Negative transcriptional regulation of the mce3 operon in Mycobacterium tuberculosis

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mce3 is one of the four mce operons in Mycobacterium tuberculosis that encode exported proteins with a probable role in the virulence of this bacterium. Upstream of mce3 there is a putative regulatory gene (Rv1963) that harbours a double tetR-family signature. To study the role of this putative regulatory gene in the transcriptional regulation of the mce3 operon, Mycobacterium smegmatis mc²155 and M. tuberculosis H37Rv strains that harboured gene fusions between the mce3 promoter region and the Escherichia coli lacZ gene, either containing or not containing the Rv1963 gene, were used. The presence of the Rv1963 gene in the strains greatly reduced β-galactosidase activity, suggesting that the Rv1963-encoded protein is a transcriptional repressor of the mce3 operon. Expression of mce3 by recombinant M. tuberculosis was increased when it was grown in a macrophage-like cell line (J774), compared to the level of expression seen when the recombinant bacterium was grown under in vitro conditions. However, no lifting of repression was induced. The mce3 promoter was defined by deletion and cloning of the Rv1963–Rv1964 intergenic region in a 200 bp DNA fragment harbouring the region upstream of the Rv1964 start codon. Gel-shift experiments determined that the Rv1963-binding site was located in this region. These results indicate that the mce3 operon is transcriptionally regulated and that under certain, unknown, conditions repression of gene expression could be lifted.

Keywords: repressor, tetR, reporter

INTRODUCTION

Tuberculosis (TB), a chronic illness caused by Mycobacterium tuberculosis, is still a major disease worldwide. According to the World Health Organization, TB is a considerable public health problem in Latin America, Asia and Africa. During the last few years, an increase in the incidence of TB has been observed and this has been attributed to weak control programmes, the AIDS pandemic, which predisposes individuals to developing TB, and the appearance of M. tuberculosis strains that are resistant to first-line antibiotics (Murray et al., 1990).

Unfortunately, many aspects of the infection and disease process of tuberculosis at the cellular and molecular level still remain unknown. According to Smith (1984), to infect and cause disease pathogenic mycobacteria must be able to (i) colonize the host’s lung tissues, (ii) enter the host’s cells, (iii) multiply in the environment of the host’s tissues, (iv) resist or interfere with the host’s defence mechanisms and (v) cause damage to the host’s tissues. Despite the formidable advances in molecular biology in recent years, the identification of the virulence factors of pathogenic mycobacteria (i.e. M. tuberculosis, Mycobacterium bovis and Mycobacterium leprae) has been delayed, when compared to the identification of the virulence factors of other infectious bacteria. Factors contributing to this situation include the lack of a phenotype clearly associated with virulence in pathogenic mycobacteria and the scarcity of genetic tools for transforming and mutating M. tuberculosis. Steps to solving the latter problem have been taken, as improved...
genetic tools have allowed the identification of virulence-related genes in M. tuberculosis (Camacho et al., 1999; Cox et al., 1999). The most-employed virulence-associated attribute of M. tuberculosis is its persistence in the infected organism or in cultured cells (Bange et al., 1999).

We have previously identified a 12.7 kb region in the genome of M. tuberculosis that is absent from the genome of M. bovis (Fisanotti et al., 1997; Zumarraga et al., 1999). This 12.7 kb fragment was present in all of the M. tuberculosis strains tested and was absent from all of the M. bovis, Mycobacterium microti and Mycobacterium africanum strains tested. The region is located near the 3′ end of the RD2 element described by Mahairas et al. (1996), a 14 kb genomic locus present in M. bovis but absent from some strains of M. bovis BCG, suggesting that this region suffers from genetic instability. Sequence analysis of ORFs within the 12.7 kb fragment of the M. tuberculosis genome demonstrated that it mostly encodes exported proteins. One of the ORFs is highly homologous to the invasin-like protein described by Riley and colleagues (Arruda et al., 1993; Chitale et al., 2001). This region was also described by Gordon et al. (1999) as RD7. The presence of genes encoding an invasin-like protein and many membrane or secreted proteins within the 12.7 kb region suggests that this region may play an essential role in the host–pathogen interaction of M. tuberculosis. The ORFs within the region are organized as a putative operon, which is similar in its sequence and organization to three other M. tuberculosis regions (operons mce1, mce2 and mce4) described by Cole et al. (1998). The lack of similarity of the genes encoded by this putative operon to genes from other bacterial species suggests that they may play a specific role in the physiology or virulence of M. tuberculosis. Flesselles et al. (1999) reported that a BCG strain mutated in mce2 exhibits a reduced ability to invade the non-phagocytic epithelial cell line HeLa, which supports the idea of a role for mce operons in virulence. Harboe et al. (1999) demonstrated production of the mce1-encoded proteins using cell extracts from M. tuberculosis and M. bovis BCG. Mce1 proteins are recognized by the antibodies of TB patients (Ahmad et al., 1999), indicating in vivo expression of the mce1 operon. At the genetic level, the four mce operons appear to have evolved from a common ancestor. The four operons may play different roles in the infection process, may be expressed at different times along growth phases or the infection process, or they may simply serve to protect essential virulence genes against mutations. In the present study, the regulation of the expression of the mce3 operon was investigated, to gain an insight into the role of this operon in M. tuberculosis. Our results show the presence of a repressor that controls mce3 transcription.

METHODS

Bacterial strains and culture media. All cloning steps were performed in Escherichia coli DH5α. E. coli BL21(DE3) was used for recombinant protein production. Regulation studies were performed in Mycobacterium smegmatis mc²155 or in M. tuberculosis H37Rv. E. coli was grown in Luria–Bertani (LB) broth or on LB agar. Both mycobacterial species were grown in either Middlebrook 7H9 medium supplemented with 0.05% Tween 80 or Middlebrook 7H11 medium supplemented with oleic acid/albumin/dextrose/catalase (OADC). When necessary, 20 µg kanamycin ml⁻¹ was added to the media. Electrocortent Mycobacterium cells were prepared according to Parish & Stoker (1998). Mycobacterial strains were transformed by electroporation using a Bio-Rad Gene Pulser, as described by Parish & Stoker (1998). Following electroporation, M. smegmatis and M. tuberculosis were plated onto Middlebrook 7H11 medium supplemented with OADC and kanamycin.

DNA manipulations. Standard methods were used for restriction-endonuclease digestion of plasmids, for DNA ligation and for other manipulations. Isolation of plasmid DNA was performed using the Wizard Miniprep SV Kit, according to the manufacturer’s instructions (Promega). DNA from M. tuberculosis was prepared according to van Soolingen et al. (1991).

Construction of lacZ reporter fusions. Details for the plasmids, vectors and primers used in this study can be found in Table 1. To create fusions with the E. coli lacZ gene, the regions containing the Rev1963–Rev1964 intergenic fragment including or not including the Rev1963 gene were amplified by PCR and cloned into the promoter-probe vector pJEM15 (Timm et al., 1994). The resulting plasmids were called p1963-P3 (plus Rev1963) and p3 (minus Rev1963). All amplified fragments were cloned into either pGEM-T (Promega) or pCRII-TOPO (Invitrogen), before being transfected to pJEM15. Fragments (100 and 206 bp in length) from upstream of the Rev1964 gene start codon were also fused to a promoterless lacZ gene, resulting in plasmids p2100 and p2100-P3, respectively (Table 1).

The template for PCR was a bacterial artificial chromosome (BAC) containing the mce3 operon, which was kindly provided by Dr S. T. Cole (Institut Pasteur, France). M. tuberculosis genomic DNA was used as a template for amplification of the mce2 operon.

Different deletions of the Rev1963–Rev1964 intergenic region were obtained as follows. The pCRIII-TOPO intermediate constructs p1963-P3 and p3 were separately digested with Ndel and SalI; the digest products were then ligated. The inserts from the resulting plasmids were transferred to BamHI-linearized pJEM15 (see Table 1), resulting in p1963-P3Ana and pP3Ana (for Ndel deletions), and p1963-P3Sal and pP3Sal (for SalI deletions). An Xmal–AegI deletion was obtained by digestion of p1963-P3 with Xmal and AegI. The digest products were ligated and introduced into linearized pJEM15, resulting in pF3AeXma/AegI (Table 1).

Cloning and expression of Rev1963. Rev1963 was amplified from M. tuberculosis BAC DNA and cloned into pRSET-A (Table 1). The resulting plasmid, pRSET1963, was introduced into E. coli BL21(DE3). E. coli BL21(pRSET1963) was then grown in LB broth at 28 °C. Expression of the Rev1963 gene was induced by the addition of 0.1 mM IPTG to the growth medium at the mid-exponential phase of growth. Soluble cell extracts from the culture were prepared by Fast Prep FP120 (Qbiogene) bead-beater disruption (40 s at 60 ms⁻¹, using Lysing Matrix B). Proteins separated by SDS-PAGE (Cataldi et al., 1994) were assayed by Western blotting using anti-histidine as the primary antibody (1:3000 dilution; Amersham Pharmacia) and alkaline-phosphatase-conjugated anti-mouse-IgG as the secondary antibody (1:2000 dilution; Sigma).
Table 1. Plasmids, vectors and primers used in this study

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Construction and characteristics</th>
<th>Origin</th>
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<tr>
<td>pJEM15</td>
<td>E. coli–mycobacterial promoter-probe shuttle vector for lacZ fusions; Km'</td>
<td>Timm et al. (1994)</td>
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<td>p1963-P3</td>
<td>PCR product from amplification with primers 1963P3up and P3rev was cloned into pCRII-TOPO and then moved to pJEM15; p1963-P3 carries the mce3 promoter region and Rv1963</td>
<td>This study</td>
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<td>p3</td>
<td>PCR product from amplification with primers P3up and P3rev was cloned into pCRII-TOPO and then moved to pJEM15; p3 carries only the mce3 promoter region</td>
<td>This study</td>
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<td>p1963-P3Sal</td>
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<td>p3Sal</td>
<td>pCRII-TOPO intermediate of p3 was digested with SalI, ligated and the BamHI insert was moved to pJEM15; p3Sal carries an SalI–SalI deletion in the intergenic region</td>
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<tr>
<td>p1963-P3ANhe</td>
<td>pCRII-TOPO intermediate of p1963-P3 was digested with Nhel, ligated and the BamHI insert was moved to pJEM15; p1963-P3ANhe carries an Nhel–Nhel deletion in the intergenic region and Rv1963</td>
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<td>p3 was digested with Nhel, ligated and the BamHI insert was moved to pJEM15; p3ANhe carries an Nhel–Nhel deletion in the intergenic region</td>
<td>This study</td>
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<td>p3AXma/Age</td>
<td>p1963-P3 was digested with XmaI and AgeI, ligated and the BamHI insert was moved to pJEM15; p3AXma/Age carries an XmaI–AgeI deletion, comprising the intergenic region and Rv1963</td>
<td>This study</td>
</tr>
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<td>p3-200</td>
<td>PCR product from amplification with primers P3200up and P3revk was cloned into pGEM-T and then moved to pJEM15; p3-200 carries a 206 bp fragment from upstream of the Rv1964 start codon (ATG)</td>
<td>This study</td>
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<td>p3-100</td>
<td>PCR product from amplification with primers P3100up and P3revk was cloned into pGEM-T and then moved to pJEM15; p3-100 carries a 100 bp fragment from upstream of the Rv1964 start codon (ATG)</td>
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<td>pRSET1963</td>
<td>PCR product from amplification with upregclo and lowregclo inserted into pGEM-T and then moved to the PRSET-A expression vector</td>
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<td>Invitrogen</td>
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<tr>
<td>pGEM-T</td>
<td>T/A cloning vector for PCR products; Ap'</td>
<td>Promega</td>
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<td>pCRII-TOPO</td>
<td>T/A cloning vector for PCR products; Ap', Km'</td>
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<tr>
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<td>Low861</td>
<td>GGATTTGATGCTGGGGCGTT</td>
<td>NA</td>
<td>56</td>
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NA, Not applicable, as used for primer-extension experiments.

PCR amplification. PCR amplifications were performed using Taq DNA polymerase (Promega) under standard conditions in a total volume of 50 µl. dNTPs were used at a concentration of 0·2 mM each; 20 pmol of each primer was used. The protocol used for amplification was as follows; denaturation at 94 °C for 3 min, followed by 35 cycles of denaturation at
performed at 42°C by using a Fastprep FP120 bead-beater for 20 s at a speed of 3000–4000 cycles per minute (DEPC)-treated water and transferred to a 2 ml screw-cap microcentrifuge tube containing 0.1 ml diameter zirconium beads and FastRNA reagents (Qiogene). Cells were disrupted by using a Fastprep FP120 bead-beater for 20 s at a speed of 609 m s⁻¹. Total RNA was then extracted from the cells following the manufacturer’s instructions. After agarose-gel electrophoresis of the total RNA and staining of the gels with ethidium bromide, the different bands of rRNA were clearly visible, indicating that the RNA preparations were of a high integrity.

**Primer extension.** This was performed using the primer Low861 (Table 1). Ten picomoles of the non-phosphorylated primer were labelled by using T4 polynucleotide kinase (Promega) in the presence of [γ⁻³²P]ATP. The specific activity of the primer was 8000 c.p.m. pmol⁻¹. M. tuberculosis H37Rv RNA (6 μg) and the labelled primer (0.1 pmol, 33 000 c.p.m. pmol⁻¹) were mixed in 7 μl of 50 mM Tris/HCl (pH 8.3) containing 0.1 M KCl. The reaction was then incubated at 94°C for 1 min, at 56°C for 10 min and then on ice for 15 min. The mixture was adjusted to a final volume of 12 μl by the addition of 1 μl of a mixture containing the dNTPs (25 mM each), 0.5 μl of RNAsin (Promega), 2.2 μl of 5X reverse transcriptase buffer [0.25 M Tris/HCl (pH 8.3), 0.2 M KCl, 36 mM magnesium acetate, 0.01 M DTT], 0.8 μl of DEPC-treated water and 0.5 μl avian myeloblastosis virus reverse transcriptase (Promega). Reverse transcription was performed at 42°C for 45 min; the reaction was stopped by the addition of 5 μl of stop buffer to the reaction mixture.

The reverse-transcription products were separated by PAGE (6% acrylamide gel containing 8 M urea), and were run alongside the sequencing products obtained with the Low861 primer. The gels were fixed by immersion in a mixture containing 5% acetic acid and 10% (v/v) methanol and 5% (v/v) acetic acid. They were then exposed to X-ray film (Kodak X-Omat RS) for 24 h at −70°C.

**Computer analyses.** Amino-acid-sequence alignments were generated by searching public databases using BLASTP (http://www.ncbi.nlm.nih.gov/BLAST). M. smegmatis BLAST searches (http://www.tigr.org/tdb/mdb/mdblinprogress.html) were used to identify an Rv1963 orthologue in this bacterium. Domain analysis was performed by using Pfam (http://www.cgr.ki.se/Pfam). Prokaryotic promoter sequences were searched by using the prokaryotic option of the Neural Network Promoter Prediction algorithm of the Berkeley Drosophila Genome Project (http://www.fruitfly.org/seq_tools/promoter.html).

**Measurements of β-galactosidase activity.** For in vitro determinations of β-galactosidase activity, 1 ml of a recombinant M. smegmatis culture or 1 ml of a recombinant M. tuberculosis culture was pelleted, resuspended in 1 ml buffer Z [0.1 M sodium phosphate (pH 7.0), 10 mM KCl, 1 mM MgSO₄ and 50 mM mercaptoethanol], disrupted using a Fast Prep FP120 bead-beater (40 s at 60 m s⁻¹, using Lysing Matrix B) and centrifuged at 13000 r.p.m. to obtain the soluble cell extract. β-Galactosidase measurements were performed on the soluble cell extract, as described by Miller (1972); results are expressed in Miller units [A₄₂₀×1000/reaction time (min) × A₄₂₀].

For determination of the β-galactosidase activity in an infected macrophage cell line, the murine macrophage-like cell line J774 was cultivated in RPMI medium 1640 with 25 mM HEPES buffer and 1-glutamine supplemented with 10% fetal calf serum in 5% CO₂ at 37°C in T25 flat-bottomed cell-culture flasks. The cell line was incubated for 18–24 h until a density of 5 × 10⁶ cells per flask was reached. Recombinant M. tuberculosis H37Rv strains were grown in Middlebrook 7H10 medium containing 20 μg kanamycin ml⁻¹. The cultures were then harvested, resuspended in RPMI medium, vortexed, sonicated for 1 min in an ultrasonic cleaner and allowed to settle. The upper part of each of the bacterial suspensions (supposedly free of clumps of bacteria) was used to infect the J774 cell line. The OD₆₀₀ value for the upper portion of the suspension was taken, and it was assumed that an OD₆₀₀ value of 0.1 was equal to 10⁶ c.f.u. ml⁻¹ (data not shown). This suspension was then used to replace the medium that the J774 cells were in, and infection of the J774 cells was performed at an m.o.i. of 100. Infected cells were incubated for 3 h, then washed five times with fresh RPMI medium. At 0, 1, 4 and 6 days post-infection, the J774 cells were scraped and lysed with 1 ml of 1% Triton X-100 for 15 min. The resulting suspension was centrifuged to obtain the mycobacterial pellet, and β-galactosidase activity was determined for the mycobacterial cells, as described above. Activity was related to the number of bacteria as determined by plating onto Middlebrook 7H11 agar supplemented with kanamycin and OADC. As a control, the β-galactosidase activity of the bacterial strains that were used for macrophage infection but grown in vitro was determined.

**Gel-shift assay.** A 100 bp and a 206 bp fragment from upstream of the start codon of Rv1964 (from mce3; see ‘Construction of lacZ reporter fusions’) and a 139 bp fragment from upstream of Rv0586 of the mce2 promoter region (obtained using primers P2up and P2low; Table 1) were used as probes in this assay. Fragments were labelled with [γ⁻³²P]ATP by using the polynucleotide kinase enzyme. Non-incorporated nucleotides were eliminated from the mixture containing the labelled probes by using Wizard PCR Prep Columns (Promega). Labelled probes were incubated with the soluble cell extract from recombinant E. coli BL21 over-expressing Rv1963 or from E. coli BL21(pRSET) (negative control) in binding buffer [4% glycerol (v/v), 1 mM MgCl₂, 0.5 mM EDTA, 0.5 mM DTT, 50 mM NaCl, 10 mM Tris/HCl (pH 7.5), 0.05 mg salmon sperm DNA ml⁻¹] for 20 min at room temperature. The samples were separated by PAGE [4% acrylamide gel containing 1X TBE (0.05 M Tris base, 0.05 M boric acid, 1 mM EDTA-Na₂·2H₂O), 0.1% bisacrylamide and 2.5% glycerol] for 3 h at 100 V, after a 30 min pre-run in a 0.5X TBE buffer tank. The gels were then dried and exposed to X-ray film.

**RESULTS**

Characterization of a putative regulatory gene for the mce3 operon

The Rv1963 gene is located upstream of the mce3 operon (Fig. 1) and encodes a hypothetical protein of 44.3 kDa (407aa). This ORF is homologous to the TetR family of regulators from several bacteria. The best
Regulation of the mce3 operon in M. tuberculosis

The Rv1963 protein downregulates mce3 transcription

To study the role of the putative regulatory gene Rv1963 in mce3 transcription, mycobacteria harbouring gene fusions between the mce3 promoter region and the Escherichia coli lacZ gene, either containing or not containing the Rv1963 gene, were used. M. smegmatis mc^3^155 was transformed with these constructs and the β-galactosidase activity of the M. smegmatis transformants was measured throughout the growth of the cultures. β-Galactosidase activity was much higher in M. smegmatis mc^3^155(p1963) (minus Rv1963) than in M. smegmatis mc^3^155(p1963-P3) (plus Rv1963) (Fig. 2a). Significantly, a similar difference in activity was observed in M. tuberculosis H37Rv transformed with the same constructs (Fig. 2b). These results indicate that the Rv1963-encoded protein negatively regulates the transcription of the mce3 operon. Consequently, we propose to redesign Rv1963 as Mce3R. β-Galactosidase activity also greatly increased during the stationary phase of growth for M. smegmatis mc^3^155(p3) (Fig. 2a). A similar increase in β-galactosidase activity was also observed for M. smegmatis mc^3^155(p1963-P3), although this activity was still at a lower level than seen for M. smegmatis mc^3^155(p3). The difference between the β-galactosidase activities of M. smegmatis mc^3^155(p3) and M. smegmatis mc^3^155(p1963-P3) remained approximately the same (17-fold) along the growth curves of the two strains. In the M. tuberculosis transformants, an increase in mce3 expression was also observed during the stationary phase, but was followed by a decline during the later periods of this growth phase (Fig. 2b).

Mapping of the mce3 promoter

To map the mce3 promoter, different segments of the mce3R–Rv1964 intergenic region were assayed for their promoter activity (Fig. 3). A strain harbouring pP3ΔXma/ΔAge expressed high β-galactosidase activity (1100 Miller units). This result could be explained by the elimination of the mce3R repressor and suggests that the mce3 promoter is located between the AgeI site and the Rv1964 start codon. Deletion of a Sall–Sall fragment (ΔSal) from the intergenic region abolished the expression of mce3, even in a strain lacking the repressor gene, suggesting that the promoter is located between the Sall sites or that it spans one of the Sall sites. Finally, strains harbouring plasmids with a NheI deletion (ΔNheI) showed no alteration in their β-galactosidase activities, demonstrating that the NheI–NheI segment

Blast hits in GenBank were with putative regulatory proteins from Streptomyces coelicolor (accession no. AL163641; 42% similarity, E-value 6e-24) and M. tuberculosis (accession no. AE007094; 43% similarity, E-value 1e-08). These data suggest that the Rv1963-encoded protein could regulate mce3 transcription. Sequence analysis of the Rv1963 gene by Pfam showed two tetR-family signatures, one located at amino acids 19–65 and one, with a lower matching, located at amino acids 223–269. A helix–turn–helix motif was identified at amino acids 36–57.
does not contain the mce3 promoter nor the repressor-binding region. To further localize the mce3 promoter of *M. tuberculosis*, 206 and 100 bp fragments from upstream of the start codon (ATG) of *Rv1964* were evaluated for their promoter activity. To do this, these fragments were cloned into pJEM15 (generating pP3-200 and pP3-100, respectively) and tested in *M. smegmatis* mc^2^155 (pP3-200). The β-galactosidase activity was 80-fold higher in *M. smegmatis* mc^2^155 (pP3-200) than in *M. smegmatis* mc^2^155 (pP3-100), indicating that a functional mce3 promoter is located between 100 and 206 bp upstream of the *Rv1964* start codon.

Primer-extension experiments (Fig. 4a) indicated that the transcription start point (TSP) of the mce3 promoter was a C base 143 nt upstream of the *Rv1964* start codon. A neural-network on-line program that searches for putative prokaryotic promoters located a probable promoter extending from −170 to −230 upstream of the ATG start codon corresponding to the first mce3 ORF (*Rv1964*). DNA STRIDER software identified putative −35 and −10 sequences in the proposed mce3 promoter region (Fig. 4b), a probable −35 sequence, TATACT (extending from −204 to −198), with 4/6 matches with the −35 consensus sequences of the *hsp60* promoter of BGC (TTGCAC) (25; 27), and a probable −10 sequence, TATATG (extending from −182 to −178), revealing 6/6 matches with the typical *E. coli* −10 consensus sequence. The localization of these putative promoter hexamers coincides with the putative promoter found by the neural network. However, the −10 element is located at −32 bp of the TSP. One less consensual sequence, TATATTA, is localized 12 bp upstream of the proposed TSP. A putative RBS was found by visual analysis of the downstream region of the proposed TSP (Fig. 4b).

**Expression of the mce3 operon in the cultured J774 cell line**

To determine whether expression of the mce3 operon was intracellularly induced, *M. tuberculosis* H37Rv transformed with p1963-P3, pP3 or pJEM15 was used to infect the J774 macrophage-like cell line. The bacterial cells used for infection came from cultures at an OD_650_ value of 1.2 for *M. tuberculosis* H37Rv (pJEM15), 1.4 for *M. tuberculosis* H37Rv (pP3), and 1.7 for *M. tuberculosis* H37Rv (p1963-P3). At 0, 1, 4 and 6 days post-infection, cell lysates of the three transformants were prepared and their β-galactosidase activities were measured. The highest β-galactosidase activity was observed during the late stages of infection (4 and 6 days post-infection) in *M. tuberculosis* H37Rv (pP3) and *M. tuberculosis* H37Rv (p1963-P3). Induction of the mce3 operon in the infected J774 cell line was suggested by the comparison of β-galactosidase activity in vitro (bacteria used for infection) to that at 6 days post-infection. However, the *M. tuberculosis* H37Rv (pP3) to *M. tuberculosis* H37Rv (p1963-P3) ratio of β-galactosidase activity was similar in bacteria growing intracellularly and in those growing in vitro (around 8:1, Table 2), indicating that intracellular growth does not induce removal of repression in the experimental conditions used here.

**Binding of the Mce3R protein to the mce3 promoter region**

The Mce3R protein was examined for its ability to bind to the mce3 promoter region by performing a gel-shift assay. mce3R was cloned into the expression vector pRSET-A; high expression recombinant mce3R was then induced in *E. coli* BL21 (pRSET1963) by the addition of IPTG to the growth medium (Fig. 5). Since
Regulation of the mce3 operon in M. tuberculosis

**Fig. 4.** (a) TSP as determined by primer extension. The TSP is indicated by an arrow; sequencing products generated by using the Low861 primer are shown alongside. (b) Predicted promoter region of the mce3 operon. The −10 (TATATG) and −35 (TAGCAA) regions are highlighted; an alternative −10 element (TATTTA) is also highlighted. A double-underlined C shows the TSP, as determined by primer extension. Letters in italics indicate putative ribosome-binding sites.

The formation of inclusion bodies by the bacterium prevented the purification of histidine-tagged Mce3R on nickel/agarose columns, we decided to work with the soluble fraction of the cell extract of E. coli BL21, which contained Mce3R (Fig. 5). Three different probes were tested in gel-shift assays on the cell extract of E. coli BL21(pRSET1963); these were 100 and 206 bp fragments upstream of the start codon (ATG) of Rv1964 and a 139 bp fragment from the mce2 promoter region. The 206 bp fragment showed Mce3R binding to the mce3 promoter region in a dose-dependent manner (Fig. 6), whereas no binding was observed with the 100 bp fragment. A cell extract from E. coli BL21 transformed with vector alone produced no retardation on the 206 bp fragment. Interestingly, Mce3R bound to the 139 bp mce2 fragment, suggesting a regulatory action of Mce3R on the mce2 promoter; however, the strength of this binding was lower than seen for Mce3R and the mce3 promoter.

**DISCUSSION**

Currently, the physiological function of Mce proteins is not known, although a protein promoting mammalian cell entry, Mcep (Arruda et al., 1993), is encoded by the mce1 operon of M. tuberculosis. Mce proteins seem to be exported by the bacterium, as suggested by their

**Table 2.** Effect of Rv1963 expression on mce3 promoter activity in recombinant strains used to infect J774 cell line

<table>
<thead>
<tr>
<th>J774 Macrophage-like cell line infected with</th>
<th>In vitro β-galactosidase activity (Miller units)*</th>
<th>β-Galactosidase activity (Miller units) at 0 d.p.i.†</th>
<th>1 d.p.i.</th>
<th>4 d.p.i.</th>
<th>6 d.p.i.</th>
</tr>
</thead>
<tbody>
<tr>
<td>M. tuberculosis H37Rv(pJEM15)</td>
<td>2</td>
<td>22</td>
<td>20</td>
<td>185</td>
<td>142</td>
</tr>
<tr>
<td>M. tuberculosis H37Rv(p1963-P3)</td>
<td>21</td>
<td>49</td>
<td>55</td>
<td>454</td>
<td>1987</td>
</tr>
<tr>
<td>M. tuberculosis H37Rv(pP3)</td>
<td>140</td>
<td>541</td>
<td>588</td>
<td>4684</td>
<td>14111</td>
</tr>
</tbody>
</table>

* Activity of bacterial cultures used as inoculum.
† d.p.i., Days post-infection.
predicted topology and by subcellular fractionation experiments (data not shown). The membrane localization of Mce proteins predicts a function for them in transmembrane transport, cell-wall synthesis or other functions associated with the bacterium–environment relationship. Genes encoding proteins homologous to those encoded by the mce operons are also present in other mycobacterial species, such as M. avium (Parker et al., 1995), M. smegmatis (http://www.tigr.org/tdb/mbd/mbdinprogress.html) and M. leprae (Cole et al., 2001). However, mce3 is absent from M. bovis and M. microti. The biological consequence of the absence of mce3 in these species is unclear, but it is important to note that although the mce3 operon is deleted in M. bovis, Rv1963 is conserved within this species. In place of the mce3 operon ORFs, the M. bovis genome has a chimeral ORF between Rv1964 and Rv1977. M. smegmatis also contains four operons with a structure similar to the mce operons of M. tuberculosis (data not shown). Surprisingly, in the M. smegmatis genome the gene most similar to Rv1963 is not upstream of the mce3-like operon, but is instead elsewhere in the genome. Also, upstream of the mce3-like operon there is another tetR-like regulator with a lesser homology to Rv1963 (data not shown).

Even though the expression of Mce proteins has been demonstrated both in vitro (Harboe et al., 1999) and in vivo (Ahmad et al., 1999), nothing is known about the regulation of production of Mce proteins. The observation of a regulatory-type gene in the vicinity of the mce3 operon prompted us to determine whether this putative regulator controls mce expression. The 0.9 kbp intergenic region between Rv1963 and Rv1964 should be the location of the mce3 promoter and the target of regulatory proteins. Progressive deletions and cloning of this region helped us to map the promoter region in a fragment extending from the Rv1964 start codon to 206 bp upstream of it. A neural-network search for putative prokaryotic promoters located a probable promoter extending from −170 to −230 upstream of the ATG start of the first mce3 ORF. As deduced from gel-shift assays, it was also observed that Mce3R binds to this region.

Using all of the published putative mycobacterial sequences, Mulder et al. (1997) calculated the mycobacterial promoter to consist of a −35 consensus sequence, TTGACG/A, and a −10 consensus sequence, TATA/GA/CT. Putative −10 (TATATG) and −35 (TAGCAA) sequences were identified in the predicted promoter region of the mce3 operon. The proposed −10 hexamer is identical to the corresponding sequence in E. coli and conserves the four first positions of the Mulder et al. (1997) consensus sequence. The putative −35 sequence conserves three positions of the Mulder et al. (1997) consensus sequence and is identical to other individual mycobacterial promoters. However, the proposed −10 sequence is far (32 bp) from the TSP identified by primer-extension experiments. Possible explanations for this large separation could be (i) an erroneous TSP was mapped because the 5′ end of the transcript was processed or degraded, or (ii) non-conserved −10 and −35 sequences are present in the mce3 promoter region. As in many actinomycete promoters, mycobacterial promoters not carrying the canonical −35 and −10 sequences have been reported. Counting upstream from the proposed start site of the mce3 promoter region there is another, less consensual, sequence, TATTTA, at a distance of −12 bp.

In general, the TetR family of bacterial regulators are repressors; many of these proteins regulate genes that encode proteins involved in membrane processes such as osmoregulation (Rkenes et al., 1996), permeability (Ma et al., 1996; Lucas et al., 1997; Namwat et al., 2001) and resistance to antibiotics or quaternary ammonium salts (Rouch et al., 1990; Grkovic et al., 1998), among other functions. The prototype TetR repressor is TetR from the Tn10 transposon of E. coli (Orth et al., 2000). There are approximately 40 tetR-family regulatory genes in M. tuberculosis (http://www.sanger.ac.uk/Projects/M_tuberculosis). To the best of our knowledge, the Rv1963-encoded protein examined in this study (as Mce3R) is the first TetR-like regulatory protein whose function has been described in M. tuberculosis. As with other TetR regulators, a helix–turn–helix motif and a tetR-family signature sequence reside in the first third of
the \textit{Rv1963} gene. Most TetR-like regulators have molecular masses ranging from 21 to 25 kDa; however, Mce3R (Rv1963) has a molecular mass $>25$ kDa. We observed that other TetR-like proteins with molecular masses $>25$ kDa contain two consensus signatures, as does Mce3R (Rv1963). The last third of Mce3R (Rv1963) shows no homology to other proteins. The two TetR-like regulators most homologous to Mce3R (Rv1963), Rv2506 and Rv3557c, are in the vicinity of lipid-metabolism-related genes of the \textit{M. tuberculosis} genome.

We could not find the inducer(s) of the \textit{mce3} operon; different conditions of stress (ethanol, SDS or low carbon) did not abolish repression of expression (data not shown). No removal of repression was observed when the \textit{J774} macrophage-like cell line was infected with recombinant \textit{M. tuberculosis}. The possibility exists that removal of repression could not be observed due to the fact that in recombinant mycobacteria carrying the reporter gene the repressor is harboured \textit{in cis} in multicopy plasmids. However, an increase in \textit{mce3} expression by \textit{M. tuberculosis} H37Rv(pP3) and \textit{M. tuberculosis} H37Rv(p1963-P3) was observed in the later stages of \textit{J774} infection, suggesting that additional factors may affect \textit{mce3} expression.

At present, it is not known whether the \textit{Rv1963}-encoded protein regulates genes other than \textit{mce3}, but gel-shift experiments indicated that Mce3R binds to the \textit{mce2} promoter region, raising the possibility that \textit{mce2} may also be negatively regulated by the \textit{Rv1963}-encoded protein. However, the binding of the recombinant protein Mce3R to the \textit{mce2} promoter seems to be weaker than binding of this protein to the \textit{mce3} promoter, suggesting that fine-tuning of regulation of the \textit{mce} operons may occur. Interestingly, a moderately homologous region of about 100 bp was found in the promoter-containing regions of \textit{mce2} and \textit{mce3} (data not shown).

The present study reveals interesting features of the control of expression of the \textit{mce} operons of \textit{M. tuberculosis}. It also poses a number of questions that need to be answered, such as (i) does the \textit{Rv1963}-encoded regulatory protein have the same effect on \textit{mce} promoters other than \textit{mce3}, and (ii) which extracellular signals are required for \textit{mce} expression? At present, it is not known whether the \textit{mce1} and \textit{mce4} promoter regions are also the target of the \textit{Rv1963}-encoded transacting regulatory factor, but the high homology between the \textit{mce} operons supports the idea of a broader regulatory mechanism.

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