functional periplasmic loop along with donor binding has been proposed to enable access to the acceptor in other glycosyltransferases such as AmT from Cupriavidus metallidurans in complex with its lipid substrate undecaprenyl phosphate (UndP) and PglB from Campylobacter lari with lipid-linked oligosaccharide (LLO) (Lizak et al., 2011; Vasilieios I. Petrou et al., 2016; Napiorkowska et al., 2017).

**EmbB-AcpM interaction**

AcpM has a four-helix topology arranged in a right-handed bundle held together by interhelical hydrophobic interactions (Wong et al., 2002) (Fig. 2C). The two AcpM molecules bind to each of the two EmbB protomers through extensive electrostatic interactions on the cytoplasmic surface of EmbB (Fig. 4A). Helix-2 and helix-3 of AcpM are intimately engaged with the cytoplasmic loop 1 (CL1) of EmbB, which is a long positively charged linker between TMH2 and TMH3 (Fig. 4A). This is consistent with the known role of helix-2 in AcpM as a contact site with its target proteins, such as AcpS (Parris et al., 2000) (Fig. S6). The AcpM attached to the DPA-bound EmbB protomer has the better-resolved structure in our cryo-EM reconstructions (Figs. S2C, S2F, and S4B). Most of its side-chains have been assigned (Table S2). Three pairs of interactions are revealed: D53 and D61 of AcpM form salt-bridges with R454TMH8i and R249CL1 of EmbB, and S41AcpM forms a hydrogen bond with R253CL1 of EmbB (Fig. 4A). R249CL1, R253CL1, and R454TMH8i in EmbB are highly conserved across mycobacterial species (Fig. S8). When a triple-alanine mutant (R249, R253, and R454) of EmbB that abolished its interaction with AcpM was transformed into Msm embB knockout strain, a moderate loss (at ~40%) of the 3-arm branching signal of AG was observed (Fig. S1G), suggesting that AcpM is most likely functionally associated to arabinosyltransferase activity in vivo, regardless the equivalent mutation had little effect on the cell-free arabinosyltransferase activity (Fig. S5A).

**Active site and possible acceptor pathway**

Glycosyltransferases are classified as either “inverting” or “retaining” based on two stereochemical outcomes in the...
formation of the new glycosidic bond at the anomeric carbon (Lairson et al., 2008). Emb proteins are believed to be inverting enzymes based on the fact that nearly all of the arabinose residues in the DPA-involved extension of AG are in an $\alpha$-configuration (Jankute et al., 2015) (except for the non-reducing end of AG catalyzed by AftB (Seidel et al., 2007)), while DPA is in a $\beta$-configuration (Lee et al., 1995).

For a conventional inverting glycosyltransferase reaction, upon both substrates (the donor and acceptor) reaching the catalytic site, a key catalytic step relies on an active site side-chain, which serves as a base catalyst that deprotonates the nucleophile of the acceptor, enabling the following nucleophilic attack at the anomeric carbon (Breton et al., 2012). In our structure, the arabinose moiety of DPA is positioned between two acidic residues D285 and E313 in the catalytic pocket (Fig. 3D). D285 belongs to the highly conserved DDx GT-C motif and is the predicted catalytically essential residue. In EmbB, D285 is located at the equivalent residue D279 in EmbC as previously reported (Berg et al., 2005). Mutation of this residue in EmbB in this study and the equivalent residue D279 in EmbC as previously reported (Berg et al., 2005) led to a complete loss of activity (Fig. S5B). In EmbB, D285 locates at the junction of two cavities, one of which harbors the arabinose moiety and phosphate group of DPA, and the other, opposite to the DPA cavity, provides polar access to the dimer interface above the membrane boundary (Figs. 5A, 5B, and 5D).

Overall, this suggests that D285 is likely the key active site residue involved in catalysis. In our structure, DPA aligns its C5 atom close to D285, whereas the C1 atom is approximately 8 Å from the side-chain of D285. It is speculated that a further conformational change is required, possibly upon acceptor binding, allowing the DPA to move deeper into the cavity and reorient its C1 atom for $\alpha(1\rightarrow3)$ glycosidic bond formation. This shift could involve a repositioning of the phosphate group much deeper into the DPA cavity and closer to D285.

EmbB catalyzes the penultimate step of AG synthesis. We have previously reported that EmbB functions in a coordinating way with EmbA (Zhang et al., 2020), nevertheless, our cell-free assay has confirmed that purified EmbB alone is functional using NV6 as acceptor. Thus, it can be inferred that EmbB may play dual roles in cells, by either forming a homodimer or a heterodimer with EmbA, depending on the physiological concentration of these proteins. Therefore, the native acceptor of EmbB could be a relatively mature arabinan chain before the terminal 3-arm branch of the characteristic hexa-arabinan motif (Fig. 1A). The possible acceptor entry pathway could be deduced based on the location of the identified donor binding cavity and the putative active site. This polar pathway as mentioned above is a tryptophan-rich region that we refer to as the “W-pathway” (Fig. 5A). This W-pathway is formed by a series of tryptophan residues W308, W504, W505, W972, and W1012. The first three tryptophan residues, located on the DDX-motif-containing PL2 and conformational change modulator PL5, extend to the arabinose moiety of DPA, while the latter two tryptophan residues are located on the mixed $\alpha/\beta$ fold subdomain of PDc. The role of W972 was previously reported to be critical in terms of both of the binding affinity with acceptor and the enzymatic activity in EmbC (W985 in EmbC corresponds to W972 in EmbB) (Alderwick et al., 2011). These tryptophan residues are only partially conserved amongst EmbA, EmbB, and EmbC. The differences might reflect the fact that Emb proteins are different enzymes with different substrate specificities. Furthermore, previous studies have attributed the C-terminal domain of the Emb proteins to a critical role in acceptor substrate recognition and arabinan chain extension (Shi et al., 2006; Alderwick et al., 2011). Consistent with this, in the active state structure, several regions of the PDc are missing in the DPA unbound EmbB protomer (Figs. 5D and S3E). The flexibility of these missing regions could be the result of the absence of the acceptor when the EmbB$_2$-AcpM$_2$ complex is activated by the donor. Consequently, this region in PDc may outline a fairly broad and open pathway leading straight into.
the W-pathway headed by W504 which locates in the dimer interface (Fig. 5D), thus indicating a macroscopic acceptor entry pathway.

**Proposed catalytic cycle for the arabinosyltransferase complex**

In this study, we have determined the structures of a substrate unbound EmbB$_2$-AcpM$_2$ complex in a presumed resting state and a donor DPA-bound pre-catalytic conformation which we define as the “active” state. The two structures of EmbB$_2$-AcpM$_2$ suggest that the binding of substrates is a sequentially coupled process with substantial conformational changes upon the binding of the two substrates.

We hypothesize that DPA binding activates the EmbB dimer by triggering conformational changes. Once the EmbB$_2$-AcpM$_2$ complex is activated, the glycosyltransferase reaction can occur in the following defined steps (Fig. 6).
A-I. The acceptor is recognized and threaded by PD_C and enters the active site through the W-pathway, forming an enzyme-donor-acceptor ternary complex (A-II) ready for the reaction. The DPA bound EmbB_2-AcpM_2 structure in this study represents an intermediate state before C1 of DPA reaches the optimal position for catalysis. Hence, to form the ternary complex a series of precisely arranged conformational changes are required to allow both substrates to be oriented optimally.

A-II. Based on the catalytically essential role of D285 and canonical mechanism of an inverting glycosyltransferase (Qasba et al., 2005; Lairson et al., 2008), the following is rationally proposed: D285 deprotonates the hydroxyl group on the C3 carbon of the acceptor and activates this hydroxyl group for a nucleophilic attack on the C1 carbon of DPA. A new glycosidic bond is formed (A-III) allowing the newly formed arabinan product and DP (the leaving group) to release from the active site.
Overall, functional studies confirm that EmbB catalyzes arabinose chain α(1→3) branching with the subsequent product utilized by AftB for the terminal β(1→2) linkage at the non-reducing end of AG. Therefore, it is plausible that product release (A-IV) could be coupled instantaneously with a new round of DPA binding (A-I).

**Structural mapping of ethambutol resistance associated mutations and its potential binding site**

In this study, we have shown that anti-TB drug ethambutol inhibits the α(1→3) arabinosyltransferase activity of purified EmbB protein. This agrees with the fact that branching of the terminal hexaarabinan motif in AG can be inhibited by ethambutol (Lee et al., 2005). Numerous mutations in *embB* are causally associated with resistance to ethambutol, but
their effects on EmbB structure and function remain unclear. The three-dimensional structure of EmbB provides an unprecedented opportunity to understand the role that the embB mutations play in the development of ethambutol resistance in *M. tuberculosis*. We selected the top 30 most frequent ethambutol-resistant mutations of EmbB in 1,814 strains from 61 studies in a manually collated drug-resistance database MycoResistance (Dai et al., 2019) (Figs. 7A and S8). Upon mapping these onto the DPA-bound EmbB structure, we find that most of the mutations concentrate in a radial region centered on the DPA-bound pocket (Fig. 7A). M306 (equivalent to *Msm* M292) in *Mtb* EmbB which is the most common clinical mutation associated with ethambutol resistance (Kamaswamy et al., 2000; Lee et al., 2005; Safi et al., 2008) is, as expected, also the most predominant (1243/2353) in our analysis (Fig. 7A). Clinical isolate mutations include M306L, M306V, M306I and M306T substitutions in *Mtb* (Lee et al., 2002; Sun et al., 2018). In *Msm*, M292T mutation results in a 60-fold increase in MIC (Lety et al., 1997). In our cell-free enzymatic activity assay, mutein M292L demonstrates clear resistance to ethambutol (Fig. S5A). Meanwhile, the binding affinity of ethambutol to this mutein also significantly decreases (Fig. 7B).

The recently reported structure of the ethambutol bound EmbA-EmbB complex enables us to analyze the structural features of the potential drug binding pockets of EmbB2 in this study. When superimposing the EmbB protomer from the EmbB2 in its resting state onto the EmbB subunit of ethambutol-bound EmbA-EmbB complex (Zhang et al., 2020), residues including the catalytic site D285 on EmbB2 and the acceptor side pockets were observed in the similar position (Figure S7A). Thus it is possible that ethambutol inhibition mode on EmbB2 similar to that on EmbA-EmbB complex by inhibiting substrate binding. Notable shifting (2.9–4.0 Å2) were observed on E313 on PL2 and H580 on PL6 (Figure S7A), likely due to ethambutol binding. The binding affinity of EmbB with ethambutol is greatly enhanced (*Kd* = 1.58 µmol/L) (Fig. 7B) when a DPA synthesis inhibitor, BTZ043 (Makarov et al., 2009), was added during cell culture to obtain overexpressed EmbB protein in a relatively low-abundance DPA environment, which could support this speculation. The competitive inhibition hypothesis of ethambutol is also in agreement with a previous DPA recognition study which demonstrated a rapid accumulation of DPA in ethambutol treated *Msm* cells (Wolucka et al., 1994).

These analyses will facilitate further experimental studies aimed at understanding how mutations in EmbB and other Emb proteins lead to ethambutol resistance. To be noted, not all ethambutol-resistant strains have *embB* mutations (Alcaide et al., 1997), suggesting that further studies on other resistance associated proteins or pathways are necessary to complete a comprehensive understanding of the mechanisms of ethambutol resistance.

**CONCLUSIONS**

In this study, cryo-EM single-particle analysis revealed conformational heterogeneity in arabinosyltransferase complex EmbB2-AcpM2 which we ascribe to evidence for a “resting” and “donor-bound active” state. An acceptor recognition and entry pathway is proposed. We have also characterized EmbB as an α(1→3) arabinosyltransferase and confirmed it is a target of ethambutol. Thus, our work not only unravels the molecular mechanisms involved in substrate recognition for this arabinosyltransferase but also provides a much-anticipated foundation for developing improved anti-TB drugs such as inert DPA analogues.

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**AUTHOR CONTRIBUTIONS**

Z.R. conceived the project. Z.R., G.S.B., Q.W., L.Z., Y.Z. and R.G. designed the experiments; L.Z., Y.Z., J.L., X.Y. cloned and purified the EmbB and mutant proteins; Y.G., L.Z. and J.L. prepared Cryo-EM samples, R.G. and Q.W. collected and processed the cryo-EM data, reconstructed the two maps, built and refined the structure model; S.S.G., N.V., K.K.B. and S.M.B. performed the enzymatic activity assay, synthesized chemical compound for activity assay and carried out the MST experiment; L.Z., Y.Z., R.G., X.Y. and W.Z. performed mass spectrum experiment and other biochemical
experiments. All the authors analyzed and discussed the results. Q. W., L.W.G., L.Z., Y.Z., R.G., G.S.B and Z.R. wrote the manuscript with the help of all the authors.

DECLARATION OF INTERESTS
All authors declare no competing interests.

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