Role of the methylcitrate cycle in propionate metabolism and detoxification in *Mycobacterium smegmatis*

Anna M. Upton and John D. McKinney

Laboratory of Infection Biology, The Rockefeller University, New York, NY 10021, USA

Catabolism of odd-chain-length fatty acids yields acetyl-CoA and propionyl-CoA. A common pathway of propionyl-CoA metabolism in micro-organisms is the methylcitrate cycle, which includes the dedicated enzymes methylcitrate synthase (MCS), methylcitrate dehydratase (MCD) and methylisocitrate lyase (MCL). The methylcitrate cycle is essential for propionate metabolism in *Mycobacterium tuberculosis*. Unusually, *M. tuberculosis* lacks an MCL orthologue and this activity is provided instead by two isoforms of the glyoxylate cycle enzyme isocitrate lyase (ICL1 and ICL2). These bifunctional (ICL/MCL) enzymes are jointly required for propionate metabolism and for growth and survival in mice. In contrast, the non-pathogenic species *Mycobacterium smegmatis* encodes a canonical MCL enzyme in addition to ICL1 and ICL2. The *M. smegmatis* gene encoding MCL (prpB) is clustered with genes encoding MCS (prpC) and MCD (prpD). Here we show that deletion of the *M. smegmatis* prpDBC locus reduced but did not eliminate MCL activity in cell-free extracts. The residual MCL activity was abolished by deletion of icl1 and icl2 in the ΔprpDBC background, suggesting that these genes encode bifunctional ICL/MCL enzymes. A ΔprpB Δicl1 Δicl2 mutant was unable to grow on propionate or mixtures of propionate and glucose. We hypothesize that incomplete propionyl-CoA metabolism might cause toxic metabolites to accumulate. Consistent with this idea, deletion of prpC and prpD in the ΔprpB Δicl1 Δicl2 background paradoxically restored growth on propionate-containing media. These observations suggest that the marked attenuation of ICL1/ICL2-deficient *M. tuberculosis* in mice could be due to the accumulation of toxic propionyl-CoA metabolites, rather than inability to utilize fatty acids per se.

**INTRODUCTION**

Accumulating evidence suggests an important role for fatty acid catabolism in mycobacteria and other microbial pathogens during infection (Boshoff & Barry, 2005; Munoz-Elias & McKinney, 2006). Consistent with this idea, the anaplerotic glyoxylate cycle, which includes the enzymes isocitrate lyase (ICL) and malate synthase (MLS) (Fig. 1b; Table 1), is required for fatty acid metabolism and virulence of diverse bacterial and fungal pathogens (Munoz-Elias & McKinney, 2006). The glyoxylate cycle is required for assimilation of acetyl-CoA units derived from beta-oxidation of fatty acids. Beta-oxidation of odd-chain-length fatty acids yields propionyl-CoA as an additional product. Several microbial pathways of propionyl-CoA metabolism have been proposed (Horswill & Escalante-Semerena, 1999; Textor et al., 1997), including the methylcitrate cycle, which mediates oxidation of propionyl-CoA to pyruvate.

Three enzymes are thought to be specific to the methylcitrate cycle: methylcitrate synthase (MCS), methylcitrate dehydratase (MCD) and methylisocitrate lyase (MCL), encoded by the prpC, prpD and prpB genes, respectively (Fig. 1a; Table 1) (Bramer & Steinbuchel, 2001; Bramer et al., 2002; Brock et al., 2000, 2001; Claes et al., 2002; Horswill & Escalante-Semerena, 1999; Textor et al., 1997). Species that operate both the glyoxylate cycle and methylcitrate cycle typically produce dedicated ICL and MCL enzymes with unique substrate specificities (isocitrate and methylisocitrate, respectively) and non-overlapping roles in their respective pathways (Bramer & Steinbuchel, 2001; Brock et al., 2001; Brock, 2005; Claes et al., 2002; Horswill & Escalante-Semerena, 1999; Liu et al., 2005; Luttik et al., 2000). The active sites of these enzymes also have characteristic catalytic motifs: K[K/Q][CGH in ICL and KRCGH in MCL (Brock et al., 2001; Brock, 2005; Grimek et al., 2003; Grimm et al., 2003).
The Mycobacterium tuberculosis and Mycobacterium bovis genomes encode MCD (prpD; mt1162; mb1161) and MCS (prpC; mt1163; mb1162) orthologues but do not encode an MCL (prpB) orthologue (Cole et al., 1998; Fleischmann et al., 2002; Garnier et al., 2003), and all three enzymes are apparently absent in Mycobacterium leprae (Cole et al., 2001), suggesting the absence of a functional methylcitrate cycle in these species. However, we found that M. tuberculosis requires the prpDC genes for in vitro metabolism of propionate and other odd-chain-length fatty acids, implying that the methylcitrate cycle is intact (Munoz-Elias et al., 2006). In contrast to other species, where ICL cannot substitute for MCL in propionate metabolism, the M. tuberculosis ICL1 (mt0483) and ICL2 (mt1966) orthologues appear to be bifunctional ICL/MCL enzymes that participate in both the glyoxylate cycle and the methylcitrate cycle, despite possessing the canonical KKCGH motif that is characteristic of monofunctional ICL (Gould et al., 2006; Munoz-Elias et al., 2006). The recently solved three-dimensional structures of ICL1 bound with the MCL substrate methylisocitrate or with the MCL reaction products (succinate and pyruvate) demonstrate that the active site of this enzyme can accommodate these moieties and catalyse the MCL reaction (Gould et al., 2006).

Consistent with the idea that ICL1/ICL2 perform essential functions in both the glyoxylate cycle and the methylcitrate cycle, these enzymes are jointly required for growth of M. tuberculosis on even- or odd-chain-length fatty acids (including acetate and propionate), and their activity is acetate- and propionate-inducible (Munoz-Elias & McKinney, 2005; Munoz-Elias et al., 2006; unpublished observations). However, in some micro-organisms the glyoxylate cycle is required for carbon anaplerosis during growth on propionate, even when propionate is metabolized by pathways other than the methylcitrate cycle (Ashworth & Kornberg, 1964; Bramer & Steinbuchel, 2001; Wang et al., 2003; Wegener et al., 1969). Thus, it is unclear whether the essential role of ICL1/ICL2 in growth and survival of M. tuberculosis during infection (Munoz-Elias & McKinney, 2005) is due to their participation in the glyoxylate cycle, the methylcitrate cycle, or both pathways. Interpretation of these observations is further complicated by studies in Aspergillus nidulans (Brock, 2005) and Salmonella typhimurium (Horswill et al., 2001), which revealed that the methylcitrate cycle intermediates methylcitrate and methyl-cis-aconitate – generated by MCS and MCD, respectively – are growth-inhibitory in these species. These intermediates would be expected to accumulate in the absence of MCL activity, and could account for the severe attenuation of ICL1/ICL2-deficient M. tuberculosis in vivo.

In order to elucidate the roles of the glyoxylate and methylcitrate cycles in mycobacterial metabolism, we carried out studies in Mycobacterium smegmatis, a fast-growing relative of M. tuberculosis, that is more amenable to genetic and biochemical analysis. In addition to ICL1 (msm0911) and ICL2 (msm3706) orthologues, the M.

![Fig. 1. The methylcitrate and glyoxylate cycles in Mycobacterium smegmatis. (a and b) Odd-chain-length fatty acids are degraded by the beta-oxidation cycle to propionyl-CoA and acetyl-CoA units, which are further metabolized by the methylcitrate cycle and the glyoxylate cycle, respectively. The methylcitrate cycle (a) converts propionyl-CoA to pyruvate on an equimolar basis. The glyoxylate cycle (b) converts two molar equivalents of acetyl-CoA to one molar equivalent of succinate. Enzymes: MCS (prpC), methylcitrate synthase; MCD (prpD), methylcitrate dehydratase; ACN, aconitase; MCL (prpB), methylisocitrate lyase; SDH, succinate dehydrogenase; FUM, fumarase; MQO, malate:quinone oxidoreductase; CIT, citrate synthase; ICL (icl1, icl2), isocitrate lyase; MLS (glcB), malate synthase. Reactions unique to the methylcitrate cycle (red arrows) or the glyoxylate cycle (blue arrows) are indicated. All other reactions (black arrows) also occur in the citric acid cycle.](image-url)
Table 1. Putative glyoxylate and methylcitrate cycle enzymes and genes in M. smegmatis, M. tuberculosis and C. glutamicum

<table>
<thead>
<tr>
<th>Protein (gene) ID</th>
<th>M. smegmatis*</th>
<th>M. tuberculosis*</th>
<th>C. glutamicum*</th>
</tr>
</thead>
<tbody>
<tr>
<td>MCL (prpB)</td>
<td>smm6646</td>
<td>–</td>
<td>cgl0760</td>
</tr>
<tr>
<td>ICL1 (icl1)</td>
<td>mss0911</td>
<td>mt0483</td>
<td>cgl2560</td>
</tr>
<tr>
<td>ICL2 (icl2)</td>
<td>mss3706</td>
<td>mt1966</td>
<td>–</td>
</tr>
<tr>
<td>MLS (glkB)</td>
<td>mss3640</td>
<td>mt1885</td>
<td>cgl2559</td>
</tr>
<tr>
<td>CIT1 (gltA)</td>
<td>mss5672</td>
<td>mt0920</td>
<td>cgl0949</td>
</tr>
<tr>
<td>CIT2 (citA)</td>
<td>mss5676</td>
<td>mt0912</td>
<td>–</td>
</tr>
<tr>
<td>MCS (prpC)</td>
<td>mss6647</td>
<td>mt1163</td>
<td>cgl0762</td>
</tr>
<tr>
<td>MCD (prpD)</td>
<td>mss6645</td>
<td>mt1162</td>
<td>cgl0759</td>
</tr>
</tbody>
</table>

*Annotated genomes can be accessed at http://www.tigr.org.
†The mtt1163-mtt1163 locus is required for propionate metabolism in M. tuberculosis (Munoz-Elias et al., 2006).
§Comparisons were made between the predicted polypeptide sequences using Vector NTI 6.0 AlignX, which uses the CLUSTAL W algorithm (Thompson et al., 1994). Values indicate the percentage amino acid identity between the M. smegmatis polypeptide and its orthologues in M. tuberculosis or C. glutamicum.
¶The cg0759-cg0872 locus is required for propionate metabolism in C. glutamicum (Kalinowski et al., 2003). A paralogous gene cluster – comprising cg0797 (prpB1), cg0798 (prpC1) and cg0796 (prpD2) – appears to be cryptic (non-functional) in this species under standard growth conditions (Kalinowski et al., 2003).

**M. smegmatis** genome potentially encodes a dedicated MCL (prpB; mss6646), which appears to be arranged in an operon (prpDBC) encoding MCS (prpC; mss6647) and MCD (prpD; mss6645) orthologues. Similarly arranged orthologues of prpDBC are present in the Mycobacterium avium (nav0346-nav0345-nav0344) and Mycobacterium marinum (mmnr1379-mmnr1380-mmnr1381) genomes (Li et al., 2005; annotated M. marinum genome available at http://genolist.pasteur.fr/Genolist/). Here, we evaluate the role of the methylcitrate cycle and the contribution of the prpDBC and icl1/icl2 gene products to propionate metabolism in M. smegmatis. We provide evidence supporting the idea that the accumulation of toxic metabolites is growth-inhibitory to ICL/MCL-deficient bacteria during growth on propionate-containing media. These observations suggest that the essential role of ICL1/ICL2 in M. tuberculosis metabolism during infection might be in propionate detoxification rather than (or in addition to) their role in fatty acid catabolism.

**METHODS**

**Bacteriology.** M. smegmatis strain mc²155 (Snapper et al., 1990) and derivative strains were stored at –80 °C in 15% glycerol. Bacteria were grown with aeration at 37 °C in Middlebrook 7H9 (DIFCO) broth containing 0.5% BSA fraction V (Fisher), 0.085% NaCl, 0.05% Tween-80 and 0.2% glucose (Sigma), or on Middlebrook 7H10 (DIFCO) agar containing 10% oleic-albumin-dextrose-catalase (DIFCO) and 0.5% glycerol. For carbon utilization experiments and preparation of cell-free extracts, bacteria were grown in M9 broth [M9 salts (DIFCO), 0.1 mM CaCl₂, 2 mM MgSO₄ (Sigma)], containing the indicated carbon substrate at 0.1% or 0.5% (w/v). Antibiotics (Sigma) were kanamycin (25 μg ml⁻¹), hygromycin (50 μg ml⁻¹) and streptomycin (20 μg ml⁻¹). Culture turbidity (OD₆₀₀) measurements were made using a Uvicspec 2000 spectrophotometer (Pharmacia) following dilution with PBS containing 0.05% Tween-80 (PBST), to give readings within the range 0.05–0.25.

**M. smegmatis cell-free extracts.** Bacteria were grown to late exponential phase (OD₆₀₀ 1.0–1.3) in M9 broth containing the indicated carbon substrate, collected by centrifugation (5000 g, 20 min), washed thrice with PBST and resuspended in the appropriate assay buffer supplemented (5% v/v) with protease inhibitor cocktail (Sigma P-8465). Cells were disrupted by bead-beating (BioSpec) with 0.1 mm zirconia-silica beads (Sigma) for 60 s at high speed. Extracts were clarified by centrifugation (18 000 g, 15 min), and the total protein concentration was determined by Bradford assay (Sigma). Cell-free extracts were stored frozen at –80 °C.

**MCS assays.** MCS activity was measured by following the accumulation of free CoA, generated by the condensation of propionyl-CoA and oxaloacetate, after reaction of CoA with 5,5'-dithiobis-(2-nitrobenzoate) (DTNB), as described (Munoz-Elias et al., 2006). Reactions were done at room temperature in a 1 ml assay volume containing 50 mM HEPES-NaOH pH 8.0, 0.1 M NaCl, 2 mM EDTA, 0.1 mM DTNB, 0.035 mM propionyl-CoA and 0.4 mM oxaloacetate. Reactions were started by addition of cell-free extract (5–300 μg total protein in 5–50 μl). Oxaloacetate-stimulated TNB anion formation, generated by the reaction of free CoA with DTNB was monitored spectrophotometrically at 412 nm, using an Uvicspec 2000 spectrophotometer (Pharmacia) and the standard extinction coefficient 13.6 mM⁻¹ cm⁻¹ for a 1 cm path length. Background was measured and subtracted by carrying out mock reactions without addition of oxaloacetate. Corrected activities below 1 nmol min⁻¹ mg⁻¹ were considered to be below the detection limit.

**ICL and MCL assays.** ICL activity was measured by following the lactate dehydrogenase (LDH)-mediated reduction of glyoxylate to glycylate with concomitant oxidation of NADH, as described...
Construction of ΔprpB, ΔprpB ΔiclI Δicl2, ΔprpDBC and ΔprpDBC ΔiclI Δicl2 strains of M. smegmatis. In-frame unmarked (non-polar) deletions of the msm6646 (prpB) and msm6645-6647 (prpDBC) ORFs were constructed in the M. smegmatis chromosome by two-step (insertion–excision) homologous recombination with the suicide vector pGI1111 (Munoz-Elias et al., 2006) containing aph (kanamycin resistance), hyg (hygromycin resistance), sacB (sucrose sensitivity) and lacZ (β-galactosidase) under the control of the M. tuberculosis antigen 85 promoter. The ΔprpB and ΔprpDBC deletions were constructed on the wild-type and ΔiclI Δicl2 genetic backgrounds. The ΔiclI Δicl2 strain was generously provided by Ernesto Muñoz-Elias and Lubomir Merkov (The Rockefeller University, New York).

The ΔprpB recombinant substrate was constructed by PCR amplification of 1 kb regions upstream (fragment A) and downstream (fragment B) of the prpB ORF. Primers introduced 5′ PacI and 3′ AvrII sites into fragment A and 5′ AvrII and 3′ AscI sites into fragment B. Primers for fragment A were 5′-ctcagagcccgacctgctc-3′ and 5′-ctcaaggccgcctagggcctg-3′ (restriction sites are underlined; prpB start codon is in bold type). Primers for fragment B were 5′-ctcagagccgtcggacacctgctc-3′ and 5′-ctcagagccgtcggacacctgctc-3′ (restriction sites are underlined; prpB stop codon is in bold type). The amplicons were digested with PacI and AvrII (fragment A) or AvrII and AscI (fragment B) and ligated together into the unique PacI and AscI sites of pGI1111 to generate pAU101.

The ΔprpDBC recombinant substrate was constructed by PCR amplification of 1 kb regions upstream of the prpD ORF (fragment C) and downstream of the prpC ORF (fragment D). Primers introduced 5′ PacI and 3′ AvrII sites into fragment C and 5′ AvrII and 3′ AscI sites into fragment D. Primers for fragment C were 5′-ctcagagccggcgctcggc-3′ and 5′-ctcagagccgctcggcctc-3′ (restriction sites are underlined; prpD start codon is in bold type). Primers for fragment D were 5′-ctcaaggccgcctcggcctc-3′ and 5′-ctcaaggccgcctcggcctc-3′ (restriction sites are underlined; prpD stop codon is in bold type). The amplicons were digested with PacI and AvrII (fragment C) or AvrII and AscI (fragment D) and ligated together into the unique PacI and AscI sites of pGI1111 to generate pAU102.

pAU101 (ΔprpB) and pAU102 (ΔprpDBC) were inserted into the M. smegmatis chromosome by electroporation and selection of transfectants on 7H10 agar containing hygromycin, kanamycin and X-Gal (50 μg ml⁻¹). Blue colonies were individually picked and amplified in 7H9 broth (no antibiotics) to allow plasmid excision, then plated on 7H10 agar containing X-Gal and 5 % sucrose (no antibiotics) to select for cells in which plasmid excision had occurred. White colonies were individually picked and amplified in 7H9 broth (no antibiotics) for genomic DNA isolation and strains in which the ΔprpB or ΔprpDBC allele had replaced the corresponding wild-type locus were identified by PCR analysis (not shown). The ΔprpB allele is a fused ORF with the sequence atgccgggagacctgctcggcctc-3′, comprising the first five and the last two codons of prpB, joined by a two-codon linker provided by the introduced AvrII site (underlined). The ΔprpDBC allele is a fused ORF with the sequence atgccgggagacctgctcggcctc-3′, comprising the first three codons of prpD and the last two codons of prpC joined by a two-codon linker provided by the introduced AvrII site (underlined).

Complementation analysis. The complementing plasmid pPRPDC, containing the M. tuberculosis prpDC genes, was described previously (Munoz-Elias et al., 2006). The complementing plasmid pPRPB was constructed by cloning the PCR-amplified M. smegmatis prpB ORF into the unique HindIII site of pEM261, an episomal vector derived from the shuttle vector pMV261 by replacing the aph kanamycin resistance cassette with the aadA streptomycin resistance cassette (Munoz-Elias et al., 2005). PCR primers, designed to introduce 5′ and 3′ HindIII sites (underlined) into the prpB amplicon, were 5′-aagtcctgacgagttggtc-3′ and 5′-aagtccttgctctcgactctc-3′. pPRPB was introduced into M. smegmatis by electroporation and selection of transformants on 7H10 agar containing streptomycin.

RESULTS

Bioinformatic analysis of the methylcitrate cycle in M. smegmatis

A cluster of three ORFs was identified in the M. smegmatis genome (msm6645-6647) whose predicted peptide products were highly similar to enzymes of the methylcitrate cycle in M. tuberculosis (Munoz-Elias et al., 2006) and the related actinomycete Corynebacterium glutamicum (Claes et al., 2002; Kalinowski et al., 2003) (Fig. 1a; Table 1). The msm6647 ORF encoded a conceptual product of 376 aa with 76 % identity to the M. tuberculosis prpC (mt1163) gene product and 54 % identity to the prpC2 (cg0762) gene product in C. glutamicum. Deletion of the mt1163 gene in M. tuberculosis eliminated all detectable MCS activity in cell-free extracts, thus confirming the assignment of the gene as a functional prpC orthologue (Munoz-Elias et al., 2006). The msm6645 ORF encoded a putative protein (460 aa) with 72 % identity to the M. tuberculosis prpD (mt1162) gene product and 66 % identity to the prpD2 (cg0759) gene product in C. glutamicum. In contrast with M. tuberculosis, which lacks a prpB orthologue, the M. smegmatis msm6646 ORF encodes a putative protein (305 aa) with 64 % identity to the C. glutamicum prpB2 (cg0760) gene product.

Role of the M. smegmatis prpDBC locus in propionate metabolism

Previously we reported that deletion of the prpDC locus eliminated growth of M. tuberculosis on media containing propionate as the carbon source (Munoz-Elias & McKinney, 2005). To investigate whether the methylcitrate cycle is also important for propionate metabolism in M.
M. smegmatis, we constructed a strain in which the putative prpDBC locus was deleted. The *M. smegmatis* *prpD*, *prpB* and *prpC* genes appear to be organized in an operon, in which the first and last codons of *prpB* overlap the last and first codons, respectively, of *prpD* and *prpC*. We generated an unmarked, non-polar chromosomal deletion encompassing all three genes, in which codon 3 of *prpD* was fused in-frame to codon 375 of *prpC* (see Methods).

Deletion of prpDBC did not alter the kinetics of *M. smegmatis* growth in standard Middlebrook 7H9 broth or in minimal M9 liquid medium supplemented with 0.1 % glucose as the sole carbon source (not shown). However, growth of the ΔprpDBC strain was substantially delayed, compared to the parental strain, when the carbon source was 0.1 % (Fig. 2a) or 0.5 % (Fig. 2b) propionate. These observations suggest that, although the prpDBC locus contributes to propionate catabolism in *M. smegmatis*, it is not essential. In contrast, the orthologous prpDC locus in *M. tuberculosis* is absolutely required for growth on propionate-containing media (Munoz-Elias et al., 2006).

**MCS activity in cell-free extracts from wild-type and ΔprpDBC bacteria**

The delayed but robust growth of ΔprpDBC bacteria on propionate suggested the existence of an alternative pathway(s) for propionate metabolism in *M. smegmatis*. To rule out the possibility of a cryptic methylcitrate cycle operating in the absence of prpDBC, we confirmed that deletion of prpDBC resulted in the loss of MCS activity by assaying cell-free extracts prepared from bacteria grown in media containing glucose or propionate as the sole carbon source. MCS activity was readily detectable in extracts from wild-type bacteria grown on propionate, but was undetectable in extracts from wild-type bacteria grown on glucose or from ΔprpDBC bacteria grown on either substrate (Table 2). These results confirm that MCS activity is propionate-inducible in *M. smegmatis*, similar to *M. tuberculosis* (Munoz-Elias et al., 2006), and suggest that *prpC* is the only gene encoding detectable MCS activity in *M. smegmatis*. Apparently, the products of the *msm5672* and *msm5676* ORFs (Table 1), which encode probable type I and type II citrate synthases that are weakly homologous to the predicted *prpC* product (28 % and 26 % identical, respectively), do not possess significant MCS activity. We cannot, however, rule out the possibility that the ΔprpDBC strain produces an alternative MCS whose activity is undetectable under the *in vitro* assay conditions that we used.

**MCL and ICL activities in cell-free extracts from wild-type and ΔprpDBC bacteria**

We also measured MCL activity in cell-free extracts prepared from wild-type and ΔprpDBC bacteria. MCL activity was barely detectable in cell-free extracts from either strain when cells were grown in media containing 0.1 % glucose as the sole carbon source (Table 2). This activity was increased dramatically in extracts from wild-type cells grown in media containing propionate at 0.1 % (80-fold induction) or 0.5 % (80-fold induction) (Table 2). Surprisingly, MCL activity was reduced only modestly (by about twofold) in extracts from propionate-grown ΔprpDBC bacteria as compared to wild-type bacteria (Table 2). These observations suggest that *M. smegmatis* possesses another gene(s), in addition to *prpB*, that encodes MCL activity.

![Fig. 2. Propionate metabolism and detoxification via the methylcitrate cycle.](http://mic.sgmjournals.org/3977)
In *M. tuberculosis*, which lacks a prpB homologue, the *icl1* and *icl2* genes encode bifunctional enzymes with ICL and MCL activities (Gould et al., 2006; Munoz-Elias et al., 2006). The *M. smegmatis* ICL1 and ICL2 proteins are highly homologous to their counterparts in *M. tuberculosis* (92% and 77% identical, respectively), suggesting that they too might be bifunctional enzymes. To test this idea, we deleted *prpDBC* in wild-type and Δicl1 Δicl2 strains of *M. smegmatis*, which grow with similar kinetics in propionate-containing media (Ernesto Munoz-Elias and Lubomir Merkov, The Rockefeller University, New York, personal communication). The ΔprpDBC Δicl1 Δicl2 strain grew normally on media containing propionate as the sole carbon source (not shown); this strain was delayed for growth on media containing propionate at 0.1% (Fig. 2a) or 0.5% (Fig. 2b), but only to a similar extent as the parental ΔprpDBC strain. We conclude that ICL1/ICL2 are not required for propionate metabolism in the presence or absence of a functional methylcitrate cycle. Nonetheless, the ICL and MCL activities that we detected in extracts from propionate-grown ΔprpDBC cells were both, apparently, due to ICL1/ICL2, because both activities were abolished in extracts from ΔprpDBC Δicl1 Δicl2 bacteria (Table 2). Consistent with this interpretation, the ratio of ICL to MCL activities in extracts prepared from ΔprpDBC bacteria was similar under all growth conditions that we tested (Table 2). These observations suggest that the *M. smegmatis* *icl1* and/or *icl2* genes encode bifunctional ICL/MCL enzymes, similar to their orthologues in *M. tuberculosis*.

Given the absence of detectable MCL and MCS activities in the ΔprpDBC Δicl1 Δicl2 cell-free extracts, it is likely that this strain lacks a functional methylcitrate cycle. This conclusion is reinforced by our observation that the presence or absence of *icl1* and *icl2* had little or no effect on the growth kinetics of ΔprpDBC bacteria in propionate-containing media, suggesting that there are no alternative sources of MCS or MCD activities other than the *prpC* and *prpD* genes, respectively. In the absence of the methylcitrate cycle, growth of the ΔprpDBC and ΔprpDBC Δicl1 Δicl2 strains on propionate might be attributable to the activity of one or more alternative pathways of propionate metabolism that have been proposed (Horswill & Escalante-Semerena, 1999; Textor et al., 1997).

### MCL deficiency sensitizes *M. smegmatis* to propionate toxicity

The observation that wild-type and Δicl1 Δicl2 strains of *M. smegmatis* grow with similar kinetics in propionate-containing media suggests that *prpB* can fully compensate for the loss of ICL1/ICL2 under these conditions. In order to determine whether the converse might also be true, we constructed an unmarked non-polar deletion of *prpB* in which codon 5 was fused in-frame to codon 303 (see Methods), leaving the *prpD* and *prpC* genes intact. As expected, deletion of *prpB* in either the wild-type or Δicl1 Δicl2 genetic background had no discernible impact on bacterial growth with glucose as the carbon source (not shown). The ΔprpB strain was partially impaired for growth on 0.1% (Fig. 2c) or 0.5% (Fig. 2d) propionate, but was more robust than ΔprpDBC or ΔprpDBC Δicl1 Δicl2 bacteria under these conditions (Fig. 2a, b), consistent with the idea that ICL1/ICL2 are bifunctional ICL/MCL enzymes that can compensate, at least partially, for the loss of *prpB*.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Carbon source</th>
<th>MCS activity*</th>
<th>MCL activity†</th>
<th>ICL activity‡</th>
<th>Ratio ICL/MCL</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT</td>
<td>0.1% Glucose</td>
<td>Undetectable</td>
<td>2.32 ± 0.31</td>
<td>15.24 ± 2.01</td>
<td>6.57</td>
</tr>
<tr>
<td>ΔprpDBC</td>
<td>0.1% Glucose</td>
<td>Undetectable</td>
<td>2.52 ± 1.51</td>
<td>11.51 ± 0.14</td>
<td>4.58</td>
</tr>
<tr>
<td>ΔprpDBC Δicl1</td>
<td>0.1% Propionate</td>
<td>ND</td>
<td>49.65 ± 3.94</td>
<td>254.33 ± 21.97</td>
<td>5.10</td>
</tr>
<tr>
<td>WT</td>
<td>0.1% Propionate</td>
<td>ND</td>
<td>124.43 ± 27.15</td>
<td>85.03 ± 6.92</td>
<td>0.68</td>
</tr>
<tr>
<td>ΔprpDBC</td>
<td>0.1% Propionate</td>
<td>ND</td>
<td>11.47 ± 0.94</td>
<td>190.40 ± 0.72</td>
<td>1.03</td>
</tr>
<tr>
<td>ΔprpDBC Δicl1</td>
<td>0.5% Propionate</td>
<td>Undetectable</td>
<td>76.02 ± 5.71</td>
<td>420.67 ± 26.57</td>
<td>5.50</td>
</tr>
</tbody>
</table>

*Units are defined as mean nanomoles of oxaloacetate-stimulated free CoA production from propionyl-CoA min⁻¹ (mg protein)⁻¹ in the cell-free extract ± SD. Detection limit: 1 nmol min⁻¹ mg⁻¹. Three measurements were made per extract. Data from one experiment are shown. Results are representative of at least two experiments with similar results.
†Units are defined as mean nanomoles of 2-methylisocitrate-stimulated NADH consumption min⁻¹ (mg protein)⁻¹ in the cell-free extract ± SD. Detection limit: 1 nmol min⁻¹ mg⁻¹. Three measurements were made per extract. Data from one experiment are shown. Results are representative of at least two experiments with similar results.
‡Units are defined as mean nanomoles of isocitrate-stimulated NADH consumption min⁻¹ (mg protein)⁻¹ in the cell-free extract ± SD. Detection limit: 1 nmol min⁻¹ mg⁻¹. Three measurements were made per extract. Data from one experiment are shown. Results are representative of at least two experiments with similar results.

WT, wild-type.
Paradoxically, ΔprpB Δicl1 Δicl2 bacteria (Fig. 2c) were much more severely impaired than ΔprpDBC Δicl1 Δicl2 bacteria (Fig. 2a) for growth on 0.1% propionate. Moreover, this strain was completely unable to grow in medium containing 0.5% propionate (Fig. 2d), although there was no loss of viability during the course of the experiment (data not shown). This striking phenotype was reversed by complementation of the ΔprpB Δicl1 Δicl2 strain with a plasmid containing an intact copy of the prpB gene, confirming that the phenotype was due to loss of MCL activity (Fig. 2 g, h). These observations suggest that the presence of prpC and/or prpD might be detrimental to growth on propionate-containing media in the absence of MCL activity. Consistent with this idea, we found that transformation of the M. smegmatis ΔprpDBC Δicl1 Δicl2 strain with a plasmid containing the M. tuberculosis prpDC genes (Munoz-Elias et al., 2006) resulted in reduced growth on 0.1% propionate (Fig. 2e) and nearly complete growth inhibition on 0.5% propionate (Fig. 2f), similar to the phenotype of ΔprpB Δicl1 Δicl2 bacteria (Fig. 2c, d). These observations indicate that in propionate-metabolizing bacteria, loss of MCL activity alone is more detrimental than loss of the entire methylcitrate cycle.

Propionate toxicity is not relieved by the addition of glucose to the growth medium

Our observations that propionate toxicity towards MCL-deficient bacteria is dose-dependent and requires MCS/MCD activity (Fig. 2) suggest that the accumulation of propionate metabolites might adversely affect the expression or activity of propionate-metabolizing pathways other than the methylcitrate cycle. Alternatively, we considered the possibility that propionate metabolites might exert more general growth-inhibitory effects, based on our previous observation that growth of prpDC-deficient M. tuberculosis on acetate- or glucose-containing media is unimpaired, whilst growth on mixtures of acetate plus propionate or glucose plus propionate is inhibited (Munoz-Elias et al., 2006). We therefore tested whether M. smegmatis strains lacking MCL and/or MCS/MCD activities were capable of growth on mixed substrates. Compared to the parental strain, growth of the ΔprpDBC (Fig. 3a), ΔprpDBC Δicl1 Δicl2 (Fig. 3a) and ΔprpB (Fig. 3b) strains was delayed and growth of the ΔprpB Δicl1 Δicl2 strain (Fig. 3b) was almost completely inhibited in medium containing a mixture of glucose plus propionate. Complementation of the ΔprpB Δicl1 Δicl2 strain with a plasmid encoding prpB restored growth on mixed-substrate media (glucose plus propionate) to nearly wild-type levels (Fig. 3d). As observed when the bacteria were grown on propionate as the sole carbon source (Fig. 2e, f), restoration of the prpDC genes to ΔprpDBC Δicl1 Δicl2 bacteria paradoxically impaired rather than enhanced growth on glucose plus propionate (Fig. 3c). These observations reinforce the idea that MCS/MCD-generated propionate metabolites exert a dominant inhibitory effect on bacterial growth that is especially pronounced in the absence of MCL activity.

DISCUSSION

Propionyl-CoA is derived from the catabolism of propionate, branched-chain amino acids and odd-chain-length fatty acids, which are abundant carbon/energy sources for soil-dwelling micro-organisms and commensals of the mammalian intestinal tract (Chauhan & Ogram, 2006; Conrad & Klose, 1999, 2000; Munoz-Elias & McKinney, 2006), but there have been few studies on the role of propionyl-CoA metabolism in pathogenic microbes. Several pathways of microbial propionate metabolism have been proposed (Horswill & Escalante-Semerena, 1999; Textor et al., 1997). Genes encoding the corresponding enzymes are found in diverse species, including some pathogenic bacteria and fungi (Horswill & Escalante-Semerena, 1999; Maerker et al., 2005; Munoz-Elias et al., 2006; Stone et al., 1999), suggesting that propionyl-CoA might be an important carbon/energy source during infection. However, propionate also possesses antifungal and antibacterial properties and propionate strongly inhibits growth of some micro-organisms, even in the presence of other carbon sources (Brock et al., 2000; Claes et al., 2002). In species that are well adapted to environments containing high levels of propionate, it is unclear whether the principal role of propionate metabolism is in carbon/energy metabolism or detoxification.
The methylcitrate cycle (Fig. 1a) is a major pathway of propionate metabolism that is widely distributed among bacteria and fungi (reviewed by Munoz-Elias & McKinney, 2006; Munoz-Elias et al., 2006). We reported previously that *M. tuberculosis* requires this pathway for propionate metabolism in *vitro*, despite encoding only two of three enzymes specific to the methylcitrate cycle, MCS (prpC) and MCD (prpD) (Munoz-Elias et al., 2006). *M. tuberculosis* lacks the final enzyme, MCL (prpB), and this activity is instead provided by two bifunctional ICL/MCL enzymes encoded by the *icl1* and *icl2* genes (Munoz-Elias et al., 2006). The bifunctional ICL1/ICL2 participate in both the glyoxylate cycle as ICL (Fig. 1b) and the methylcitrate cycle as MCL (Fig. 1a) and are therefore required for growth in *vitro* on either acetate or propionate, respectively (Gould et al., 2001; Munoz-Elias & McKinney, 2005; Munoz-Elias et al., 2006). At least one of these pathways appears to be essential for bacterial metabolism during infection because ICL1/ICL2 are jointly required for survival of *M. tuberculosis* in macrophages and mice (Munoz-Elias & McKinney, 2005). Selective disruption of the glyoxylate cycle could be accomplished by deletion of the *glcB* gene encoding MLS, which is not involved in the methylcitrate cycle. Selective disruption of the methylcitrate cycle by deletion of the prpDC locus paradoxically attenuates *M. tuberculosis* replication in macrophages but not in mice (Munoz-Elias et al., 2006), suggesting that loss of the methylcitrate cycle might be buffered by induction of another pathway for propionate metabolism when the bacteria are grown in *vivo*.

Several lines of evidence suggest that fatty acids might serve as an important source of carbon and energy for *M. tuberculosis* during infection (reviewed by Bosshoff & Barry, 2005; Munoz-Elias & McKinney, 2006), which could explain why ICL1/ICL2 are required for *in vivo* survival. However, recent studies on the mechanism of propionate toxicity in other micro-organisms (Brock & Buckel, 2004; Brock, 2005; Horswill et al., 2001) suggested the possibility that ICL1/ICL2 might also serve a critical role in the removal of potentially toxic propionate metabolites in *vivo*. Here, using *M. smegmatis*, a fast-growing relative of *M. tuberculosis*, we provide evidence that ICL/MCL activity is indeed required for removal of toxic methylcitrate cycle metabolites during growth on propionate-containing media, even in the presence of other carbon sources (such as glucose) that are metabolized by non-overlapping pathways. Unlike *M. tuberculosis* (Munoz-Elias et al., 2006), *M. smegmatis* apparently uses but does not absolutely require the methylcitrate cycle for growth on propionate-containing media, indicating the existence of an alternative pathway(s) for propionate metabolism in this species.

Among microbes that metabolize propionate via the methylcitrate cycle, *M. smegmatis* is so far unique in producing a monofunctional MCL (prpB) as well as bifunctional ICL/MCL (*icl1, icl2*). In other well-characterized species that operate both the glyoxylate and methylcitrate cycles, ICL and MCL activities are encoded by distinct genes with non-overlapping functions (Bramer & Steinbuchel, 2001; Brock et al., 2001; Brock, 2005; Claes et al., 2002; Horswill & Escalante-Semerena, 1999). The *M. smegmatis* prpB gene product contains the active site catalytic motif KRGC, which is characteristic of MCL (Brock et al., 2001), and this enzyme apparently cannot substitute for ICL1/ICL2 in the glyoxylate cycle (Ernesto Munoz-Elias and Lubomir Merkov, personal communication). In contrast, although the *M. smegmatis* icl1 and icl2 gene products contain the KK/QCGH motif previously associated only with monofunctional ICL (Brock et al., 2001), they appear to participate in both the glyoxylate cycle and the methylcitrate cycle, like their orthologues in *M. tuberculosis* (Munoz-Elias et al., 2006). The participation of mycobacterial ICL1/ICL2 in both pathways might reflect a unique ability of these enzymes to cleave isocitrate as well as methylisocitrate (Gould et al., 2006), or might instead reflect differential regulation of ICL expression in mycobacteria as compared to other species.

Also in contrast to some other microbes, which require the glyoxylate cycle (Fig. 1b) for carbon anaplerosis during propionate metabolism (Ashworth & Kornberg, 1964; Bramer & Steinbuchel, 2001; Wang et al., 2003; Wegener et al., 1969), we found that growth of *M. smegmatis* on propionate as the sole carbon source was not affected by deletion of *icl1* and *icl2*, in either the presence or absence of the methylcitrate cycle (see below), nor by deletion of the *glcB* gene encoding MLS (unpublished observations). Anaplerotic enzymes that might substitute for the glyoxylate cycle under these conditions include malic enzyme (mez; *msm5055*), pyruvate carboxylase (*eca; msm2412, msm6648*), or PEP synthase (*msm3934*) and PEP carboxylase (*msm3097*). Although ICL1/ICL2 were not required for growth of *M. smegmatis* on propionate as the sole carbon source, the upregulation of their activities under these conditions suggests that the glyoxylate cycle might be a preferred (but not essential) anaplerotic route in cells metabolizing propionate. The highest levels of ICL activity were observed in extracts from ΔprpDBC bacteria, suggesting the possibility of regulatory crosstalk between the *icl* and *prp* loci.

Unexpectedly, we found that deletion of the prpDBC locus reduced, but did not eliminate, growth of *M. smegmatis* on propionate as the sole carbon source. In contrast, *M. tuberculosis* absolutely requires the prpDC locus for growth on propionate-containing media (Munoz-Elias et al., 2006). These observations suggest that *M. smegmatis* possesses an alternative route(s) of propionate metabolism that is absent or less efficient in *M. tuberculosis*. Potential routes of propionate metabolism include the methylmalonyl-CoA pathway, which dominates propionyl-CoA metabolism in mammalian cells. The *M. smegmatis* genome contains orthologues of all of the genes specific to the methylmalonyl-CoA pathway, as does the *M. tuberculosis* genome (Cole et al., 1998; Fleischmann et al., 2002), and propionyl-CoA carboxylase, catalysing the first dedicated reaction in this pathway, has been demonstrated in cell-free
extracts from both species (Wheeler et al., 1992). Further work is required to determine whether the methylmalonyl-CoA pathway is responsible for growth of the M. smegmatis ΔprpDBC strain on propionate-containing media and, if so, why this pathway apparently cannot support growth of the M. tuberculosis ΔprpDC strain under these conditions. The delayed growth of ΔprpDC M. smegmatis after transfer to propionate-containing media might reflect the time required for induction of alternative metabolic pathways. Delayed growth was observed when ΔprpDBC bacteria were transferred to media containing propionate alone or a mixture of glucose plus propionate. In the latter case, glucose metabolism might be blocked by the accumulation of propionyl-CoA, which has been shown to inhibit pyruvate dehydrogenase in Aspergillus spp. (Brock & Buckel, 2004; Maerker et al., 2005) and Rhodobacter sphaeroides (Maruyama & Kitamura, 1985).

Paradoxically, we found that the residual growth of ΔprpDBC Δicl1 Δicl2 bacteria in media containing propionate, or a mixture of propionate plus glucose, was abolished by restoration of the prpDC genes. Growth inhibition of this strain by propionate was also dose-dependent, suggesting that the propionate metabolites generated by MCS/MCD are toxic in the absence of MCL activity. Substrate-dominant growth inhibition by propionate has also been observed in methylcitrate cycle mutants of A. nidulans (Brock, 2005) and S. typhimurium (Horswill et al., 2001), which accumulate MCS/MCD-generated propionate metabolites. Although the mechanism of growth inhibition by propionate metabolites is unknown, proposed molecular targets include isocitrate dehydrogenase, aconitase and citrate synthase (Brock, 2005; Cheema-Dhadli et al., 1975).

Our discovery that MCL activity is critical for detoxification of MCS/MCD-generated propionate metabolites in M. smegmatis calls for a re-evaluation of our earlier studies on propionate metabolism. Consistent with this interpretation, a recent analysis of cell wall-associated lipids in M. tuberculosis recovered from mouse lungs suggests that the bacteria accumulate high levels of propionyl-CoA during growth in this environment (Jain et al., 2007). This conclusion is also suggested by the marked increase in expression of the prpDC locus when M. tuberculosis is grown in macrophages or in the lungs of mice (Mattow et al., 2006; Schnappinger et al., 2003). These observations suggest that deletion of ICL1/ICL2 might result in growth inhibition due to accumulation of toxic MCS/MCD-generated propionate metabolites. If this hypothesis is correct, then deletion of prpDC should paradoxically relieve, in whole or in part, the in vivo requirement for ICL1/ICL2. In this context it is noteworthy that deletion of prpD alone might attenuate the growth of M. tuberculosis in mice (unpublished preliminary data cited in Mattow et al., 2006), whereas deletion of both prpC and prpD did not (Muñoz-Elias et al., 2006), suggesting that MCS-generated propionate metabolites might be growth inhibitory in the absence of MCD activity. In light of the new findings reported here, further studies are needed to clarify whether the essential function of M. tuberculosis ICL1/ICL2 during infection is attributable to their role in the glyoxylate cycle (fatty acid catabolism), the methylcitrate cycle (propionyl-CoA metabolism/detoxification), or both pathways.

ACKNOWLEDGEMENTS

The authors thank Ernesto Muñoz-Elias and Lubomir Merkov for generously providing the M. smegmatis Δicl1 Δicl2 strain and for communicating their unpublished results. This work was supported by National Institutes of Health Grant HL088906 (to J.D.M.).

REFERENCES


Complex with product and with isocitrate inhibitor provide insight into lyase substrate specificity, catalysis and evolution. Biochemistry 44, 2949–2962.


Edited by: G. S. Besra