Involvement of the \textit{fadD33} gene in the growth of \textit{Mycobacterium tuberculosis} in the liver of BALB/c mice

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The potential pathogenic role of \textit{Mycobacterium tuberculosis} H37Rv \textit{fadD33}, a gene encoding an acyl-CoA synthase that is underexpressed in the attenuated strain H37Ra, was investigated. In a first approach, \textit{fadD33} was cloned and expressed in strain H37Ra to restore gene expression and \textit{fadD33}-complemented bacteria were used to investigate whether \textit{fadD33} might confer any growth advantage to \textit{M. tuberculosis} H37Ra in an infection model of BALB/c mice. No differences were found in the growth rates of \textit{M. tuberculosis} H37Rv, H37Ra and \textit{fadD33}-complemented H37Ra in the lungs and spleen. In contrast, in the liver, where the attenuated strain H37Ra showed impaired growth compared to the virulent strain H37Rv, complementation of the attenuated strain H37Ra with \textit{fadD33} restored bacterial replication. In a further approach, the \textit{fadD33} gene of strain H37Rv was disrupted by allelic exchange mutagenesis and the virulence of the mutant strain was tested by mouse infection. It was found that disruption of \textit{fadD33} decreased \textit{M. tuberculosis} H37Rv growth in the liver, but not in the lungs or spleen, and complementation of the \textit{fadD33}-disrupted mutant with \textit{fadD33} restored bacterial replication in the liver, but did not affect replication in the lungs and spleen. These findings suggest that \textit{fadD33} plays a role in \textit{M. tuberculosis} virulence by supporting bacterial growth in the liver.

**Keywords:** virulence genes, experimental infection

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**INTRODUCTION**

Although tuberculosis remains one of the leading causes of death worldwide, the mechanisms by which \textit{Mycobacterium tuberculosis} establishes progressive disease are not well understood. Identification of the virulence factors of \textit{M. tuberculosis} is of fundamental importance for the development of new vaccines and drugs against this pathogen.

A widely used experimental model for the investigation of \textit{M. tuberculosis} virulence factors at the gene level is represented by the virulent strain H37Rv and the attenuated mutant H37Ra, originally derived from the classical \textit{M. tuberculosis} strain H37 (Steenken et al., 1934). A number of extensive studies have been tried so far to identify the genetic basis for the attenuation of \textit{M. tuberculosis} H37Ra. For example, by transforming \textit{M. tuberculosis} H37Ra with a cosmid library of \textit{M. tuberculosis} H37Rv, Pascopella et al. (1994) identified a locus that enhanced growth and survival of \textit{M. tuberculosis} H37Rv in the spleens of infected mice. Furthermore, comparison of \textit{M. tuberculosis} H37Rv with \textit{M. tuberculosis} H37Ra revealed differences in gene expression (Kinger & Tyagi, 1993; Rindi et al., 1999; Rivera-Marrero et al., 1998), transposition of insertion elements (Lari et al., 1999, 2001) and genomic polymorphisms and deletions (Brosch et al., 1999), but the reason(s) for the decreased virulence of \textit{M. tuberculosis} H37Ra have not been determined.

By comparing gene expression of the H37Rv and H37Ra strains by mRNA differential display, Rindi et al. (1999) reported a number of genes that appear to be down-regulated in strain H37Ra. Sequences of these genes...
were found only in species belonging to the M. tuberculosis complex, i.e. M. tuberculosis, Mycobacterium bovis, including the BCG strain, and Mycobacterium microti, thus indicating their association with the most virulent mycobacteria (Rindi et al., 2001). One of these genes, fadD33 (also called Rev1345), is one of 36 homologues of the fadD gene of Escherichia coli identified in the M. tuberculosis genome (Cole et al., 1998). In E. coli, the fadD gene product is an acyl-CoA synthase responsible for the activation of free fatty acids to acyl-CoA thioesters, which represents the first step of fatty acid degradation (Clark & Cronan, 1996; Nunn, 1987). Predictively, mycobacterial fadD33 encodes an acyl-CoA synthase as well, but the precise biochemical function of FadD33 is not defined at present.

The purpose of the study presented here was to address the question of whether fadD33 plays a role in M. tuberculosis infection. For this purpose, we cloned and expressed the fadD33 gene of M. tuberculosis H37Rv in the attenuated strain H37Ra to restore gene expression; furthermore, we constructed a mutant of strain H37Rv with a disrupted fadD33 gene. Virulence of fadD33-complemented M. tuberculosis H37Rv and fadD33-disrupted M. tuberculosis H37Rv was then tested by experimental mouse infection.

METHODS

Bacterial strains and growth conditions. M. tuberculosis H37Rv and H37Ra were from a collection maintained at our Department. The IS6110-RFLP patterns of the strains have been reported previously (Lari et al., 1999, 2001) and correspond to genotypes RV4 and RA1 of the H37 variants defined by Bifani et al. (2000). The H37Rv and H37Ra strains were grown in liquid Middlebrook 7H9 medium (Difco) defined by Bifani et al. (2000). These strains were grown on solid or in liquid Luria–Bertani (LB) medium (Sigma) and used for recombinant DNA studies and plasmid propagation. The resulting plasmid pMY9 was then tested by experimental mouse infection.

Construction of the M. tuberculosis H37Rv-fadD33::Kan mutant. A 2971 bp Xbal–ClaI fragment containing fadD33 was cloned in E. coli into pBluescript KS(+) by standard methods (Sambrook et al., 1989) and a 275 bp intragenic fragment of fadD33 was then used to transform by electroporation M. tuberculosis H37Ra and the H37Rv-fadD33::Kan mutant (see below). Transformants were selected by growth at 37°C on Middlebrook 7H10 agar plates containing 100 µg hygromycin B ml⁻¹. The integrity of the coding region was verified by sequencing the inserted DNA fragment using an automated apparatus (ALFexpress DNA sequencer; Pharmacia Biotech), using the Cy5 Thermo Sequenase dye Terminator Kit (Pharmacia). The recombinant plasmid pROLYHG-fadD33 was then used to transform by electroporation M. tuberculosis H37Rv and the H37Rv-fadD33::Kan mutant (see below). Transformants were selected by growth at 37°C on Middlebrook 7H10 agar containing 100 µg hygromycin B ml⁻¹.

Recombinant DNA techniques. Extraction of mycobacterial genomic DNA, molecular cloning and restriction endonucl ease digestions were performed by standard techniques (Sambrook et al., 1989). Cloning vectors used were pBluescript KS(+) (Stratagene), pPROLYHG, pMY9 and pPR27 (Pellicet et al., 1997). Plasmid pPROLYHG was obtained from the shuttle plasmid pHYG16R1 (Garbe et al., 1994) by the addition of the pBluescript-II-SK polynucleoty in the KpnI site. Plasmid pMY9 was constructed by cloning the Tn903 apr gene conferring kanamycin-resistance (Kan⁶) into EcoRI-digested pUC8 (Yanisch-Perron et al., 1985). The Kan⁶ cassette was amplified by PCR from pMD31 (Donnelly-Wu et al., 1993) using EcoRI-tailed primers (5'-GGCGATTCTCTTTTCTGACTGGT-GA-3' and 5'-GGCGAATTCCTCGAGAATCTGGTTG-3') and digested with EcoRI. Restriction endonucleases and other enzymes (Roche Molecular Biochemicals) were used according to the manufacturers’ instructions.

Cloning of fadD33 and complementation of M. tuberculosis H37Rv and the H37Rv-fadD33::Kan mutant. A 1809 bp fragment of M. tuberculosis H37Rv chromosomal DNA, including the full-length fadD33 gene (GenBank accession no. Q11015; sequence positions 1509281–1510843), was amplified by PCR. Primers PKup (5'-ACGTCGTGAGGATCTGT-3') and PKlow (5'-CAGCACTCTACCTGAGC-3'), annealing to bases 217–199 upstream (in order to include the promoter) and bases 9–26 downstream of the fadD33 reading frame, respectively, were used. The primers had a base mutation (C replaced by G) to create HpaI restriction sites. The PCR-generated fragment was cloned in E. coli XL-1 Blue into the E. coli–Mycobacterium shuttle vector pROLYHG, encoding hygromycin resistance, which had been digested with BamHI (Boehringer), according to standard protocols (Sambrook et al., 1989). The resulting plasmid (pROLYHG-fadD33) was propagated in E. coli XL-1 Blue after selection on LB agar containing 100 µg hygromycin B ml⁻¹ (Sigma).
10 ng DNA per 50 µl of reaction mixture. PCR amplification was performed with an OmniGene temperature cycler (Hybrid) set for one cycle of 3 min at 94 °C, 25 cycles of 1 min at 94 °C, 1 min at 60 °C and 2 min at 72 °C, with a final cycle for 4 min at 72 °C. Aliquots (10 µl) of PCR products were analysed by 2% agarose gel electrophoresis.

**Electrotransformation.** *M. tuberculosis* H37Rv and H37Ra were prepared for electroporation as described by Pelicic et al. (1997), with minor modifications. Briefly, cells were grown in 200 ml Middlebrook 7H9/ADC/Tween 80 for 3 weeks at 37 °C, washed three times in 10% (v/v) glycerol, resuspended in 1 ml of 10% glycerol and stored at −80 °C until needed. Aliquots (100 µl) of competent cells were mixed with approximately 1 µg recombinant DNA in a Bio-Rad cuvette with a 0.2 cm gap width and electrotransformed with a Bio-Rad Gene Pulser and Pulse Controller set at 25 µF, 200 Ω and 2.5 kV.

**Gene expression analysis by RT-PCR.** Total RNA was extracted from the pellet of mycobacterial cells growing in liquid Middlebrook medium essentially as described by Chomczynski & Sacchi (1987) with minor modifications (Rindi et al., 1998). RNA reverse transcription was carried out by using oligo(dT)-primed reverse transcriptase (RT), as described previously (Rindi et al., 1998). Briefly, a 1 µg sample of bacterial RNA, dissolved in diethyl pyrocarbonate (DEPC)-treated water, was heated at 65 °C for 15 min and then cooled on ice before cDNA synthesis. Oligo(dT)$_15$ (Pharmacia Biotech) was used to initiate the first strand cDNA synthesis, using 200 U M-MLV RT (Gibco) in a buffer containing 50 mM Tris (pH 8.3), 75 mM KCl, 3 mM MgCl$_2$, 10 mM DTT, 0.5 mM each dNTP, 20 µg RNAse inhibitor and 25 pmol primer for 1 h at 37 °C in a total volume of 20 µl. The reaction was stopped by incubation at 95 °C for 5 min. A 175 bp fadD33-specific target sequence of the generated cDNAs was PCR-amplified using oligonucleotide primers PK1 (5′-TGGTTGCCAGCTTGTAC-3′) and PK2 (5′-ACCAGGTAAACCAGCATTAC-3′), which anneal to bases 980–999 (upstream) and bases 1135–1154 (downstream), respectively, of the fadD33 reading frame. Briefly, PCR was performed in 0.5 ml microcentrifuge reaction tubes in a final volume of 50 µl containing 10 mM Tris/HCl (pH 8.8), 1.5 mM MgCl$_2$, 50 mM KCl, 0.1% Triton X-100, 250 ng each primer, 0.2 mM each dNTP and 1.25 U Taq polymerase (DNAzyme). PCR amplification was performed with an OmniGene temperature cycler (Hybrid) set for one cycle of 3 min at 94 °C, 25 cycles of 1 min at 94 °C, 1 min at 60 °C and 2 min at 72 °C, with a final cycle of 4 min at 72 °C. For Rv0441c expression studies, a 225 bp specific target of the *M. tuberculosis* Rv0441c gene encoding the 65 kDa antigen (Shinnick et al., 1987). The identity of the amplified cDNA obtained by using primers PK1 and PK2 was verified by sequencing. As shown in Fig. 1, fadD33-specific bands were detected for all of the mRNA transcripts; the signal for the fadD33 messenger from strains H37Rv and H37Ra (pROLHYG-fadD33) and wild-type H37Rv, while the RNA transcripts for the constitutively expressed 65 kDa antigen gene yielded bands of equivalent intensity in all of the strains.

**RESULTS**

**Cloning of fadD33**

A 1809 bp DNA fragment, including the 1563 bp fadD33 gene and its promoter, was PCR-amplified from *M. tuberculosis* H37Rv genomic DNA by using a pair of specific primers. The amplified product was cloned in *E. coli* XL-1 Blue into the *E. coli*–*Mycobacterium* shuttle expression vector pROLHYG and 60 colonies were examined for the presence of the insert by restriction analysis. *E. coli* transformants, which harboured pROLHYG containing the insert of the expected length, were sequenced. Five of these showed nucleotide sequences with 1–3 single base mutations determining an incorrect fadD33 gene product; one transformant, selected for the present study, showed a nucleotide sequence encoding the expected product of fadD33, although a silent single base mutation (C→T) was found at gene position 430.

**Complementation of *M. tuberculosis* H37Ra**

The recombinant shuttle plasmid pROLHYG-fadD33 was electroporated into *M. tuberculosis* H37Rv and the expression of fadD33 in these cells was analysed by RT-PCR. In particular, total DNase-treated RNA from *M. tuberculosis* H37Rv(pROLHYG-fadD33), *M. tuberculosis* H37Ra(pROLHYG), *M. tuberculosis* H37Ra and *M. tuberculosis* H37Rv was transcribed into cDNA by using oligo(dT)-primed reverse transcriptase. The reaction products were then probed by PCR employing primers specific for the fadD33 gene and for a constitutively expressed gene, i.e. *Rv0441c*, which encodes the 65 kDa antigen (Shinnick et al., 1987). The identity of the amplified cDNA obtained by using primers PK1 and PK2 was verified by sequencing. As shown in Fig. 1, fadD33-specific bands were detected for all of the mRNA transcripts; the signal for the fadD33 messenger from strains H37Rv and H37Ra (pROLHYG) was markedly weaker than that obtained from *M. tuberculosis* H37Ra(pROLHYG-fadD33) and wild-type H37Rv, while the RNA transcripts for the constitutively expressed 65 kDa antigen gene yielded bands of equivalent intensity in all of the strains.

**Mouse infection by fadD33-complemented *M. tuberculosis* H37Ra**

As a first attempt to examine the role of fadD33 on *in vivo* growth and survival, BALB/c mice were infected intravenously with *M. tuberculosis* H37Rv, *M. tuberculosis* H37Ra and fadD33-complemented H37Ra. The mice were killed at 1, 21 and 42 days post-infection, and the number of c.f.u.s per entire organ was reported as the log$_{10}$ value. The significance of the difference in the mean number of c.f.u.s per organ was calculated by the ANOVA test according to the instat software package (GraphPad); all P values less than 0.05 were considered to indicate statistical significance.
determined (Fig. 2). As to virulent *M. tuberculosis* H37Rv, the number of c.f.u.s increased by approximately 1 \( \log_{10} \) in the spleen, 1–5 \( \log_{10} \) in the lung and 0–5 \( \log_{10} \) in the liver during the first 3 weeks of infection. Thereafter, the bacillary load stabilized at approximately \( 10^{5–6} \) c.f.u.s in the three organs. In the lungs and spleen, the \( \log_{10} \) c.f.u. counts of strain H37Ra, as well as those of the fadD33-complemented H37Ra, were comparable to H37Rv at any tested time, which might indicate that the H37Rv strain employed in our experiments is not as virulent as expected. In the liver, however, the \( \log_{10} \) c.f.u. counts for strain H37Ra were significantly lower than those for strain H37Rv at 21 and 42 days post-infection (\( P < 0.001 \)), and those of the fadD33-complemented H37Ra strain were significantly higher than those of strain H37Ra (\( P < 0.01 \)), and not statistically different from strain H37Rv. No animal deaths were recorded during the whole experimental period. These results demonstrate that complementation of strain H37Ra with fadD33 conferred a growth advantage to the attenuated strain H37Ra in the liver.

**Construction of the *M. tuberculosis* H37Rv-fadD33::Kan mutant**

A fragment of the fadD33 gene of *M. tuberculosis* H37Rv was replaced with a Kan\(^R\) gene by allelic exchange using ts–sacB counterselection technology (Pelicic et al., 1997). The recombinant plasmid pPR27-fadD33::Kan was introduced into *M. tuberculosis* H37Rv by electroporation, and transformants were selected at 32 °C on 7H10/kanamycin. Several transformants were grown in liquid culture and then plated at 39 °C onto 7H10/kanamycin containing 2% sucrose. Various colonies were grown in 7H9 medium and genomic DNA was extracted and analysed by PCR using a pair of primers flanking the deletion site (Fig. 3). *M. tuberculosis* H37Rv DNA, which was included as a control, showed one amplification band of 753 bp in size. As expected for allelic exchange mutants, all of the clones presented a single fragment approximately 700 bp longer than that in the wild-type strain. This 700 bp increase corresponded to the size of the Kan\(^R\) gene.
Fig. 3. fadD33 region in M. tuberculosis allelic exchange mutants (H37Rv-fadD33::Kan). (Left panel) PCR products obtained from DNA of four clones of H37Rv-fadD33::Kan mutants (lanes 1–4) and wild-type H37Rv. Lanes also include a molecular mass marker (100 bp ladder) and PCR carried out in the absence of cDNA (H2O). (Right panel) The fadD33 region of the M. tuberculosis H37Rv-fadD33::Kan mutant and M. tuberculosis H37Rv is outlined. Dark-grey, light-grey and solid bars represent the bacterial chromosome, the fadD33 gene and the Kan\(^\mu\) box, respectively. The arrows indicate the PCR primer positions; the expected amplicon sizes are also shown.

(1 kbp) that was inserted in place of a 275 bp fragment of the fadD33 gene. The wild-type and mutant strains of M. tuberculosis H37Rv showed similar colony morphology, growth characteristics and drug susceptibility profiles (data not shown).

As a control, the M. tuberculosis H37Rv-fadD33::Kan mutant was complemented with fadD33 by electroporation with the recombinant plasmid pROLHYG-fadD33 (as described above). The expression of fadD33 in these cells was analysed by an oligo(dT)-primed RT-PCR assay (Rindi et al., 1998). For this purpose, total DNase-treated RNA from M. tuberculosis H37Rv-fadD33::Kan, M. tuberculosis H37Rv-fadD33::Kan(pROLHYG-fadD33) and M. tuberculosis H37Rv was transcribed into cDNA by using oligo(dT)-primed reverse transcriptase. The reaction products were then probed by PCR employing primers specific for the fadD33 and Rv0441c genes. Sequence-verified fadD33-specific bands were detected for the mRNA transcripts of M. tuberculosis H37Rv-fadD33::Kan(pROLHYG-fadD33) and M. tuberculosis H37Rv, but not from M. tuberculosis H37Rv-fadD33::Kan; the RNA transcripts for Rv0441c yielded the expected bands in all of the strains (Fig. 4).

**Mouse infection by the M. tuberculosis H37Rv-fadD33::Kan mutant**

BALB/c mice were infected intravenously with M. tuberculosis H37Rv, M. tuberculosis H37Rv-fadD33::Kan mutant and M. tuberculosis H37Rv-fadD33::Kan(pROLHYG-fadD33), and the number of c.f.u.s in the lungs, spleen and liver at various time points post-infection was determined. In the representative experiment reported in Fig. 5, although the counts of the inocula yielded the expected numbers of c.f.u.s (approx. 10\(^8\)), the mean number of c.f.u.s of the M. tuberculosis H37Rv-fadD33::Kan mutant found in the spleen at 1 day post-injection was almost 0.4 log\(_{10}\) lower than that of the other strains injected, while it did not differ significantly from the other strains in the lungs and liver. At 14, 42 and 123 days post-infection, the c.f.u. counts of the strains tested were comparable in the lungs and spleen, while the number of c.f.u.s of the M. tuberculosis H37Rv-fadD33::Kan mutant was approximately 0.5 to 0.7 log\(_{10}\) lower than those of the parent strain H37Rv in the liver (P < 0.02 at least, by ANOVA). Notably, in the liver, the c.f.u. numbers of the M. tuberculosis H37Rv-fadD33::Kan mutant complemented with fadD33 were significantly higher (0.6–1 log\(_{10}\)) than those of the fadD33-disrupted mutant at 14, 42 and 123 days post-infection (P < 0.01, at least) and similar to those of strain H37Rv. No animal deaths were recorded during the whole experimental period. In another preliminary experiment, the survey of the c.f.u. counts in the organs of infected mice was done at 1, 14, 21 and 42 days post-infection, with results comparable to those reported above. Taken together, our findings indicate that disruption of fadD33 influences the growth of M. tuberculosis H37Rv in the liver, but not in the lungs and spleen.
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We then used a further experimental approach to test the role of fadD33 in M. tuberculosis virulence. We prepared a fadD33-disrupted M. tuberculosis H37Rv mutant and the relative fadD33-complemented control, and tested them by mouse infection. This approach confirmed the involvement of fadD33 in the growth of M. tuberculosis H37Rv in the liver of BALB/c mice. Indeed, disruption of fadD33 reduced the growth of M. tuberculosis H37Rv in the liver, but not in the lungs and spleen; moreover, complementation of the fadD33-disrupted mutant with fadD33 completely restored bacterial replication in the liver.

An unexpected finding in infection experiments (Fig. 2) was that strains H37Rv and H37Ra replicated to a comparable extent in the lungs and spleen of infected BALB/c mice, although they differed significantly in the liver. Indeed, M. tuberculosis H37Rv would be expected to grow rapidly in immunocompetent mice (more than a 2 log increase in the c.f.u. count) in the lungs and spleen in the first 2–3 weeks post-infection. The low rate of replication of M. tuberculosis H37Rv in our experiments might indicate that the strain we used is not as virulent as others, as also suggested by the results from in vitro experiments aimed at investigating the growth of strains H37Rv and H37Ra in human phagocytes. In fact, while M. tuberculosis H37Rv was expected to grow significantly faster than H37Ra in human macrophages (McDonough et al., 1993; North & Izzo, 1993; Zhang et al., 1998), in our hands, strains H37Rv and H37Ra showed comparable growth in human peripheral blood monocytes; in activated monocyte-derived THP-1 cells, H37Rv was slightly more resistant than H37Ra to intracellular killing, as judged by the higher number of c.f.u.s detected in cell lysates 2 days post-infection, but grew intracellularly at the same rate as H37Ra thereafter (L. Rindi, unpublished observations). The relatively low rate of replication of our M. tuberculosis H37Rv strain in organs of infected mice and in cultured macrophages might be due to the fact that the strain had not been recently passaged in vivo nor in macrophages in vitro; alternatively, it is also possible that the Rv4 genotype of H37Rv, the variant that we employed in our study (Bifani et al., 2000), is actually poorly virulent for BALB/c mice, a strain considered highly resistant to M. tuberculosis (Medina & North, 1998), as well as being only moderately able to grow within macrophages.

Taken together, the experiments employing the fadD33-complemented H37Ra and fadD33-disrupted H37Rv mutants point to the conclusion that fadD33 plays a role in M. tuberculosis virulence in mice by supporting bacterial growth in the liver. The involvement of mycobacterial fadD genes in M. tuberculosis tropism is not unprecedented. In fact, it has been reported that the products of genes fadD26 and fadD28 participate in the biosynthesis of phthiocerol dimycocerosate, a complex cell-wall-associated lipid found only in pathogenic mycobacteria (Brennan & Nikaido, 1995; Kolattukudy et al., 1997), which determines tissue-specific replication in the lungs (Camacho et al., 1999; Cox et al., 1999). The

Fig. 5. Experimental infection of BALB/c mice with M. tuberculosis H37Rv (■), the M. tuberculosis H37Rv-fadD33::Kan mutant (▲) and the M. tuberculosis H37Rv-fadD33::Kan mutant complemented with fadD33 (●). The data are expressed as the geometric means ± S.D. of the log10 c.f.u. counts obtained from four to eight mice per group per time point.

**DISCUSSION**

In the present study, we have investigated the potential pathogenic role of fadD33, a gene of M. tuberculosis that is underexpressed in H37Ra, the attenuated strain derived from H37.

As a first step, we tested the possibility that restoration of fadD33 expression in strain H37Ra might confer growth advantages in a mouse infection model. These experiments showed that complementation of strain H37Ra with fadD33 restored its replication to the levels of H37Rv in the liver, but not in the lungs and spleen, where the c.f.u. counts were the same for strains H37Ra and H37Rv.
reasons why fadD33 expression might influence M. tuberculosis growth in the mouse liver are unknown at present. However, one has to consider that there are 36 fadD genes encoding proteins with acyl-CoA synthase activity in M. tuberculosis H37Rv and the same number of fadE genes encoding putative acyl-CoA dehydrogenases (Cole et al., 1998). It is therefore likely that such a large number of fadD/fadE genes in the M. tuberculosis genome reflects the necessity of M. tuberculosis to load a large variety of lipids onto CoA, some of which have to be transported to specific enzymes for lipid degradation and others of which have to be used for biosynthesis. As fadD33 is located just upstream of fadE14 and downstream of an acyl carrier protein gene (Rv1344) in the H37Rv genome (Cole et al., 1998), it may be hypothesized that, after intracellular transport, the proteins FadD33 and FadE14 participate in the activation and subsequent oxidation of liver-specific fatty acids needed as a source of carbon and energy by M. tuberculosis; the products of these enzymes would be then oxidized further in the two pathways required for fatty acid metabolism in bacteria, i.e. β-oxidation and the glyoxylate shunt (Clark & Cronan, 1996). The importance of fatty acid metabolism in M. tuberculosis experimental infection in mice has been underscored by McKinney et al. (2000) and Sharma et al. (2000), who showed that isocitrate lyase, one of the glyoxylate shunt enzymes, plays a pivotal role for survival of M. tuberculosis in the lungs of mice during the persistent phase of infection, entailing a metabolic shift in the carbon source to two-carbon compounds generated by β-oxidation of fatty acids.

Alternatively to a role in the degradation of fatty acids, the enzyme FadD33 might participate, similarly to FadD26 and FadD28 in the lungs (Cox et al., 1999), in the biosynthesis of lipids or other metabolites specifically required for growth of M. tuberculosis in the liver of infected mice. Recently, it has been shown that some fad and fadD genes are induced in M. tuberculosis following detergent-induced surface stress (Manganelli et al., 2001), which might suggest a possible role of their products in the biosynthesis of cell-wall lipids. In this context, we also have to consider that FadD33 is similar to the putative polyketide biosynthesis protein PKSJ of Bacillus subtilis (Albertini et al., 1995), as it shows a 27.1% identity in an overlap of 468 aa (http://genolist.pasteur.fr/TubercuList/). As microbial polyketide metabolites have shown potent biological activities in different models, acting as virulence factors, antibiotics, immunosuppressants and toxins (George et al., 1999; Kolattukudy et al., 1997; Motamedi et al., 1997), it is tempting to consider that mycobacterial FadD33 might be involved in the synthesis of polyketides that play a role in M. tuberculosis infection in the liver. The involvement of certain polyketide metabolites in M. tuberculosis infection has been reported by Graham & Clark-Curtiss (1999), who showed that pks2, one of the 18 polyketide synthase genes of M. tuberculosis H37Rv, is expressed in infected human macrophages but not in bacteria growing in culture broth, and by De Voss et al. (2000), who demonstrated that the mycobactin siderophores produced by polyketide synthase enzymes are essential for M. tuberculosis growth in macrophages. Analyses of the lipid profiles of strains H37Rv and H37Ra, as well as the definition of the cellular localization of the fadD33 gene product, are likely to provide insights into understanding the precise biochemical function of FadD33 and its role in M. tuberculosis infection.

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