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Biosynthesis of mycobacterial arabinogalactan: identification of a novel α(1→3)
arabinofuranosyltransferase

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Key words: Corynebacterium glutamicum, Mycobacterium tuberculosis, arabinogalactan, arabinofuranosyltransferase, cell wall

Running Title: Identification of a novel arabinofuranosyltransferase
Summary

The cell wall mycolyl-arabinogalactan-peptidoglycan complex is essential in mycobacterial species, such as *Mycobacterium tuberculosis* and is the target of several anti-tubercular drugs. For instance, ethambutol targets arabinogalactan biosynthesis through inhibition of the arabinofuranosyltransferases Mt-EmbA and Mt-EmbB. A bioinformatics approach identified putative integral membrane proteins, MSMEG2785 in *Mycobacterium smegmatis*, Rv2673 in *Mycobacterium tuberculosis* and NCgl1822 in *Corynebacterium glutamicum*, with 10 predicted transmembrane domains and a glycosyltransferase motif (DDX), features that are common to the GT-C superfamily of glycosyltransferases. Deletion of *M. smegmatis* MSMEG2785 resulted in altered growth and glycosyl linkage analysis revealed the absence of AG α(1→3)-linked arabinofuranosyl (Araf) residues. Complementation of the *M. smegmatis* deletion mutant was fully restored to a wild type phenotype by MSMEG2785 and Rv2673, and as a result, we have now termed this previously uncharacterized open reading frame, arabinofuranosyltransferase C (*aftC*). Enzyme assays using the sugar donor β-D-arabinofuranosyl-1-monophosphoryl-decaprenol (DPA) and a newly synthesized linear α(1→5)-linked Ara₅ neoglycolipid acceptor together with chemical identification of products formed, clearly identified AftC as a branching α(1→3) arabinofuranosyltransferase. This newly discovered glycosyltransferase sheds further light on the complexities of *Mycobacterium* cell wall biosynthesis, such as in *M. tuberculosis* and related species and represents a potential new drug target.
Introduction

Tuberculosis (TB) affects a third of the world population and causes 1.8 million fatalities annually (Dye, 2006). The spread of TB has been facilitated in recent years due to the susceptibility of HIV infected individuals to *Mycobacterium tuberculosis*, the etiological agent of TB (Paolo and Nosanchuk, 2004). The problem has also been compounded by the emergence of multi-drug resistant TB (MDR-TB) (Kaye and Frieden, 1996) and extensively drug-resistant (XDR)-TB strains (Shah *et al.*, 2007). *M. tuberculosis* and other mycobacteria have a distinct cell wall which has a lipid-rich outer layer that is highly impermeable (Minnikin, 1982). One of the major components of this outer envelope are mycolic acids, long chain \( \alpha \)-alkyl, \( \beta \)-hydroxy fatty acids that are essential for bacterial survival (Vilcheze *et al.*, 2000; Portevin *et al.*, 2004; Bhatt *et al.*, 2005; Parish *et al.*, 2007). These are found either esterified to the non-reducing termini of arabinogalactan (AG), or are present as trehalose esters, such as trehalose dimycolate (TDM) (Brennan and Nikaido, 1995; Dover *et al.*, 2004).

A common feature of members of the *Corynebacterianeae* is that they all possess this unusual cell wall architecture (McNeil *et al.*, 1990, 1991; Besra *et al.*, 1995). Apart from mycolic acids, the cell wall is dominated by a second macromolecule, an essential heteropolysaccharide termed arabinogalactan (AG), which is linked to both mycolic acids and peptidoglycan, forming the mycolyl-arabinogalactan-peptidoglycan (mAGP) complex (Daffé *et al.*, 1990; McNeil *et al.*, 1990; McNeil *et al.*, 1991; Besra *et al.*, 1995). The formation of the arabinan domain (\( \alpha 1 \rightarrow 5 \), \( \alpha 1 \rightarrow 3 \) and \( \beta 1 \rightarrow 2 \) glycosyl linkages) of AG results from the subsequent addition of arabinofuranose (Araf) residues by a set of unique arabinofuranosyltransferases including, the Emb proteins of which 3 paralogues exist in *Mycobacterium avium* (Belanger *et al.*, 1996) and
M. tuberculosis (Telenti et al., 1997), AftA (Alderwick et al., 2006a) and AftB (Seidel et al., 2007a). The lipid linked sugar donor β-D-arabinofuranosyl-1-monophosphoryldecaprenol (DPA) (Wolucka et al., 1994; Lee et al., 1995; Lee et al., 1997), serves as the substrate molecule for these complex membrane bound glycosyltransferases.

The anti-tuberculosis drug ethambutol (EMB) was shown to specifically inhibit AG biosynthesis (Takayama and Kilburn, 1989). The precise molecular target of EMB occupies the embCAB locus in M. tuberculosis (Telenti et al., 1997). To further define the role of EmbCAB proteins in cell wall arabinan biosynthesis, embA, embB and embC were individually inactivated in Mycobacterium smegmatis (Escuyer et al., 2001; Zhang et al., 2003). All three mutants were viable, however, the non-reducing terminal Ara₆ motif which is the template for mycolylation in AG (McNeil et al., 1991) was altered in both the Ms-embA and Ms-embB mutants (Escuyer et al., 2001), whilst Ms-embC was shown to be involved in the formation of the arabinan domains of lipoarabinomannan (LAM) (Zhang et al., 2003). Attempts to obtain deletion mutants of embA (Amin et al., 2008) and embB in M. tuberculosis and embAB in M. smegmatis have proved unsuccessful (G.S. Besra, unpublished results). In contrast, deletion of the single Cg-emb orthologue and chemical analysis of the cell wall revealed a novel truncated AG structure possessing only terminal (t)-Araf residues with a corresponding loss of cell wall bound mycolic acids (Alderwick et al., 2005). The presence of a novel enzyme responsible for “priming” the galactan domain for further elaboration by Emb proteins led to the identification of AftA (Alderwick et al., 2006a). Recently, a retaining GT-C enzyme was identified, now termed AftB, which is responsible for the attachment of terminal β(1→2) Araf residues, and marks the “end point” for AG arabinan biosynthesis (Figure 1) before decoration with mycolic acids (Seidel et al., 2007a).
It is clear that additional arabinofuranosyltransferases involved in AG and LAM biosynthesis still remain to be identified. Indeed, Liu and Musheginan (2003) identified fifteen members of the GT-C superfamily residing in *M. tuberculosis*, representing candidates involved in the biosynthesis of cell wall related glycans and lipoglycans (Liu and Mushegian, 2003). We have continued our earlier studies (Alderwick *et al.*, 2006a; Alderwick *et al.*, 2006b; Seidel *et al.*, 2007a) to identify genes required for the biosynthesis of the core structural elements of the mAGP complex by studying mutants of *M. smegmatis* and the orthologous genes and enzymes of *M. tuberculosis* and *C. glutamicum*. Herein, we present MSMEG2785, Rv2673c and NCgl1822 as a new distinct arabinofuranosyltransferase of the GT-C superfamily, which is responsible for the transfer of Ara\(^f\) residues from DPA to the arabinan domain to form \(\alpha(1\rightarrow3)\)-linked Ara\(^f\) residues, which result in the branched arabinan domain distal to the non-reducing terminal Ara\(_6\) motif characteristic of mycobacterial AG.
Results

Genome comparison of the Rv2673 locus

The arabinofuranosyltransferases EmbA, EmbB, and EmbC are vital for *M. tuberculosis* and represent a target for the established drug EMB (Mikusova *et al.*, 1995; Belanger *et al.*, 1996; Telenti *et al.*, 1997). Structural considerations of these proteins and a search for new drug targets resolved that more than 16 related proteins are present in *M. tuberculosis*, possibly also acting as glycosyltransferases (Liu and Mushegian, 2003). In our systematic analysis of GT-C glycosyltransferases, focusing on those present in *M. tuberculosis* and *C. glutamicum*, we have previously identified the arabinofuranosyltransferases AftA (Alderwick *et al.*, 2006a) and AftB (Seidel *et al.*, 2007a), as well as several α-mannosyltransferases (Mishra *et al.*, 2007; Mishra *et al.*, 2008). Each of these glycosyltransferases plays a specific yet decisive role in cell wall biosynthesis and assembly. *In silico* analysis of one of the putative glycosyltransferases of *M. tuberculosis*, Rv2673, highlighted that orthologues are present in a range of species belonging to the sub-order *Corynebacterianeae*, including the families *Mycobacteriaceae*, *Corynebacteriaceae* and *Nocardiaceae* (Figure 2A). Furthermore, the organization of the gene locus is largely retained. The adjacent genes are largely of unknown function. *RibD* encodes a bifunctional deaminase-reductase domain, followed by a gene product containing a hydrolase domain, which is however absent in *Corynebacterium*, and downstream of Rv2673 a gene of unknown function is present. The wide distribution of Rv2673, its syntenic organization, and the fact that it is retained even in *M. leprae*, strongly indicates a fundamental function of its product. According to our experimental analysis (see below) we annotated this gene *arabinofuranosyltransferase C (aftC)*.
AftC of *M. tuberculosis* is 433 amino acid residues long. It is a hydrophobic protein and is predicted to possess 10 transmembrane-spanning segments (Figure 2B). However, in contrast to AftA, AftB or EmbC, it is characterized by the absence of a periplasmic carboxyterminal extension. The amino acid sequence among the *Corynebacterianeae* is very well conserved, and there are 43% identical residues shared by the *M. tuberculosis* and *C. glutamicum* proteins. The degree of conservation is particularly high in the loop regions, for instance between helix 1 and 2, 3 and 4, or 6 and 7 (Figure 2B). The fully conserved aspartyl (D) and glutamyl (E) residues, which we propose to be involved in catalysis or substrate binding, are located in the first extended loop region (Liu and Mushegian, 2003), as we have demonstrated for similarly located aspartyl (D) residues of Cg-Emb and AftB (Seidel *et al.*, 2007a; Seidel *et al.*, 2007b). Interestingly, the long transmembrane helix 8 is well conserved and it is within this region that there is a strong identity to a membrane protein of *Vibrio parahaemolyticus* (CpsG). Furthermore, this gene is located in a gene cluster involved in the biosynthesis of a capsular polysaccharide within this pathogen (Guvener and McCarter, 2003).

**Construction and growth of mutants**

In order to delete *aftC* and study for possible consequences we generated a null mutant of *M. smegmatis mc²155 MSMEG2785* (ortholog of *Rv2673*) using specialized transduction (Figure 3A). In contrast to our *C. glutamicum* studies (see below) growth of *M. smegmatis ΔaftC* in comparison to *M. smegmatis* was poor in liquid medium (Figure 3B) and sensitive to the addition of Tween-80 on agar plates (>0.005%). Complementation of *M. smegmatis ΔaftC* with either pMV261-Ms-*aftC* or pMV261-Mt-*aftC* restored the mutant to a wild type phenotype (Figure 3B). On solid media *M. smegmatis ΔaftC* had a smooth and glossy appearance in comparison to
the typical crenulated colony morphology found for wild type *M. smegmatis* (Figure 3C) and failed to stain as ‘acid-fast’ positive (data not shown). In addition, susceptibility of *M. smegmatisΔaftC* to EMB and the hydrophobic antibiotics rifampicin and chloramphenicol was enhanced (minimal inhibitory concentration of 2, 100 and 10 µg/ml for wild type *M. smegmatis* in comparison to 0.4, 4 and 5 µg/ml for *M. smegmatisΔaftC*, respectively) indicating increased permeability and that *M. smegmatisΔaftC* had an altered cell wall. To study the function of the corynebacterial AftC the non-replicative plasmid pK19 mobsacBΔaftC was constructed. This was used to transform *C. glutamicum* to kanamycin resistance, indicating integration in its chromosome (Supplementary Figure S1A). Loss of vector was obtained by selection for sucrose-resistance yielding clones with *aftC* deleted. A PCR analysis with primer pairs P5 and P6 resulted in the expected fragment of 2160 bp for the wild type and of 1065 bp for the deletion mutant, which was termed *C. glutamicumΔaftC*. Colonies of this mutant were more erose compared to the usual glossy appearance of the wild type colony (data not shown). In contrast to *M. smegmatisΔaftC* the growth of the *C. glutamicumΔaftC* mutant on the salt medium CGXII possessed only a slightly reduced growth rate of 0.32 h⁻¹, whereas, that of the wild type *C. glutamicum* was 0.39⁻¹ h⁻¹ (Supplementary Figure S1B).


To study the function of mycobacterial *aftC* deletion, defatted cells were analyzed qualitatively for AG esterified mycolic acids and cell wall associated lipids from an equivalent starting amount of biomass for each strain due to differences in growth rate (Figure 3B). As expected, *M. smegmatis* exhibited a typical profile of cell wall bound α, α’ and epoxy-mycolic acid methyl
esters (MAMEs), whereas, these products were drastically reduced in *M. smegmatisΔaftC* (Figure 4A). In addition, complementation of *M. smegmatisΔaftC* with either pMV261-Ms-*aftC* or pMV261-Mt-*aftC* (Figure 4A), led to the restoration of normal ‘levels’ of cell wall bound mycolic acids. Analysis of cell wall associated lipids in several independent experiments highlighted an apparent increase in TDM for the *aftC* deletion mutant. This was confirmed quantitatively through [14C]acetate labeling of cultures and equal loading of radioactivity of extractable free lipids from *M. smegmatis*, *M. smegmatisΔaftC* and the complemented *M. smegmatisΔaftC* strain using plasmids pMV261-Ms-*aftC* and pMV261-Mt-*aftC* (Figure 4B). Typically, wild type *M. smegmatis* synthesized 5250 cpm, whereas *M. smegmatisΔaftC* afforded 14676 cpm of TDM after equivalent loading of radioactivity and quantitative analysis by phosphorimaging. Complementation of *M. smegmatisΔaftC* with either pMV261-Ms-*aftC* or pMV261-Mt-*aftC* restored the phenotype of the deletion mutant back to that of wild type *M. smegmatis* (Figure 4B). These results demonstrated that Ms-*aftC* and Mt-*aftC* are involved in a key aspect of arabinan biosynthesis, whereby deletion substantially perturbs tethering of mycolic acids to AG, which results in an increase in TDM production.

The cell wall core (mAGP) was prepared from *M. smegmatis* and *M. smegmatisΔaftC* as described (Daffè *et al.*, 1990; Besra *et al.*, 1995; Alderwick *et al.*, 2005) and the ratio of Ara to Gal in mAGP determined by gas chromatography (GC) analysis of alditol acetates (Daffè *et al.*, 1990; Besra *et al.*, 1995; Escuyer *et al.*, 2001; Alderwick *et al.*, 2005) (Figure 5). The glycosyl composition was calculated based on a single rhamnosyl (Rha) residue per AG chain (McNeil *et al.*, 1990). The glycosyl compositional analysis revealed a relative molar ratio of Rha:Ara:Gal of 1:71:31 and an Ara:Gal ratio of 2.3:1 which is in accord with previous data (Escuyer *et al.*, 2001). The *M. smegmatisΔaftC* mutant yielded AG with a significant reduction in Ara content
concomitant with a relative increase in the amount of Gal. The *M. smegmatisΔaftC* yielded an AG with a Rha:Ara:Gal ratio of 1:22:56 and an Ara:Gal ratio of 0.4:1. Complementation of *M. smegmatisΔaftC* with either pMV261-Ms-*aftC* or pMV261-Mt-*aftC*, restored the Rha:Ara:Gal ratio to that of wild type *M. smegmatis*. Gas chromatography mass spectrometry (GC/MS) analysis of per-O-methylated alditol acetate derivatives prepared from *M. smegmatis* and *M. smegmatisΔaftC* indicated the complete absence of 3,5-Araf branching residues and a significant reduction in t-Araf, 2-Araf and 5-Araf-linkages (Figure 6). Complementation of *M. smegmatisΔaftC* with either plasmid encoding Ms-*aftC* or Mt-*aftC* restored the glycosyl linkage profile to that of wild type *M. smegmatis* (Figure 6). These results demonstrate that MSMEG2785 and Rv2673, are functionally equivalent and are involved in the synthesis of 3,5-Araf branching residues. Interestingly, LAM preparations from *M. smegmatisΔaftC* were truncated in size on SDS-PAGE analysis to ‘full-size’ LAM from wild type *M. smegmatis*. Further purification and detailed chemical analyses of LAM from the *aftC* mutant strain are currently being undertaken and will be reported separately (H.L. Birch, unpublished results).

In contrast to the mycolic acid studies performed with the mycobacterial *aftC* deletion mutant, *C. glutamicumΔaftC* cells were analyzed quantitatively for AG esterified corynemycolic acids due to similar growth rates between strains (Supplementary Figure S1B). Wild type *C. glutamicum* exhibited the known profile of corynemycolic acid methyl esters (CMAMEs, 35345 cpm) (Supplementary Figure S2), whereas, cell wall bound CMAMEs were significantly reduced in *C. glutamicumΔaftC* (8023 cpm). The above data was reassuring as the qualitative (*M. smegmatisΔaftC*) and quantitative (*C. glutamicumΔaftC*) analyses were comparable in terms of a reduction in cell wall bound mycolic acids (Figure 4A and Supplementary Figure S2). Importantly, these results have also shown that Cg-*aftC* is involved in a key aspect of arabinan
biosynthesis, whereby deletion perturbs tethering of corynomycolic acids to AG. The GC/MS profiles of per-O-methylated alditol acetate derivatives of *C. glutamicum* and *C. glutamicum*Δ*aftC* are shown in Supplementary Figure S3 with *C. glutamicum*Δ*aftC* also clearly devoid of 3,5-Araf branching residues.

*In vitro* arabinofuranosyltransferase activity with extracts of *M. smegmatis*, *M. smegmatis*Δ*aftC* and complemented strains

Initial attempts to develop an *in vitro* assay using either purified recombinant expressed AftC or *E. coli* membranes expressing *aftC*, have thus far proved unsuccessful, probably due to the hydrophobic nature of the protein. In an alternative approach, we assessed the capacity of membrane preparations from *M. smegmatis*, *M. smegmatis*Δ*aftC* and *M. smegmatis*Δ*aftC* complemented with pMV261-Mt-*aftC* to catalyze arabinofuranosyltransferase activity in the presence of exogenous synthetic acceptors (Lee *et al.*, 1997; Seidel *et al.*, 2007a).

We first assessed whether *M. smegmatis*Δ*aftC* was deficient in α(1→5) and β(1→2) arabinofuranosyltransferase activity using an α-D-Araf-(1→5)-α-D-Araf-O-(CH2)7CH3 (Ara2) synthetic acceptor (Lee *et al.*, 1997) and DP[14C]A as a sugar donor based on an established assay format for determining α(1→5) and β(1→2) arabinofuranosyltransferase activities (Lee *et al.*, 1998). TLC/autoradiographic analysis of the products which were only synthesized in the presence of Ara2, when assayed with *M. smegmatis* membranes resulted in the formation of two products (A and B) (Figure 7A and B). The enzymatic synthesis of products A and B are consistent with our previous studies using mycobacterial (Lee *et al.*, 1997) and corynebacterial (Seidel *et al.*, 2007a) membrane preparations resulting in trisaccharide products as a result of
α(1→5) and β(1→2) Araf linkages to the Ara₂ acceptor (Figure 7A). Addition of EMB in several experiments, even at high concentrations of up to 1 mg/ml to the reaction mixture, resulted in a decrease in only the in vitro synthesized α-D-[^14]C]Araf-(1→5)-α-D-Araf-(1→5)-α-D-Araf-O-(CH₂)₇CH₃ product A (Figure 7A and B). Assays performed with membranes from M. smegmatisΔaftC and the pMV261-Mt-aftC complemented strain using the Ara₂ synthetic acceptor gave a similar profile to that of wild type M. smegmatis (Figure 7B). The data clearly show that the M. smegmatisΔaftC strain possesses comparable levels of EMB-sensitive α(1→5) and EMB-resistant β(1→2) arabinofuranosyltransferase activity.

The lack of α(1→3) arabinofuranosyltransferase activity in the previously reported Ara₂ and α-D-Araf-(1→5)-α-D-Araf-(1→5)-α-D-Araf-O-(CH₂)₇CH₃ (Ara₃) acceptor based assays (Lee et al., 1997) required the development of an arabinofuranosyltransferase assay using the Ara-extended synthetic acceptor α-D-Araf-(1→5)-α-D-Araf-(1→5)-α-D-Araf-(1→5)-α-D-Araf-(1→5)-α-D-Araf-(1→5)-α-D-Araf-O-(CH₂)₈NH₂ (Ara₅) (Supplementary Experimental and Supplementary Figure S4) and DP[^14]C]A as a sugar donor (Lee et al., 1998). TLC/autoradiographic analysis of the products which are only synthesized in the presence of Ara₅, when assayed with M. smegmatis membranes resulted in the formation of a single product X (Figure 8A) through the transfer of a single[^14]C]Araf residue, with a retardation factor (Rₙ) consistent with a synthetic Ara₆ acceptor (Appelmelk et al., 2008) standard (Figure 8B). In addition, the synthesis of product X in overexpression studies was enhanced. Consistently from two independent membrane preparations and assays performed in triplicate from M. smegmatis pMV261-Mt-aftC produced product X (6453 cpm) in comparison to membranes from wild type M. smegmatis (4289 cpm) in the above assays demonstrating that AftC was functionally involved in the synthesis of product X. The inclusion of EMB in several experiments, even at high concentrations of up to 1 mg/ml to the
reaction mixture did not inhibit the synthesis of this in vitro synthesized \[^{14}\text{C}]\text{Araf}-\text{Ara}_5\) (Figure 8A, Product X) illustrating that the \(\text{Ara}_5\) acceptor was not extended via an EMB-sensitive \(\alpha(1\rightarrow5)\) arabinofuranosyltransferase. Interestingly, membranes prepared from the \(\text{M. smegmatis}\Delta\text{aftC}\) strain were unable to synthesize the in vitro product to the same level of activity that was observed with wild type membranes prepared from \(\text{M. smegmatis}\) (Figure 8A). This was to be expected, since our earlier in vivo and in vitro studies would have anticipated residual \(\text{Ara}_6\) product formation, considering that \(\text{M. smegmatis}\Delta\text{aftC}\) possesses \(\beta(1\rightarrow2)\) arabinofuranosyltransferase activity. Assays performed with membranes from the \(\text{M. smegmatis}\Delta\text{aftC}\text{pMV261-Mt-aftC}\) complemented strain, gave a similar profile to that of wild type \(\text{M. smegmatis}\) (Figure 8A).

To establish that the \(\text{Ara}_5\) acceptor is being utilized by two different arabinofuranosyltransferases, presumably establishing \(\beta(1\rightarrow2)\) and \(\alpha(1\rightarrow3)\) linkages, assays similar to that used before were scaled up (see Experimental Procedures) and product X extracted and purified through preparative TLC for each membrane preparation. GC (Sassaki et al., 2005) and GC/MS (Alderwick et al., 2005) analyses of the partially per-\(O\)-methylated, per-\(O\)-acetylated alditol acetate derivatives of product X in assays performed with \(\text{M. smegmatis}\) membranes revealed the addition of \(\beta(1\rightarrow2)\) [\(R_t\ 11.75\) min; \(m/z\ 129, 130, 161, 190\)] and \(\alpha(1\rightarrow3)\) [\(R_t\ 12.39\) min; \(m/z\ 118, 129, 130, 190, 202, 233\)] linked \(\text{Araf}\) residues (Figure 9A and B). Therefore, the product migrating below \(\text{Ara}_5\) and co-incident with the \(\text{Ara}_6\) acceptor standard on TLC (Figure 8A and B) is in fact a mixture of two products (Figure 9B). The addition of \(\beta(1\rightarrow2)\)-linked \(\text{Araf}\) residues can be attributed to the function of AftB. The presence of \(\alpha(1\rightarrow3)\)-linked \(\text{Araf}\) residues in this assay using an \(\text{Ara}_5\) acceptor clearly highlights the role of a novel arabinofuranosyltransferase(s) capable of functioning in an \(\alpha(1\rightarrow3)\) capacity. Importantly, the
level of $\alpha(1\rightarrow3)$ activity when the Ara$_5$ acceptor is incubated with membranes prepared from *M. smegmatis*ΔaftC is completely abolished (Figure 9A). However, $\beta(1\rightarrow2)$ activity is clearly present in *M. smegmatis*ΔaftC (Figure 9A). In addition, *M. smegmatis*ΔaftC complemented with pMV261-Mt-aftC restores $\alpha(1\rightarrow3)$ arabinofuranosyltransferase activity to wild type *M. smegmatis* (Figure 9A). The results clearly establish both from *in vivo* and *in vitro* experiments that AftC catalyzes the addition of an $\alpha(1\rightarrow3)$-Araf unit *via* an $\alpha(1\rightarrow3)$ arabinofuranosyltransferase and that this enzyme is also resistant to EMB (Figure 8A).
Discussion

The mAGP complex represents one of the most important cell wall components of the *Corynebacterianeae* and is essential for the viability of *M. tuberculosis* (Vilcheze et al., 2000; Pan et al., 2001; Gande et al., 2004; Mills et al., 2004). It is therefore not surprising that one of the most effective anti-mycobacterial drugs, EMB, targets its synthesis through inhibition of AG biosynthesis. However, the emergence of MDR-TB and XDR-TB has accelerated the need to discover new drug targets (Brennan and Nikaido, 1995). One of the strategies is to identify genes involved in AG biosynthesis. Based on this strategy we previously identified the presence of a new “priming” enzyme, now termed AftA, which would link the initial Araf unit with the C-5 OH of a β(1→6) linked Galf of a pre-synthesized galactan core (Alderwick et al., 2005), and more recently identified the AftB enzyme responsible for β(1→2) Araf residues.

The previously described Emb (Alderwick et al., 2005), AftA (Alderwick et al., 2006a) and AftB proteins (Seidel et al., 2007a) are distinct arabinofuranosyltransferases. Thus, despite some functional relationship, these glycosyltransferases have inherent specific features as evident from the insensitivity of AftA and AftB towards EMB, whereas the single Cg-Emb (Alderwick et al., 2005; Radmacher et al., 2005), and Mt-Emb proteins are sensitive towards EMB (Telenti et al., 1997; Belanger et al., 1996). The number of arabinofuranosyltransferases that are required for mycobacterial arabinan biosynthesis has been a matter of speculation to date depending on how the arabinan chains are assembled. The primary structure of AG (Besra et al., 1995; Daffé et al., 1990) would suggest at least five distinct arabinofuranosyltransferases are required for the complete formation of AG. Interestingly, *M. smegmatis* embA and embB mutants were found to possess reduced amounts of the non-reducing terminal disaccharide β-D-Araf-(1→2)-α-D-Araf
and result in the removal of the dominant terminal non-reducing Ara\textsubscript{6} branched motif in the mutant being replaced by a linear Ara\textsubscript{4} motif (Escuyer et al., 2001). The authors of this study concluded that the \textit{M. smegmatis embA} and \textit{embB} mutants result in a lack of 3-arm branching off the main \textalpha(1\rightarrow5)-arabinan chain proximal to the non-reducing and attachment site of mycolic acids in AG (Escuyer et al., 2001). Initially, it was proposed that the \textbeta-D-Araf-(1\rightarrow2)-\alpha-D-Araf disaccharide was assembled using EmbA and EmbB. However, the recent identification of AftB, the development of specific \textit{in vitro} assays in combination with mutant strains, and recent structural studies have fuelled speculation that EmbA/B act as \textalpha(1\rightarrow5) arabinofuranosyltransferases (Bhamidi et al., 2008; Seidel et al., 2007a; Alderwick et al., 2005).

In this study, we have identified MSMEG2785 (also Rv2673 and NCgl1822), which we have termed AftC, as a novel branching arabinofuranosyltransferase. More precisely, AftC catalyzes the addition of \textalpha(1\rightarrow3) Ara\textsubscript{f} residues as shown through both \textit{in vivo} and \textit{in vitro} experiments, ultimately resulting in 3,5-Ara\textsubscript{f} residues after further \textalpha(1\rightarrow5) extension, characteristic of AG.

For instance, incubation of membranes prepared from \textit{M. smegmatis} with DP\textsuperscript{[14C]}A and a linear \textalpha(1\rightarrow5)-Ara\textsubscript{5} neoglycolipid acceptor resulted in the synthesis of an Ara\textsubscript{6} product. Further chemical characterization of the product by glycosyl linkage analysis established that the \textalpha(1\rightarrow5)-Ara\textsubscript{5} acceptor was extended \textit{via} an EMB resistant \textalpha(1\rightarrow3) arabinosfuranosyltransferase giving rise to 3-linked Ara\textsubscript{f} residues and corroborated our earlier cell wall analysis of the \textit{M. smegmatis}\textalpha{AfC} mutant. Since, it is now established that only \textalpha(1\rightarrow5) arabinofuranosyltransferase(s) are EMB-sensitive it can be further speculated that EmbA and EmbB function in the assembly of the linear \textalpha(1\rightarrow5) arabinan segments as presented in Figure 10, which is in accordance with previous data and the phenotype of a Cg-Emb mutant.
(Alderwick et al., 2005). It is clear that further studies are required to establish the precise role of EmbA and EmbB in mycobacteria.

The analysis of the *M. smegmatis*Δ*aftC* mutant to date and based on the Ara:Gal ratio would suggest that the residual arabinan segment in the mutant consists of approximately five Ara\(^f\) residues: \[\beta\text{-D-Ara}-(1\rightarrow2)-\alpha\text{-D-Ara}-(1\rightarrow5)-\alpha\text{-D-Ara}-(1\rightarrow5)-\alpha\text{-D-Ara}-(1\rightarrow5)-\alpha\text{-D-Ara}\]

located at three branches on the galactan chain (Alderwick et al., 2005; Besra et al., 1995). This is consistent with the recent primary structure of AG (Bhamidi et al., 2008), with a ‘non-variable’ terminal non-reducing Ara\(_{17}\) motif, introduction of a 3,5-Ara\(^f\) residue distal to this non-reducing end by AftC and further extension by a linear \(\alpha(1\rightarrow5)\)Araf domain (Figure 10). The latter appears to be variable (up to 12/13 residues). However, based on *M. smegmatis*Δ*aftC* and the subsequent Ara:Gal compositional analysis a dominant Ara\(_{22}\)/Ara\(_{23}\) motif would be consistent with recent (Bhamidi et al., 2008) and previous (Besra et al., 1995) structural data on AG and this is represented in terms of biosynthetic considerations in Figure 10. It is also possible that AftC or a second distinct \(\alpha(1\rightarrow3)\) arabinofuranosyltransferase (shown as AftD in Figure 10) may be involved in late stages of AG synthesis i.e. the non-reducing Ara\(_{6}\) motif and is consistent with our data and the model presented in Figure 10.

The discovery of AftC has now shed new light on the key arabinofuranosyltransferases to build an arabinan domain typical for *Corynebacterianae*. In this context, the genomic organization in the genomes of the *Corynebacterianae* sequenced is intriguing, revealing high synteny of the *M. tuberculosis* aftC locus to the maps of all other *Mycobacterium* and *Corynebacterium* species. The identification of new cell wall biosynthetic drug targets is of great importance, especially with the emergence of MDR-TB. This newly discovered DPA dependent arabinofuranosyl
transferase represents, along with a straightforward *in vitro* enzyme assay, a promising candidate for further exploitation as a potential drug target.
Experimental procedures

**Bacterial strains and growth conditions.** *C. glutamicum* ATCC 13032 (referred to the remainder of the text as *C. glutamicum*) and *Escherichia coli* DH5αmer were grown in Luria-Bertani broth (LB, Difco) at 30°C and 37°C, respectively. The recombinant strains generated in this study were grown on complex Brain Heart Infusion medium (BHI, Difco), and the salt medium CGXII used for *C. glutamicum* as described (Eggeling and Bott, 2005). Kanamycin and ampicillin were used at a concentration of 50 µg/ml. *M. smegmatis* strains were grown in Tryptic Soy Broth (TSB; Difco) containing 0.005 % Tween80 (TSBT). Solid media were made by adding 1.5 % agar to the above-mentioned broths. The concentrations of antibiotics used for *M. smegmatis* were 100 µg/ml for hygromycin and 20 µg/ml for kanamycin. Minimal inhibitory concentrations were determined by plating cells on solid media supplemented with various concentrations of EMB, rifampicin and chloramphenicol. The minimal inhibitory concentration was defined as the first concentration of drug that would inhibit 100% of growth after 5 days of incubation (Belanger et al., 1996). *M. tuberculosis* H37Rv DNA was obtained from the NIH Tuberculosis Research Materials and Vaccine Testing Contract at Colorado State University. All other chemicals were of reagent grade and obtained from Sigma-Aldrich.

**Construction of plasmids and strains.** Approximately 1 kb of upstream and downstream flanking sequences of *MSMEG2785* were PCR amplified from *M. smegmatis* mc²155 genomic DNA using the primer pairs MS2785LL (TTTTTTTTCCATAAATTGGATCCGCTGACCGACCTCATC) and MS2785LR, MS2785RL (TTTTTTTCCATTTTCTTGCGAGCCCGAGCCTCAAGTTG), and MS2785RR (TTTTTTTCCATAGATTGGTCTCCTGCTGCTGCCCTTGG) and MS2785RR.
(TTTTTTTTCCATCTTTTGCGAATCTCAGCGCGATTTCAC), respectively (all primers are given in 5’ to 3’ direction). Following restriction digestion of the primer incorporated Van91I sites, the PCR fragments were cloned into Van91I-digested p0004S to yield the knockout plasmid pΔMSMEG2785 which was then packaged into the temperature sensitive mycobacteriophage phAE159 as described previously (Bardarov et al., 2002) to yield phasmid DNA of the knockout phage phΔMSMEG2785. Generation of high titre phage particles and specialized transduction were performed as described earlier (Bardarov et al., 2002; Stover et al., 1991). Deletion of MSMEG2785 in one hygromycin resistant transductant was confirmed by Southern blot. To enable expression of MSMEG2785 and Rv2673, in the deletion mutant, these were amplified using primer pairs designed for subsequent cloning into the mycobacterial-shuttle vector pMV261 (Stover et al., 1991). All cloned fragments were verified by sequencing.

To construct the deletion vector pK19mobsacBΔaftC (NCgl1822), crossover PCR was applied with primer pairs AB (A, CGTTAAGCTTCGATCTTGTTGATGTGGCATCACACG; B, CCCATCCACTAAACTAAACAGCGCCATCAACAACATGG) and CD (C, TGTITAAGTTTGGATGGGTGATCCAACGCACGACCATC; D, GCATGGATCCACGCATACCGAGGGAAAGATCTTC) and C. glutamicum genomic DNA as template. Both amplified products were used in a second PCR with primer pairs AD to generate a 656 bp fragment consisting of sequences adjacent to Cg-aftC, which was ligated with BamHI-HindIII-cleaved pK19mobsacB. All plasmids were confirmed by sequencing. The chromosomal deletion of Cg-aftC was performed as described previously using two rounds of positive selection (Schafer et al., 1994), and its successful deletion was verified by use of two different primer pairs.
Isolation of the mAGP complex, glycosyl composition and linkage analysis of alditol acetates by GC and GC/MS. The thawed cells were resuspended in phosphate buffered saline containing 2% Triton X-100 (pH 7.2), disrupted by sonicaton and centrifuged at 27000 x g (Besra et al., 1995; Alderwick et al., 2005). The pelleted material was extracted three times with 2% SDS in phosphate buffered saline at 95°C for 1 h, washed with water, 80% (v/v) acetone in water, and acetone, and finally lyophilized to yield a highly purified cell wall preparation (Besra et al., 1995; Alderwick et al., 2005). Cell wall or per-O-methylated cell wall preparations (Alderwick et al., 2005) were hydrolyzed in 2 M TFA, reduced with NaB\(_2\)H\(_4\) and the resultant alditols per-O-acetylated and examined by GC and GC/MS as described previously (Besra et al., 1995; Alderwick et al., 2005).

Extraction and analysis of cell wall bound mycolic acids. In terms of \(M.\) \textit{smegmatis} strains equivalent amounts of freeze-dried bacilli (100 mg) were processed as described previously (Seidel et al., 2007a) following two consecutive CHCl\(_3\)/CH\(_3\)OH/H\(_2\)O (10:10:3, v/v/v) extractions for 4 h at 50°C in the analysis of cell wall associated lipids, and cell wall bound MAMEs. Alternatively, \(M.\) \textit{smegmatis} and \(C.\) \textit{glutamicum} cultures (5 ml) were grown and metabolically labelled at mid-logarithmic phase of growth using 1 µCi/ml [1,2-\textsuperscript{14}C]acetate (50-62 mCi/mmol, GE Healthcare, Amersham Bioscience) for 4 h at either 30°C or 37°C with gentle shaking, harvested, washed and freeze-dried. Cells were then extracted by two consecutive extractions with 2 ml of CHCl\(_3\)/CH\(_3\)OH/H\(_2\)O (10:10:3, v/v/v) for 4 h at 50°C to provide cell wall associated lipids and analyzed as described previously (Seidel et al., 2007a). The crude lipid extracts were resuspended in CHCl\(_3\)/CH\(_3\)OH (2:1) and equivalent aliquots (50,000 cpm) analyzed by TLC using silica gel plates (5735 silica gel 60F\(_{254}\), Merck) developed in CHCl\(_3\)/CH\(_3\)OH:NH\(_4\)OH (80:20:2, v/v/v) to separate [\textsuperscript{14}C]-labeled TDM and phospholipids (Mikusova et al., 1995).
Lipids were visualized by autoradiography by overnight exposure of Kodak X-Omat AR film to the TLC plates to reveal labelled lipids, quantified by phosphorimaging and compared to know standards (Mikusova et al., 1995). The bound MAMEs/CMAMEs from the above de-lipidated extracts were released by the addition of 2 ml of 5% aqueous solution of tetra-butyl ammonium hydroxide followed by overnight incubation at 100°C. After cooling, water (2 ml), CH₂Cl₂ (4 ml) and CH₃I (500 µl) were added and mixed thoroughly for 30 min. The lower organic phase was recovered following centrifugation and washed three times with water (4 ml), dried and resuspended in diethyl ether (4 ml). After centrifugation the clear supernatant was again dried and resuspended in CH₂Cl₂ (100 µl). An aliquot (5 µl) from each strain was subjected to scintillation counting and an equivalent (5 µl) aliquot analyzed by TLC using silica gel plates (5735 silica gel 60F254, Merck), developed in petroleum ether/acetone (95:5, v/v) and either visualized by autoradiography by exposure of Kodak X-Omat AR film to the TLC plates to reveal [14C]-labeled MAMEs/CMAMEs, or charred following spraying with 5% molybdophosphoric acid in ethanol at 100°C and compared to know standards.

Arabinofuranosyltransferase activity with membrane preparations of M. smegmatis, M. smegmatis pMV261-Mt-aftC, M. smegmatisΔaftC and M. smegmatisΔaftC pMV261-Mt-aftC. Membranes were prepared as described previously (Lee et al., 1997; Alderwick et al., 2006a) and resuspended in 50 mM MOPS (pH 7.9), containing 5 mM β-mercaptoethanol and 10 mM MgCl₂ (buffer A) to a final concentration of 15-10 mg/ml. The neoglycolipid acceptors used in this study were α-D-Araφ-(1→5)-α-D-Araφ-(1→5)-α-D-Araφ-(1→5)-α-D-Araφ-O-(CH₂)₈NH₂ (Ara₅, see Supplementary Material) and α-D-Araφ-(1→5)-α-D-Araφ-O-(CH₂)₇CH₃ (Ara₂) (Lee et al., 1995; Lee et al., 1998). The acceptors (either Ara₂ or Ara₅) and DP[¹⁴C]A (Lee et al., 1995; Lee et al., 1998) (stored in CHCl₃/CH₃OH, 2:1, v/v) were aliquoted into 1.5 ml
eppendorf tubes to a final concentration of 2 mM and 200,000 cpm (90 µM), respectively, and dried under nitrogen. The arabinofuranosyltransferase assay was carried out as described previously (Lee et al., 1997) with modifications. IgePal™ (Sigma-Aldrich) was added (0.1%, v/v) with the appropriate amount of buffer A (final volume 80 µl). Tubes were sonicated for 15 min to resuspend lipid linked substrates and then mixed with the remaining assay components, which included membrane protein from either *M. smegmatis, M. smegmatis* pMV261-Mt-aftC, *M. smegmatis*ΔaftC or *M. smegmatis*ΔaftC pMV261-Mt-aftC (1 mg), 1 mM ATP, 1 mM NADP and in some cases EMB (0-1 mg/ml). Assays were incubated for 1 h at 37°C and quenched by the addition of 533 µl CHCl₃/CH₃OH (1:1, v/v). After mixing and centrifugation at 27000 x g for 15 min at 4°C, the supernatant was removed and dried under nitrogen. The residue was then resuspended in 700 µl of CH₃CH₂OH/H₂O (1:1, v/v) and loaded onto a 1 ml SepPak strong anion exchange cartridge (Supelco), pre-equilibrated with CH₃CH₂OH/H₂O (1:1, v/v). The column was washed with 2 ml CH₃CH₂OH and the eluate collected, dried and partitioned between the two phases arising from a mixture of *n*-butanol (3 ml) and water (3 ml). The resulting organic phase was recovered following centrifugation at 3,500 x g and the aqueous phase again extracted twice with 3 ml of water-saturated *n*-butanol. The pooled extracts were back-washed twice with *n*-butanol-saturated water (3 ml). The *n*-butanol fraction was dried and resuspended in 200 µl butanol. The extracted radiolabeled material was quantified by liquid scintillation counting using 10 % of the labeled material and 5 ml of EcoScintA (National Diagnostics, Atlanta). The incorporation of [¹⁴C]Araf was determined by subtracting counts present in control assays (incubations in the absence of acceptor). The remaining labeled material was subjected to thin-layer chromatography (TLC) using either isopropanol:acetic acid:water (8:1:1, v/v/v) for the assays utilizing the Ara₅ acceptor or CHCl₃:CH₂OH:H₂O:NH₄OH (65:25:3.6:0.5, v/v/v/v) in the case of the Ara₂ acceptor on aluminum-backed Silica Gel 60 F₂₅₄ plates (Merck, Darmstadt,
Germany). Autoradiograms were obtained by exposing TLCs to X-ray film (Kodak X-Omat) for 3 days.

Characterization of α(1→3)-arabinofuranosyltransferase activity with membranes prepared from *M. smegmatis*, *M. smegmatisΔaftC* and *M. smegmatisΔaftC* pMV261-Mt-aftC. Large-scale reaction mixtures containing cold DPA (200 µg, 0.75 mM) (Lee et al., 1997) and 50 mM of the acceptor Ara₂ were mixed and given an initial incubation at 37°C with membranes prepared from either *M. smegmatis*, *M. smegmatisΔaftC* or *M. smegmatisΔaftC* pMV261-Mt-aftC for 1 h. The assays were replenished with fresh membranes (1 mg) and re-incubated for 1 h at 37 °C with the entire process repeated thrice. Products were extracted from reaction mixtures by *n*-butanol/water phase separation as described earlier to extract products. Products were applied to preparative TLC plates, developed in isopropanol:acetic acid:water (8:1:1, v/v/v) and sprayed with 0.01% 1,6-diphenylhexatriene in petroleum-ether:acetone (9:1, v/v), and the products localized under long-wave (366 nm) UV light (Lee et al., 1997). The plate was then re-developed in toluene to remove the reagent and the bands recovered from the plates by extraction with *n*-butanol. The butanol phases were washed with water saturated with *n*-butanol and the dried products subjected to GC (Sassaki et al., 2005) and GC/MS as described (Lee et al., 1997; Alderwick et al., 2006a).
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Abbreviations

The abbreviations used are: AG, Arabinogalactan; Ara, arabinose; Cg, C. glutamicum; 2D-TLC, two-dimensional thin-layer chromatography; DPA, decaprenol phosphoarabinose; EMB, ethambutol; f, furanose; Gal, galactose; GC, gas chromatography; GC/MS, gas chromatography mass spectrometry; LB, Luria-Bertani; MAME, mycolic acid methyl ester; mAGP, mycolyl-arabinogalactan-peptidoglycan; Man-LAM, mannose capped LAM; MS, M. smegmatis; Mt, M. tuberculosis; OD, Optical Density; TLC, thin-layer chromatography.
Figure Legends

Fig. 1. Biosynthetic pathway leading to arabinan formation in *M. tuberculosis* AG.

Fig. 2. Comparison of the *aftC* locus within the *Corynebacterianeae*. (A) The locus in the bacteria analyzed consists of *aftC* which in *M. tuberculosis* has the locus tag Rv2673 and in *C. glutamicum* NCgl1822. The genomic region displayed encompasses 7 kb, and orthologous genes are highlighted accordingly. Abbreviations: *M. marinum*, *Mycobacterium marinum*; *M. av subsp. par.*, *Mycobacterium avium* subsp. *paratuberculosis*; *C. efficiens*, *Corynebacterium efficiens*; *C. jeikeium*, *Corynebacterium jeikeium*; *Nocardia farcina*, *Nocardia farcina* IFM 10152; *Rhodococcus*, *Rhodococcus* sp. strain RHA1. (B) AftC is a hydrophobic protein predicted to span the membrane 10 times and the transmembrane helices are numbered accordingly. The lower part of the figure shows the degree of conservation of the orthologues given in A as analysed by the DIALIGN method (Brudno *et al.*, 2003). Also shown is the approximate position of the fully conserved aspartyl (D) and glutamyl (E) residues.

Fig. 3. Generation of a *MSMEG2785* null mutant. (A) A map of the *MSMEG2785* region in the parental *M. smegmatis* strain and its corresponding region in the Δ*MSMEG2785* mutant. *res*, γδ resolvase site; *hyg*, hygromycin resistance gene from *Streptomyces hygroscopicus*; *sacB*, sucrose counter-selectable gene from *Bacillus subtilis*. Digoxigenin-labelled probes were derived from ~1kb upstream and downstream flanking sequences that were used to construct the knockout plasmid, and are indicated by thick lines with square ends. *SacI* digested bands expected in a Southern blot are indicated in roman numerals with sizes in brackets. The inset shows the Southern blot of *SacI* digested genomic DNA from the two strains with expected
bands indicated by arrows. (B) Growth of wild type of \textit{M. smegmatis} (◇), \textit{M. smegmatis}\text{Δ}aft\text{C} (□), \textit{M. smegmatis}\text{Δ}aft\text{C} pMV261-Ms-aft\text{C} (△), and \textit{M. smegmatis}\text{Δ}aft\text{C} pMV261-Mt-aft\text{C} (○) on TSB medium. (C) Colony morphology of wild type \textit{M. smegmatis} and \textit{M. smegmatis}\text{Δ}aft\text{C} on TSB/agar plates. Black bar represents 1 mm.

**Fig. 4. Analysis of cell wall associated lipids and bound MAMEs from \textit{M. smegmatis}, \textit{M. smegmatis}\text{Δ}aft\text{C}, \textit{M. smegmatis}\text{Δ}aft\text{C} pMV261-Ms-aft\text{C} and \textit{M. smegmatis}\text{Δ}aft\text{C} pMV261-Mt-aft\text{C}.** (A) Analysis of cell wall bound MAMEs from \textit{M. smegmatis}, \textit{M. smegmatis}\text{Δ}aft\text{C}, \textit{M. smegmatis}\text{Δ}aft\text{C} pMV261-Ms-aft\text{C} and \textit{M. smegmatis}\text{Δ}aft\text{C} pMV261-Mt-aft\text{C}. The bound mycolic acids from an equivalent amount of freeze-dried cells (100 mg), which were initially de-lipidated using two consecutive extractions of CHCl\textsubscript{3}:CH\textsubscript{3}OH:H\textsubscript{2}O (10/10/3; v/v/v) at 50\textdegree C for 4 h, were released by the addition of tetra-butylammonium hydroxide at 100\textdegree C overnight, and methylated as described in the “Experimental Procedures”. An equivalent aliquot from each strain was subjected to TLC using silica gel plates (5735 silica gel 60F\textsubscript{254}, Merck), and developed in petroleum ether/acetone (95:5, v/v) and charred to reveal MAMEs and compared to known standards (Gande \textit{et al.}, 2004). (B) Quantitative analysis of extractable \textsuperscript{14}C-lipids from \textit{M. smegmatis}, \textit{M. smegmatis}\text{Δ}aft\text{C}, \textit{M. smegmatis}\text{Δ}aft\text{C} pMV261-Ms-aft\text{C} and \textit{M. smegmatis}\text{Δ}aft\text{C} pMV261-Mt-aft\text{C}. Lipids were extracted from cells by a series of organic washes as described in ‘Experimental Procedures’ (Seidel \textit{et al.}, 2007a). An equivalent aliquot (50, 000 cpm) from each strain was subjected to TLC using silica gel plates (5725 silica gel 60F\textsubscript{254}, Merck) developed in CHCl\textsubscript{3}:CH\textsubscript{3}OH:NH\textsubscript{4}OH (80:20:2, v/v/v) and quantified using phosphorimaging and compared to known standards (Mikusova \textit{et al.}, 1995) after exposure to Kodak X-Omat film for 24 hours.
Fig. 5. GC analysis of cell walls of *M. smegmatis*, *M. smegmatis∆*aft*C*, *M. smegmatis∆*aft*C* pMV261-Ms-*aft*C and *M. smegmatis∆*aft*C* pMV261-Mt-*aft*C*. Samples of purified cell walls were hydrolyzed with 2M TFA, reduced, per-O-acetylated and analyzed as described under “Experimental Procedures” (Besra *et al.*, 1995; Alderwick *et al.*, 2005).

Fig. 6. GC/MS analysis of cell walls of *M. smegmatis*, *M. smegmatis∆*aft*C*, *M. smegmatis∆*aft*C* pMV261-Ms-*aft*C* and *M. smegmatis∆*aft*C* pMV261-Mt-*aft*C*. Samples of per-O-methylated cell walls were hydrolyzed with 2M TFA, reduced, per-O-acetylated and analyzed as described under “Experimental Procedures” (Besra *et al.*, 1995; Alderwick *et al.*, 2005).

Fig. 7. Arabinofuranosyltransferase activity utilizing an Ara₂ acceptor and membranes prepared from *M. smegmatis*, *M. smegmatis∆*aft*C* and *M. smegmatis∆*aft*C* pMV261-Mt-*aft*C*. (A) Biosynthetic reaction scheme of products A and B formed in arabinofuranosyltransferase assays using the neoglycolipid Ara₂ acceptor. (B) Arabinofuranosyltransferase activity was determined using the synthetic Ara₂ acceptor in a cell-free assay with and without EMB (1 mg/ml) as previously described (Lee *et al.*, 1997). The products of the assay were resuspended prior to scintillation counting (10 %) and the remaining subjected to TLC using silica gel plates (5735 silica gel 60F₂₅₄, Merck) in CHCl₃:CH₃OH:H₂O:NH₄OH (65/25/3.6/0.5, v/v/v/v) with the reaction products visualized by autoradiography. The TLC autoradiogram is representative of several independent experiments.

Fig. 8. Arabinofuranosyltransferase activity utilizing an Ara₅ acceptor and membranes prepared from *M. smegmatis*, *M. smegmatis∆*aft*C* and *M. smegmatis∆*aft*C* pMV261-Mt-*aft*C*. (A) Arabinofuranosyltransferase activity was determined using the synthetic Ara₅ acceptor
in a cell-free assay with and without EMB (1 mg/ml). The products reflective of three independent enzyme preparations and assays were resuspended prior to scintillation counting (10%) and the remaining subjected to TLC using silica gel plates (5735 silica gel 60F254, Merck) in isopropanol:acetic acid:water (8/1/1/, v/v/v) with the reaction product X visualized by autoradiography. The TLC autoradiogram is representative of three independent experiments. 

(B) Ara₅ and Ara₆ (Appelmelk et al., 2008) acceptor standards were subjected to TLC using silica gel plates (5735 silica gel 60F254, Merck) in isopropanol:acetic acid:water (8/1/1/, v/v/v) with the reaction products visualized by staining with α-naphthol followed by charring.

Fig. 9. GC characterization of in vitro synthesized product X from the arabinofuranosyltransferase assays utilizing the Ara₅ acceptor. (A) GC analysis of the partially per-O-methylated, per-O-acetylated alditol acetate derivative of product X obtained from assays containing membranes prepared from either M. smegmatis, M. smegmatisΔaftC or M. smegmatisΔaftC pMV261-Mt-aftC (Sassaki et al., 2005). (B) Panel illustrates the structure(s) of product X.

Fig. 10. Mycobacterial arabinan biosynthesis and the role of AftC.


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117x252mm (300 x 300 DPI)
AftB  AftC/AftD?  EmbA/ EmbB or  AftE?

Site of mycolic acid attachment

254x190mm (300 x 300 DPI)