Mycobacterium marinum MMAR_2380, a predicted transmembrane acyltransferase, is essential for the presence of the mannose cap on lipoarabinomannan

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Lipoarabinomannan (LAM) is a major glycolipid in the mycobacterial cell envelope. LAM consists of a mannosylphosphatidylinositol (MPI) anchor, a mannan core and a branched arabinan domain. The termini of the arabinan branches can become substituted with one to three α(1→2)-linked mannosyl residues, the mannose cap, producing ManLAM. ManLAM has been associated with a range of different immunomodulatory properties of Mycobacterium tuberculosis during infection of the host. In some of these effects, the presence of the mannose cap on ManLAM appears to be crucial for its activity. So far, in the biosynthesis of the mannose cap on ManLAM, two enzymes have been reported to be involved: a mannosyltransferase that adds the first mannosyl residue of the mannose caps to the arabinan domain of LAM, and another mannosyltransferase that elongates the mannose cap up to three mannosyl residues. Here, we report that a third gene is involved, MMAR_2380, which is the Mycobacterium marinum orthologue of Rv1565c. MMAR_2380 encodes a predicted transmembrane acyltransferase. In M. marinum ΔMMAR_2380, the LAM arabinan domain is still intact, but the mutant LAM lacks the mannose cap. Additional effects of mutation of MMAR_2380 on LAM were observed: a higher degree of branching of both the arabinan domain and the mannan core, and a decreased incorporation of [1,2-14C]acetate into the acyl chains in mutant LAM as compared with the wild-type form. This latter effect was also observed for related lipoglycans, i.e. lipomannan (LM) and phosphatidylinositol mannosides (PIMs). Furthermore, the mutant strain showed increased aggregation in liquid cultures as compared with the wild-type strain. All phenotypic traits of M. marinum ΔMMAR_2380, the deficiency in the mannose cap on LAM and changes at the cell surface, could be reversed by complementing the mutant strain with MMAR_2380. Strikingly, membrane preparations of the mutant strain still showed enzymic activity for the arabinan mannose-capping mannosyltransferase similar to that of the wild-type strain. Although the exact function of MMAR_2380 remains unknown, we show that the protein is essential for the presence of a mannose cap on LAM.

Abbreviations: Ara6, hexaarabinofuranoside; Araf, arabinofuranosyl unit; AraLAM, LAM with linked arabinosyl units; BCA, bicinchoninic acid; CE, capillary electrophoresis; LAM, lipoarabinomannan; LM, lipomannan; ManLAM, mannose-capped LAM; Manp, mannopyranosyl residue; MPI, mannosylphosphatidylinositol; PIMs, phosphatidylinositol mannosides; PIM2, phosphatidylinositol dimannosides; PIM4, phosphatidylinositol tetramannosides; PIM6, phosphatidylinositol hexamannosides; PM–CW, plasma membrane–cell wall domain.

Six supplementary figures and a supplementary table, with supplementary references, are available with the online version of this paper.
INTRODUCTION

The complex mycobacterial cell envelope contains an exceptionally high amount of lipids. One of the major glycolipids present is lipoarabinomannan (LAM) (Briken et al., 2004; Chatterjee & Khoo, 1998; Nigou et al., 2002, 2003). With its mannosylphosphatidylinositol (MPI) anchor, LAM is probably inserted in both the cytoplasmic membrane and the outer membrane (Hoffmann et al., 2008; Pitarque et al., 2008). The glycans portion of LAM comprises a mannan core, which consists of a mannan core, which consists of (1→6)-linked mannosyl residues substituted at some positions with single (1→2)-linked mannosyl linkages, and an arabinan domain consisting of (1→5)-linked arabinose (see Supplementary Fig. S1). This latter domain is branched with side chains that always end in (1→2)-linked arabinosyl units (AraLAM). In mannose-capped LAM (ManLAM), a part of these terminal arabinosyl residues is substituted with an (1→5)-linked mannosyl residue which can be further elongated by the addition of one or two (1→2)-linked mannosyl residues, forming the mannose cap (Supplementary Fig. S1). Whether mannose caps are present on LAM depends on the Mycobacterium species (Pitarque et al., 2005).

Several immunomodulating properties of LAM have been reported which could codetermine the host–pathogen interaction during infection with pathogenic mycobacteria, such as Mycobacterium tuberculosis. Some of these have been linked specifically to the presence of the mannose cap on LAM, e.g. the binding of ManLAM to pattern recognition receptors such as the dendritic cell-specific intercellular adhesion molecule-3-grabbing nonintegrin (DC-SIGN) (Geijtenbeek et al., 2003; Maeda et al., 2003) and the macrophage mannose receptor (MMR) (Schlesinger et al., 1994), and its role in phagosome maturation arrest (Kang et al., 2005; Welin et al., 2008).

So far, two mannosyltransferases have been identified as being involved in the biosynthesis of the mannose cap on ManLAM. The first, encoded by Rv1635c, adds the first mannosyl residue of the mannose cap to the non-reducing arabian termini (Dinadayala et al., 2006). Rv2181 encodes the second, cap-elongating mannosyltransferase, which besides lengthening the mannose cap, substitutes the mannan core of LAM with the single (1→2)-linked mannosyl moieties (Kaur et al., 2006, 2008). Both enzymes use polyprelyosphosphomannose (PPM) as a sugar donor (Appelmelk et al., 2008; Kaur et al., 2006). A potential glycosyltransferase function of these enzymes has been predicted using bioinformatics tools. Although very successful, this approach is biased towards finding glycosyltransferases directly involved in the biosynthesis of glycolipids or glycoproteins, and proteins that exert more unexpected functions may be missed.

In an alternative approach to identify novel genes with a role in the biosynthesis of ManLAM, we have used a colony blot screen of a transposon-insertion mutant library in Mycobacterium marinum in which single-transposon mutants were probed with mannose cap-recognizing mAb 55.92.1A1 (Appelmelk et al., 2008). As recently described, this screen yielded the mutant in MMAR_2439, the M. marinum orthologue of Rv1635c. Subsequent mannosyltransferase assays and chemical analysis confirmed that the function of MMAR_2439 is the addition of the first mannosyl residue of the mannose cap to LAM, identical to Rv1635c (Appelmelk et al., 2008).

We have extended our search using the screening approach with the mannose cap-recognizing mAb. In this paper, we reveal a third gene involved in the biosynthesis of the mannose cap on LAM. In M. marinum ΔMMAR_2380, the LAM molecule is still intact, apart from lacking its mannose cap. Additional effects of the mutation of MMAR_2380 were seen in a higher degree of branching of both the arabinan domain and the mannan core in mutant LAM, decreased [1,2-14]acetate incorporation in the acyl chains of mutant LAM and related lipoglycans, and an altered cell surface of the mutant strain as compared with wild-type M. marinum. MMAR_2380 encodes a predicted transmembrane acyltransferase, and here we explored potential roles for MMAR_2380 in the biosynthesis of LAM in M. marinum.

METHODS

Bacterial strains and growth conditions. M. marinum strain E11 (Puttinaowarat et al., 1999) and Mycobacterium smegmatis mc²155 were grown in Middlebrook 7H9 broth (Difco) with 10 % Middlebrook albumin dextrose catalase (ADC) enrichment (BBL) and 0.05 % (v/v) Tween 80, or on Middlebrook 7H10 agar (Difco) with 10 % Middlebrook oleic acid albumin dextrose catalase (OADC) enrichment (BBL) at 30 and 37 ºC, respectively. Escherichia coli DH5α was grown on LB at 37 ºC. Mycobacterial growth was measured by determining OD₆₀₀ with a UV/visible spectrophotometer (Jenway). The concentrations of antibiotics used were 25 µg kanamycin ml⁻¹ and 50 µg hygromycin ml⁻¹ for mycobacteria, and 100 µg hygromycin ml⁻¹ for E. coli.

Immunoblotting assay. Bacteria were grown until the late-exponential phase and disrupted with a Beadbeater (BioSpec). Protein concentration was measured with a bicinchoninic acid (BCA) Protein Assay (Pierce). Supernatants were run on a 10 % SDS-PAGE gel and immunostained after electroblotting on a PVDF membrane (Millipore). Murine mAbs of the IgM class were used. mAb F30-5 recognizes the branches of the arabian domain of LAM (Appelmelk et al., 2008; Kolk et al., 1984). mAb 55.92.1A1 binds the mannose cap on ManLAM (Appelmelk et al., 2008). First the PVDF membranes were incubated in 0.5 % (w/v) blocking reagent (Boehringer) for 1 h at 37 ºC, followed by incubation of 2 h with the mAb diluted in 1:1 blocking buffer and PBS + 0.05 % (v/v) Tween 80 (PBST). After thorough washing in PBST, the membranes were incubated with horseradish peroxidase (HRP)-labelled goat anti-mouse IgM (American Qualex) in PBST with 0.5 % (v/v) normal goat serum. After washing, the membranes were stained with 4-chloro-1-naphthol (4-CN; Bio-Rad) and 3,3’-diamobenzidine.4HCl (DAB; Sigma).

Identification of a novel M. marinum mutant deficient in the biosynthesis of the mannose cap on LAM. A transposon insertion mutant library was created in M. marinum E11 with the
Himα1-based mariner transposon, which has little insertion site specificity (dinucleotide TA) (Rubin et al., 1999). The transposon was introduced via phagemid φMycoMar17, as described by Sassetti et al. (2001). Mutants selected on kanamycin were screened in a colony blot assay for the absence of the mannose cap on LAM using mAb 55.92.1A1, as described previously (Appelmelk et al., 2008). In brief, single colonies were transferred to PVDF membranes with sterile toothpicks, after which the membranes were baked for 1 h at 70 °C and subsequently treated as in the immunoblotting assay described above. Mutants that were repeatedly negative with 55.92.1A1 in colony blots were examined further by SDS-PAGE and immunostaining. The location of the transposon insertion was determined by ligation-mediated PCR, as described previously (Abdallah et al., 2006). The exact insertion position of the transposon in gene \( \text{MMAR}_2380 \) was confirmed by standard PCR with the pMyco1-primer and a second primer, cap-RV, which binds about 210 bp downstream from \( \text{MMAR}_{2380} \). The PCR product was sequenced on an ABI Prism 300 DNA sequencer (Applied Biosystems). To determine the direction of the kanamyacin-resistance cassette in the transposon in \( \text{MMAR}_{2380} \), two primers were used, MMAR_2380-FW and MMAR_2380-RV, with a binding site upstream or downstream of the transposon in gene \( \text{MMAR}_{2380} \), respectively, and two primers binding to sequences within the transposon (the kanamyacin cassette), Kana-FW and Kana-RV. See Supplementary Table S1 for primer sequences.

**Chemical analysis of the mannose cap on LAM.** The presence of the mannose cap in \( \text{M. marinum} \) wild-type and \( \text{M. marinum} \) \( \Delta \text{MMAR}_{2380} \) strains was determined by subtracting counts present in control assays (reaction components incubated in the absence of acceptor Ara\(_g\)) (Appelmelk et al., 2008).

**NMR analysis of the mannose cap, arabinoxylan domain and mannose core of LAM.** NMR spectra of LAM from \( \text{M. marinum} \) wild-type and \( \text{M. marinum} \) \( \Delta \text{MMAR}_{2380} \) were recorded on a Bruker DMX-500 NMR spectrometer equipped with a double resonance (1H/X)-BBI z-gradient probe head. All samples were exchanged in \( \text{D}_2\text{O} \) (99.97 % D, Euriso-top, with intermediate lyophilization, and then dissolved in 0.5 ml \( \text{D}_2\text{O} \) and analysed at 313 K. The \( ^1\text{H} \) and \( ^13\text{C} \) NMR chemical shifts were referenced relative to internal acetone at 2.225 and 34.00 p.p.m. respectively. All the details concerning NMR sequences used and experimental procedures have been described in previous studies (Gilleron et al., 2000).

**Glycosidic linkage analysis of LAM.** Glycosyl linkage composition was performed according to the modified procedure of Ciucanu & Kerek (1984). The per-O-methylated LAM was hydrolysed using 500 μl 2 M trifluoroacetic acid (TFA) at 110 °C for 2 h, reduced using 350 μl 10 mg ml\(^{-1}\) sodium borodeuteride [\( \text{NaBD}_4 \)] (1 M \( \text{NaOH}: \text{C}_2\text{H}_5\text{OH}: 1:1, \text{v/v} ) and per-O-acetylated using 300 μl acetic anhydride for 1 h at 110 °C. The resulting alditol acetates were solubilized in cyclohexane before analysis by GC and GC/MS.

**[1,2-\(^{14}\text{C}]\)Acetate incorporation in total lipids.** \( \text{M. marinum} \) strains were grown as described above and metabolically labelled using 5 μCi ml\(^{-1}\) [1,2-\(^{14}\text{C}]\)acetate [50–62 mCi mmol\(^{-1}\) (1850–2294 MBq mmol\(^{-1}\)], GE Healthcare, Amersham Bioscience] at OD\(_{600}\) 0.4, and cultures were grown for a further 4 h at 37 °C with gentle shaking. Cells were harvested by centrifugation and washed once with PBS, and a small-scale apolar and polar lipid extraction was performed as described by Dobson et al. (1985). The lipid extracts were dried and resuspended in \( \text{CH}_2\text{Cl}_2: \text{CH}_3\text{OH} \) (2:1), and equal amounts of crude lipid (25000 c.p.m.) were applied to the corners of 6.6 × 6.6 cm pieces of Merck 5554 aluminium-backed TLC plates. The plates were developed using solvent system E for polar lipids: chloroform: methanol: water (60:30:6, by vol.) in the first direction, and chloroform:acetic acid: methanol:water (40:25:3:6, by vol.) in the second direction (Besra, 1998; Dobson et al., 1985). Plates were dried and autoradiograms were produced by overnight exposure of Kodak X-Omat AR film to the TLC plates to reveal [1,2-\(^{14}\text{C}]\)acetate-labelled lipids.
C2H5OH. The sample was dried using a Savant Speedvac concentrator concentrated to approximately 1 ml and precipitated using 5 ml acetate and 50 % propan-1-ol). The eluent was collected and removal of neutral glycans, followed by buffer B (50 mM ammonium acetate and 15 % propan-1-ol) and subjected to Octyl Sepharose CL-4B chromatography. The column (2.5 × 50 cm) was washed initially with four column volumes of buffer A to ensure removal of neutral glycans, followed by buffer B (50 mM ammonium acetate and 50 % propan-1-ol). The eluent was collected and concentrated to approximately 1 ml and precipitated using 5 ml C2H5OH at 68 °C. The aqueous phase was dialysed and dried, followed by extensive treatments with α-amylase, DNase, RNase, chymotrypsin and trypsin to degrade any contamination. This fraction was dialysed to remove the low-molecular-mass breakdown products formed after the enzyme treatment, thus yielding the crude lipoglycan fraction. The crude lipoglycan extract was dried and resuspended in buffer A to remove the low-molecular-mass breakdown products formed after the enzyme treatment, thus yielding the crude lipoglycan fraction.

RESULTS AND DISCUSSION

M. marinum MMAR_2380 is essential for the presence of the mannose cap on LAM

Two genes have been reported to be involved in the biosynthesis of the mannose cap on ManLAM, Rv1635c and Rv2181 (Dinadayala et al., 2006; Kaur et al., 2008). An M. marinum mutant strain in which the homologue of Rv1635c (MMAR_2439) is mutated has also been isolated in a colony blot screen with mannose cap-recognizing mAb 55.92.1A1 (anti-ManLAM; α-ManLAM) (Appelmelk et al., 2008).

By continuing with this screen, we identified a novel gene involved in mannose-capping. LAM from an M. marinum mutant strain with a transposon inserted in MMAR_2380 at 91 bp upstream of its 3’ end (Supplementary Fig. S2) reacted well with an anti-AraLAM (α-AraLAM) mAb (mAb F30-5) which recognizes the arabinan branches of LAM, but not with α-ManLAM (Fig. 1a). The absence of the mannose cap on LAM in M. marinum ΔMMAR_2380 was further verified by chemical analysis. Both the mono- and di-mannoside caps, which are the dominant cap-lengths in the wild-type strain of M. marinum (Pitarque et al., 2005), were not detectable in the mutant strain (Fig. 1b). By complementing M. marinum ΔMMAR_2380 with a wild-type copy of MMAR_2380 (region indicated in Supplementary Fig. S2), the biosynthesis of the mannose cap on LAM was restored (Fig. 1a). This also excluded the possibility that the transposon affected the treXYZ-operon located downstream of MMAR_2380 rather than MMAR_2380 (Supplementary Fig. S2).

Mannosyltransferase capping enzymic activity is still present in the M. marinum ΔMMAR_2380 mutant strain

Since the full-length mannose cap is missing in the mutant strain, we checked the potential capability of the latter to

![Fig. 1](http://mic.sgmjournals.org)
add the first mannosyl unit of the cap. We used a mannosyltransferase assay previously set up to characterize the enzymic activity of the MMAR_2439 (Rv1635c) gene product (Appelmelk et al., 2008). A membrane preparation from M. marinum wild-type cells is able to transfer mannosyl from an in situ-produced decaprenylphospho-mannose donor to a synthetic Araβ acceptor, but a membrane preparation of M. marinum ΔMMAR_2439 does not show this enzyme activity (Appelmelk et al., 2008). In contrast to this previous mutant, a membrane preparation from M. marinum ΔMMAR_2380 was able to produce a mannosylated Araβ acceptor similar to that of the wild-type strain (Fig. 2). This means that the arabinan mannosylcapping enzymic activity is still present in the membrane of M. marinum ΔMMAR_2380; in other words, the gene product of MMAR_2380 is not involved in the direct functioning of the LAM-capping mannosyltransferase.

**Structural differences between the glycan parts of wild-type and mutant LAM**

To investigate whether an alteration in the structure of the arabinan domain of mutant LAM might have caused the inability of the mutant strain to add the mannosyl cap, the glycan part of wild-type and mutant LAM was analysed by NMR. The NMR profile showed that the mutant LAM contained all mannosyl (Man\(\beta\)) and arabinosyl (Ara\(\beta\)) residues that are present in the wild-type LAM, even the single \(\alpha(1\rightarrow2)\)-linked mannoses added to the mannan core (Fig. 3). Most importantly, the \(\beta\)-arabinosyl residues which form the non-reducing termini of the branches of the arabinan domain and which are the acceptors for the mannosyl-capping enzyme MMAR_2439 (Supplementary Fig. S1), were still part of M. marinum ΔMMAR_2380 LAM, and hence could, at least in theory, become substituted with a mannosyl cap.

Further analysis, however, did indicate an increase in the degree of branching of the mannan core in the mutant LAM, as revealed by the \(2,6-\alpha\)-Manp: (2,6-\(\alpha\)-Manp+6-\(\alpha\)-Manp) ratio, which was 78% in the mutant and 28% in the wild-type LAM. In a similar way, the arabinan domain of the mutant LAM seemed to harbour more lateral branches, with a 2-\(\alpha\)-Araf:5-\(\alpha\)-Araf ratio of 0.35 in the mutant as compared with 0.29 in the wild-type LAM. Methylation analysis corroborated these conclusions, although the ratio values were somewhat different: the 2,6-\(\alpha\)-Manp: (2,6-\(\alpha\)-Manp+6-\(\alpha\)-Manp) ratio was 50% for mutant LAM and 36% for the wild-type LAM, and the 2-\(\alpha\)-Araf:5-\(\alpha\)-Araf ratio was 0.23 and 0.15 for the mutant and wild-type LAM, respectively.

Accordingly, in the biosynthesis of ManLAM, the function of the MMAR_2380 protein appears essential for the presence of the mannosyl cap, but its mutation also results in increased branching of both the mannan core and the arabinan domain of LAM.

**Acylation patterns of lipoglycans from wild-type and mutant strains**

As MMAR_2380 is predicted to contain an acyltransferase domain, the acylation of mutant LAM was examined. To investigate this, M. marinum was cultured in the presence of \([1,2\]^{14}\)Cacetate, after which lipoglycans were extracted and counted for the incorporation of \([1,2\]^{14}\)Cacetate in the acyl chains (Fig. 4a). The data show that as compared with lipoglycans from wild-type M. marinum, lipoglycans from M. marinum ΔMMAR_2380 have a reduced \([1,2\]^{14}\)Cacetate incorporation. The complementation of M. marinum ΔMMAR_2380 with wild-type MMAR_2380 resulted in an increase of \([1,2\]^{14}\)Cacetate incorporation. LAM and the related lipoglycan lipomannan (LM) were further examined by SDS-PAGE/autoradiography (Fig. 4a), which also confirmed the reduction of \([1,2\]^{14}\)C acetate incorporation in the mutant LAM and showed a similar effect for mutant LM.

As similar effects of mutation of MMAR_2380 on \([1,2\]^{14}\)Cacetate incorporation were seen for LM and LAM, we also analysed acylation of the structurally related phosphatidylinositol mannosides (PIMs). \([1,2\]^{14}\)Cacetate-labelled lipid extracts were examined by 2D TLC using solvent system E for polar lipids (Besra, 1998; Dobson et al., 1985), which indeed showed differences in the polar lipid profiles of the wild-type and mutant strains. The lipid extract from wild-type M. marinum showed \([1,2\]^{14}\)Cacetate incorporation into phosphatidylinositol (PI), tri- and tetra-acylated phosphatidylinositol dimannosides (Ac\(_1\)/Ac\(_2\)/PIM\(_2\)) and phosphatidylinositol hexamannosides (Ac\(_3\)/Ac\(_4\)/PIM\(_6\)) (Fig. 4b). Interestingly, in the lipid profile of M. marinum ΔMMAR_2380, a subtle but reproducible reduction in \([1,2\]^{14}\)Cacetate incorporation in both Ac\(_1\)/PIM\(_6\) and
Ac2PIM6 could be observed (Fig. 4b). The incorporation of [1,2-14C]acetate in Ac1/Ac2PIM2, however, showed some variations between the experiments, and therefore was less clear.

Phosphatidylinositol dimannosides (PIM2) have been hypothesized to be precursors for phosphatidylinositol hexamannosides (PIM6) as well as LAM and LM, with phosphatidylinositol tetramannosides (PIM4) as a putative branching point (Besra et al., 1997; Kovacevic et al., 2006), and therefore alterations at or before this point of the biosynthesis pathway of LAM may carry forward into the final structure of LAM, as well as LM and PIM6. Because [1,2-14C]acetate incorporation analysis only provides information on potential quantitative differences between the wild-type and mutant lipoglycans, and to verify the results obtained from the TLC assays, we also subjected extracted PIMs to direct structural analysis by MALDI-TOF MS in an independent experiment. This technique can discriminate between the various forms of PIMs in terms of mannosylation and acylation (Gilleron et al., 2006). The crude lipid extract from the mutant strain M. marinum DMMAR_2380 contained all the different forms of PIMs present in the wild-type strain but with an apparent reduction of the most acylated forms (Supplementary Fig. S3), which might explain the decrease of [1,2-14C]acetate incorporation in the mutant.

Hence, while LAM, LM and all forms of PIMs are present in the mutant strain, small quantitative differences in [1,2-14C]acetate incorporation in PIMs, LM, and LAM between the wild-type and the mutant strain can be observed, which might arise from a reduction of the relative abundance of the most acylated forms.

M. marinum DMMAR_2380 has altered cell-surface properties

Along with the biosynthesis by M. marinum DMMAR_2380 of LAM that is devoid of the mannose cap, another phenotypic trait was observed for this mutant strain. As compared with the wild-type strain, M. marinum DMMAR_2380 showed severe aggregation. When grown as liquid cultures in 7H9 medium supplemented with 0.05% (v/v) Tween 80, the mutant strain showed a reduced OD600 over time as compared with both its parent and the complemented strain (Fig. 5a). While the wild-type and complemented strain showed smooth yellow suspensions, the mutant strains showed aggregation and irregular pink clumps (Fig. 5b, and Supplementary Fig S4 for colour pictures). We cannot determine whether DMMAR_2380 is essential for optimal growth in vitro or, alternatively, whether the reduced OD600 in liquid cultures is solely due to aggregation. On 7H10 agar plates, the mutant strain showed the same colony morphology and growth rate as the wild-type strain (not shown). The effect of mutation of DMMAR_2380 on the cell-surface properties of M. marinum DMMAR_2380 in liquid cultures was consistent with earlier reported results for a Mycobacterium avium mutant strain in which the homologous gene was mutated (Yamazaki et al., 2006a, b). This M. avium mutant was impaired in its ability to produce large, wild-type amounts of biofilm (Yamazaki et al., 2006b), which also negatively influenced its invasiveness of human bronchial epithelial cells (Yamazaki et al., 2006a). On the other hand, in a designer arrays for defined mutant analysis (DeADMAN) screen of a transposon mutant library in M. tuberculosis CDC1551 for survival in mice, the mutant strain with a transposon in the homologous gene (ΔMT1616) was tested and did not...
appear to be attenuated in in vivo growth (Lamichhane et al., 2005).

The glycolipid profile and mannosylation pattern of proteins in M. marinum ΔMMAR_2380 appear identical to wild-type patterns

The above-mentioned effect of the transposon insertion in MMAR_2380, the aggregation of the mutant strain, suggested a more pleiotropic effect on the bacterial surface, and hence could have affected, for example, the biosynthesis of glycolipids other than LAM. Other alterations in phenotypic traits, such as morphology, smooth/rough transition of colonies and biofilm formation, have often been linked to changes in glycolipid constituents (Belisle et al., 1993; Belisle & Brennan, 1989; Daffé et al., 1991; Howard et al., 2006). Therefore, we performed an extensive lipid profile study in which polar and apolar extractable lipids were run in a range of four different TLC solvent systems, A to D, in addition to system E discussed above. Strikingly, no differences between the wild-type and the mutant strain could be observed (Supplementary Fig. S5).

Next, we checked for the mannosylation of proteins in M. marinum ΔMMAR_2380 as compared with the wild-type strain, because of the specific role of MMAR_2380 in the mannose-capping of LAM. Whole-cell lysates were exam-
grown cultures per strain; error bars represent standard deviation. (b) OD600 measurements during growth in 7H9 + 0.05 % Tween 80 with agitation. Shown are means of three independently grown cultures per strain; error bars represent standard deviation.

Fig. 5. Physical appearance of liquid-grown *M. marinum* wild type, ΔMMAR_2380 and complemented ΔMMAR_2380 (ΔMMAR_2380 comp.). (a) OD600 measurements during growth in 7H9 + 0.05 % Tween 80 with agitation. Shown are means of three independently grown cultures per strain; error bars represent standard deviation. (b) *M. marinum* ΔMMAR_2380 shows increased aggregation as compared with the wild-type and the complemented strains (see Supplementary Fig. S4 for colour pictures).

**Prediction of gene function**

*MMAR_2380* encodes a 729 aa predicted transmembrane protein of unknown function (Supplementary Fig. S2). Therefore, a standard BLASTP search was performed against the nonredundant (nr) database at NCBI for the protein MMAR_2380 along with a search against the Conserved Domain Database (CDD) (Marchler-Bauer et al., 2009). In contrast to the mannose-capping enzyme Rv1635c, MMAR_2380 (Rv1565c) is also present with high similarity in *Mycobacterium* species known to produce LAM without a mannose cap, e.g. in *M. smegmatis* mc²155 (MSMEG_3187; identities 75 %, positives 85 %). Its homologue in *M. tuberculosis* strain CDC1551 (MT1616) is annotated as putative lipopolysaccharide biosynthesis protein WbpC. Unfortunately, the exact function of the WbpC protein has not yet been determined. At present, WbpC is annotated as a possible O-acetyltransferase in the O-antigen biosynthesis cluster of *Pseudomonas aeruginosa* (King et al., 2009). The N-terminal half of the protein contains a putative conserved domain of the acyltransferase-3 superfamily (Supplementary Fig. S2). As expected, many hits were found with predicted lipopolysaccharide biosynthesis acyltransferases from other non-mycobacterial species that contain the same conserved domain. MMAR_2380 was further predicted to be a protein with 10 transmembrane helices and a large C-terminal tail of approximately 300 amino acids in the periplasm (TMHMM 2.0) (Sonnhammer et al., 1998).

Considering the effects of mutation of *MMAR_2380* described above, we postulate three hypotheses for how mutation of *MMAR_2380* may affect the biosynthesis of LAM and the related lipoglycans, LM and PIMs. The first possibility is that MMAR_2380 is a redundant acyltransferase involved in the acylation of LAM, LM and PIMs. The phosphatidylinositol synthase required for the MPI anchor is PgsA1 (encoded by *Rv2612c*; *MMAR_2090* in *M. marinum*) (Briken et al., 2004; Jackson et al., 2000), and acyltransferase *Rv2611c* has been shown to be involved in further acylation of PIMs (position C6 of the Manp linked to the C2 of the inositol) (Kordula et al., 2003). Importantly, the *Rv2611c*-mutant *M. smegmatis* strains still produce tri- and tetra-acylated PIMs (Kordula et al., 2003), and hence other acyltransferases are yet to be identified. From the TLC pattern (Fig. 4b), it is not possible to determine the position of acylation at which MMAR_2380 may be involved (position C3 of the inositol or position C6 of the Manp linked to the C2 of the inositol). However, the differences of [1,2-14C]acetate incorporation in PIMs, LAM and LM were small, and other effects of mutation of *MMAR_2380* were observed, suggesting a different function for *MMAR_2380*.

A second function for MMAR_2380 could be as a regulatory protein in the biosynthesis of LAM and related lipoglycans. The biosynthesis pathway of LAM has recently become better characterized. Not only glycosyltransferases directly involved in the addition of mannose and arabinose have been discovered, but also proteins with a role in the regulation of this pathway. One of these proteins is lipoprotein LpqW, which directs PIM₄ into the biosynthesis route of LAM (Crellin et al., 2008; Kovacevic et al., 2006). Furthermore, the production of PIM₄ and PIM₆ has been shown to be compartmentalized in separate cell domains, a plasma membrane domain (PM₇) and a plasma membrane–cell wall domain (PM–CW), respectively, each.
containing the enzymes required specifically for their biosynthesis (Morita et al., 2005). Hence, as mutation of MMAR_2380 resulted in a small quantitative decrease of [1,2-14C]acetate incorporation in mutant LAM as well as LM and PIM6 (Fig. 4), MMAR_2380 may also have a regulatory function in the metabolic pathway of these lipoglycans, e.g. in the recruitment of specific enzymes to the different membrane/cell wall fractions. In addition, as it is a regulatory protein, mutation of MMAR_2380 could be the cause of the higher branching degrees of the mutant LAM, which could subsequently affect the LAM-capping activity in the mutant strain. Regarding the potential regulatory role of MMAR_2380, it has been reported that for certain enzymes additional processing such as acetylation is essential for proper transport and localization or for the activity of the enzyme (Banaei et al., 2009; Fukuda et al., 2002; Tschumi et al., 2009), and MMAR_2380 may function in this way.

Finally, considering the altered growth of the mutant strain (Fig. 5), it cannot be excluded that mutation of MMAR_2380 has a pleiotropic effect on the organization of the whole cell wall, and that it thus disturbs the compartmentalized biosynthesis of the higher-order PIM₆, LAM and LM, and/or the transport of lower-order PIM₂ from the PM₆ domain to the PM–CW fraction as precursor for the other lipoglycans, possibly resulting in the inability of the mutant strain to produce LAM with a mannosse cap.

Summarizing, we have identified a novel gene involved, possibly indirectly, in the biosynthesis of the mannosse cap on LAM, MMAR_2380, which is the M. marinum orthologue of Rv1565c. The mutant LAM was not only devoid of the mannosse cap, but also displayed a higher degree of branching in both the mannan core and the arabinan domain as compared with wild-type LAM. In addition, mutation of MMAR_2380 caused small quantitative differences in [1,2-14C]acetate incorporation in LAM, LM and PIMs, while all the different acylated forms of the PIMs seen in the wild-type strain were still present. Furthermore, another effect was seen: M. marinum ΔMMAR_2380 showed increased aggregation in liquid cultures as compared with the wild-type strain, a phenotypic trait which was not observed for the previous mutant M. marinum ΔMMAR_2349, which produced ‘capless’ LAM. Hence, in all likelihood, MMAR_2380 encodes an acyltransferase, although neither the length of the acyl chain transferred nor the acceptor can be predicted. Acylation activity by MMAR_2380 may be important for the biosynthesis of the mannosse cap in a way which has yet to be determined.

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REFERENCES


