Molecular cloning of a *Coxiella burnetii* gene encoding a macrophage infectivity potentiator (Mip) analogue

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The gene encoding a protein that reacted with antibodies specific for *Legionella pneumophila* macrophage infectivity potentiator (LpMip) was cloned from *Coxiella burnetii*, the obligate intracellular rickettsia that causes Q fever in humans. Nucleotide sequencing analysis revealed an ORF encoding a gene product of 230 amino acids with a molecular mass of 25.5 kDa and a predicted pI of 10.7. The predicted amino acid sequence from the ORF shows similarity with Mip/Mip-like proteins of *Legionella* (46%) and *Chlamydia* (30%). Moreover, like LpMip, the amino acid sequence of the C terminus of this protein has over 35% identity to prokaryotic and eukaryotic FK506-binding proteins (FKBPs) that belong to a superfamily of immunophilins and are peptidyl-prolyl cis-trans isomerases (PPIases). When overproduced in *Escherichia coli*, the *C. burnetii* protein also exhibited PPIase activity. Taken together, these results demonstrate that *C. burnetii* encodes a Mip analogue (CbMip). A putative leader peptide at the N terminus of CbMip was detected by computer analysis. Furthermore, *TnphoA* mutagenesis demonstrated that in *E. coli* CbMip was secreted. In view of the role of Mip/Mip-like proteins in the pathogenesis of *Legionella* and *Chlamydia*, CbMip may be a *C. burnetii* virulence factor.

Keywords: *Coxiella burnetii*, Mip, virulence factor

INTRODUCTION

*Coxiella burnetii* is an obligate intracellular bacterium that causes Q fever in humans (Baca & Paretsky, 1983). During the infectious process, *C. burnetii* is taken up by host cells into phagosomes which then fuse with primary lysosomes to form phagolysosomes. After several cycles of replication, the vacuoles become loaded with bacteria which are released into the extracellular environment upon bursting of the host cell. Formation of the phagolysosome is a critical step during infection because the acidic environment of the phagolysosome appears to activate the metabolism of *C. burnetii* (Hackstadt & Williams, 1981). Therefore, microbial biochemical factors that support initiation of infection or phagolysosomal survival can be considered to be important virulence factors. While several factors have been proposed to contribute to the virulence of *C. burnetii* (Baca et al., 1993; Heinzen et al., 1992; Hendrix et al., 1993), little is known about its mechanisms of uptake and survival in phagolysosomes.

As a group, intracellular bacteria have evolved strategies for invasion, intracellular survival and growth (Moulder, 1985) and consequently, they may have similar infection or survival mechanisms. Although *C. burnetii* is a phylogenetically distinct organism, a comparison of 16S ribosomal RNA sequences suggests that facultatively intracellular bacteria of the genus *Legionella* are most closely related to *C. burnetii* (Weisburg et al., 1989). Indeed, the organisms share similar intracellular growth compartments at least at the early stages of infection. In searching for virulence factors of *Legionella pneumophila*, Cianciotto et al. (1989) identified a gene encoding a 24 kDa surface protein involved in macrophage infection which they designated *mip* (macrophage infectivity potentiator). Since then *mip*-like genes have been cloned from other
intracellular bacteria, including *Chlamydia trachomatis*, and the gene products shown to possess amino acid sequence similarity to *Legionella pneumophila* Mip (Bangsborg et al., 1991; Cianciotto et al., 1990a; Fischer et al., 1992; Lundemose et al., 1992). Genetic data indicate that Mip plays an important role as a virulence factor in *L. pneumophila*, since mutations of the *mip* gene cause a reduction in intracellular infection (Cianciotto et al., 1990b, 1995a; Cianciotto & Fields, 1992).

Recently Mip/Mip-like proteins have been shown to belong to the FK506-binding protein (FKBP) family within the superfamily of immunophilins (see review by Hacker & Fischer, 1993). Although Mip/Mip-like proteins are large molecules (≥ 24 kDa) compared to eukaryotic FKBP's, the proteins share significant amino acid sequence similarity and are peptidyl-prolyl cis-trans isomerases (PPlases). PPlase, in free form, catalyses the slow conformational interconversion of peptidyl-prolyl bonds in oligopeptides and proteins (Fischer & Schmid, 1990), suggesting a function in protein folding and trafficking. To date a number of FKBP's have been characterized from different sources and all possess PPlase activity which is inhibited by the immunosuppressive drugs FK-506 and rapamycin (Etzkorn et al., 1993). While the actual function of the PPlase is not yet clear, the enzymic activity of Mip/Mip-like proteins appears to be related to the ability of the organisms to initiate infection. For instance, pretreatment of *Citrobacter kochii* with FK506 or rapamycin significantly reduces the infection of host cells in cell culture (Lundemose et al., 1993).

We have previously reported the possible occurrence of a Mip analogue in *C. burnetii* and other rickettsiae, including the genus *Rochalimaea*, based on DNA hybridization and immunoblotting data (Cianciotto et al., 1995b). In this paper we describe the cloning, nucleotide sequence and expression of the *C. burnetii* *mip* gene (*cbmip*). The identified *C. burnetii* Mip analogue (CbMip) represents a new member of the Mip/Mip-like protein family.

**METHODS**

**Bacterial strains, plasmids, media and growth conditions.** Bacterial isolates (*C. burnetii*, *Escherichia coli* and *L. pneumophila*) and plasmids used in this study are listed in Table 1. *E. coli* cultures were routinely maintained in Luria–Bertani (LB) medium at 37 °C; SOC medium (1° 20 g bacitracin–tryptone, 5 g bac-to-yeast extract, 0.5 g NaCl, 20 mM glucose; Ausubel et al., 1989) was used for growing *E. coli* strain Top10 (Invitrogen) carrying the *cbmip* gene on pTrcB expression vectors (Invitrogen). *L. pneumophila* was grown on buffered charcoal–yeast extract agar medium (Cianciotto et al., 1989) at 37 °C. *C. burnetii* was grown in embryonated yolk sacs and purified as previously described (Hendrix & Mallavia, 1984). When needed, antibiotics were incorporated into media at the following concentrations to maintain plasmids in *E. coli*: ampicillin, 100 μg ml⁻¹; kanamycin, 50 μg ml⁻¹ and tetracycline, 24 μg ml⁻¹.

**Screening of the *C. burnetii* genomic library.** Preparation of *L. pneumophila* Mip (LpMip)-specific polyclonal antibodies from rabbits has been described elsewhere (Cianciotto et al., 1990a). The LpMip-specific antibodies were used to screen a bacteriophage λZAPII (Stratagene) genomic DNA library of the *C. burnetii* Nine Mile isolate for clones expressing a Mip analogue. The *C. burnetii* genomic DNA library (Mo & Mallavia, 1994) was constructed with EcoRI-digested λZAPII arms. Bacteriophage λZAPII was mixed with *E. coli* strain XL1-Blue (Bullock et al., 1987) in LB containing 0.7% agar at ~ 500 viruses per plate and poured over a bottom layer of LB agar (1.5%). Plates were incubated for 4 h at 42 °C when plaques were just visible. Induction was done with IPTG (Gibco) by overlaying the plates with a nitrocellulose membrane (Schleicher & Schuell) impregnated with 10 mM IPTG and incubating for further 10 h at 37 °C. The membrane was analysed as for Western blotting (Ausubel et al., 1989) using LpMip-specific antibodies (see below). Once positive plaques were identified, secondary screening was conducted to obtain pure, positive clones which were excised in vivo in the presence of helper phage R408 (Russe l et al., 1986). Positive clones were verified by incubating *E. coli* harbouring an appropriate plasmid in LB broth supplemented with 1 mM IPTG at 37 °C overnight with shaking at 250 r.p.m. and analysing cell lysates by Western blotting using the LpMip-specific antibodies (see below).

**Recombinant DNA techniques.** A positive clone, pYMAl, isolated from the genomic library, contained a 5·3 kb EcoRI DNA fragment in pSK (Fig. 1). Physical mapping and subcloning showed that the putative *cbmip* gene was within a 1·7 kb EcoRI–Clal fragment of a pSK recombinant, designated pYMAl.1 (Fig. 1). pYMAl.1 was used as a DNA template for sequencing. Digestion of pYMAl.1 with HindIII and self- ligation resulted in pYMAl.4 which carried a DNA insert of 187 bp encompassing the upstream region of the *cbmip* gene and the coding region for the first 44 amino acids of the CbMip (Fig. 1). pYMAl.6 was constructed by ligating the cloned 1·7 kb EcoRI–Clai fragment of pYMAl.1 into pUC19 such that the *cbmip* gene was in the opposite orientation to the lac promoter on the vector. Deletion of the 1·7 kb EcoRI–Clai fragment of pYMAl.1 and religation resulted in pYMAl.10. To overproduce the CbMip protein, plasmids pYMAl.14-1 and pYMAl.14-2 were constructed. A 694 bp DNA fragment (nucleotides 65–759, see Results, Fig. 3a) was first amplified from pYMAl.1 by PCR using a primer pair A1-R1 (5' GAAACGTTTACCCAGGAATCTGATCTG). The product was separated on a 1·5% agarose gel, purified using GeneClean kit II (Biorad) and cloned into pCR-Blunt (Invitrogen). *E. coli* strain INVaF’ (Invitrogen) carrying recombinant plasmids were identified as white colonies on ampicillin-containing LB agar plates supplemented with X-Gal. An insert of the recombinant plasmid was excised by digestion with EcoRI and the fragment ligated into EcoRI-digested pTrcB previously treated with shrimp alkaline phosphatase (Amersham). Insert orientation was determined by restriction mapping. The plasmid, pYMAl.14-1, had the *cbmip* gene fused in-frame with the sequence encoding the leader peptide of the vector derived from bacteriophage T7 gene 10 and gene expression was controlled by the IPTG-inducible trc promoter on pTrcB. pYMAl.14-2 contained the same DNA fragment in pTrcB, but in an opposite orientation. Using the same strategy, a 582 bp DNA fragment amplified using primers A1-R1 (5' GAAACGTTTACCCAGGAATCTGATCTG) and cloned into pCR-Blunt (Invitrogen). pYMAl.14-2 contained the same DNA fragment in pTrcB, but in an opposite orientation. Using the same strategy, a 582 bp DNA fragment amplified using primers A1-R1 (5' GAAACGTTTACCCAGGAATCTGATCTG) and cloned into pCR-Blunt (Invitrogen). pYMAl.14-2 contained the same DNA fragment in pTrcB, but in an opposite orientation. Using the same strategy, a 582 bp DNA fragment amplified using primers A1-R1 (5' GAAACGTTTACCCAGGAATCTGATCTG) and cloned into pCR-Blunt (Invitrogen). pYMAl.14-2 contained the same DNA fragment in pTrcB, but in an opposite orientation. Using the same strategy, a 582 bp DNA fragment amplified using primers A1-R1 (5' GAAACGTTTACCCAGGAATCTGATCTG) and cloned into pCR-Blunt (Invitrogen). pYMAl.14-2 contained the same DNA fragment in pTrcB, but in an opposite orientation. Using the same strategy, a 582 bp DNA fragment amplified using primers A1-R1 (5' GAAACGTTTACCCAGGAATCTGATCTG) and cloned into pCR-Blunt (Invitrogen).
**Table 1. Bacterial strains and plasmids**

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Relevant characteristics</th>
<th>Source or reference</th>
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<tr>
<td><strong>E. coli</strong></td>
<td></td>
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<tr>
<td>XL1-blue</td>
<td>endA1 hisR17 ((t_b^e) m&lt;sub&gt;b&lt;/sub&gt;) supE44 thi-1 recA gyrA96 relA (lac') [F' proAB&lt;sup&gt;s&lt;/sup&gt; lacZAM15 Tn10(Tc&lt;sup&gt;46&lt;/sup&gt;)]</td>
<td>Stratagene</td>
</tr>
<tr>
<td>INVaF&lt;sup&gt;+&lt;/sup&gt;</td>
<td>endA1 hisR17 ((t_b^e) m&lt;sub&gt;b&lt;/sub&gt;) supE44 thi-1 recA gyrA96 relA [(80) lacZAM15 (\Delta) (lacZYA-argF) U169 deo R']</td>
<td>Invitrogen</td>
</tr>
<tr>
<td>Top10</td>
<td>mer.A (\Delta) mrr- (\Delta) rpsL (\Delta) rpsI (\Delta) rpsK (\Delta) rpsL (\Delta) rpsI (\Delta) rpsK</td>
<td>Invitrogen</td>
</tr>
<tr>
<td>CC118</td>
<td>araD139 (\Delta) (ara len)7697 (\Delta) lacX74 dox recA1 araD139 (\Delta) (ara len)7697 galU galK rpsL recA1 napG</td>
<td>Manoil &amp; Beckwith   (1985)</td>
</tr>
<tr>
<td><strong>L. pneumophila</strong></td>
<td></td>
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<tr>
<td>130b</td>
<td>Clinical isolate (Wadsworth strain) (mip^e)</td>
<td>Cianciotto et al.   (1989)</td>
</tr>
<tr>
<td><strong>C. burnetii</strong></td>
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<td>Nine Mile</td>
<td>Acute disease isolate plasmid QpHI</td>
<td>Samuel et al.       (1985)</td>
</tr>
<tr>
<td>K</td>
<td>Chronic disease isolate plasmid QpRS</td>
<td>Samuel et al.       (1985)</td>
</tr>
<tr>
<td>Priscilla</td>
<td>Goat abortion isolate plasmid QpRS</td>
<td>Samuel et al.       (1985)</td>
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<td>S</td>
<td>Chronic disease isolate, plasmid-less</td>
<td>Samuel et al.       (1985)</td>
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<td><strong>Plasmid</strong></td>
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<td>pUC19</td>
<td>Ap&lt;sup&gt;+&lt;/sup&gt; cloning vector</td>
<td>BRL</td>
</tr>
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<td>Ap&lt;sup&gt;+&lt;/sup&gt; cloning vector</td>
<td>Stratagene</td>
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<td>Ap&lt;sup&gt;+&lt;/sup&gt; Km&lt;sup&gt;+&lt;/sup&gt; PCR cloning vector</td>
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<tr>
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<td>Ap&lt;sup&gt;+&lt;/sup&gt; expression vector</td>
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<td>pYMA1</td>
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<td>This study</td>
</tr>
<tr>
<td>pYMA1.1</td>
<td>pSK carrying (cbmip) on a 1.7 kb ClaiI-EcoRI fragment</td>
<td>This study</td>
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<tr>
<td>pYMA1.4</td>
<td>pSK carrying 187 bp containing the upstream region and the region encoding the first 44 amino acids of the (cbmip) gene product</td>
<td>This study</td>
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<tr>
<td>pYMA1.6</td>
<td>pUC19 carrying same (cbmip) as pYMA1.1 but opposite in orientation to lac promoter</td>
<td>This study</td>
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<td>pYMA1.10</td>
<td>pSK carrying a 3.6 kb partially digested (ClaiI-EcoRI) fragment from pYMA1</td>
<td>This study</td>
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<td>pYMA1.14-1</td>
<td>pTrcB carrying (cbmip) in frame</td>
<td>This study</td>
</tr>
<tr>
<td>pYMA1.14-2</td>
<td>Same as pYMA1.14-1 except opposite orientation</td>
<td>This study</td>
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<tr>
<td>pYMA1.35-1</td>
<td>pTrcC carrying (cbmip) missing the coding sequence for the 39 amino acids at the N terminus of the gene product</td>
<td>This study</td>
</tr>
<tr>
<td>pYMA1.201</td>
<td>(cbmip::TnphoA) in pYMA1.6</td>
<td>This study</td>
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\(TnphoA\) mutagenesis (Manoil & Beckwith, 1985). \(E. coli\) strain CC118 (\(PhoA^-\)) was first transformed with pYMA1.6 and then transfected with \(\lambda::TnphoA\). Potential \(cbmip::TnphoA\) fusions were selected on ampicillin-containing LB agar plates supplemented with 5-bromo-4-chloro-3-indolyl-phosphate (X-P) and identified by physical mapping of the plasmids (pYMA1.201). When necessary, the fine structure of \(TnphoA\) inserts in the target plasmid was determined by nucleotide sequencing using the primer (5' CCGGTTTTTCCAGAACCAG) complementary to the DNA sequence of the 5' end of the \(phoA\) gene (Manoil & Beckwith, 1985).

**DNA sequencing, sequence analysis and protein sequencing.** Nucleotide sequences were determined by the method of Sanger et al. (1977) using Sequenase version 2.0 (Amersham). In addition to M13 universal and reverse primers (Yanisch-Perron et al., 1985), the following customized sequencing primers were used: A1-R0 (see above), A1-R1 (see above), A1-R2 (5' AAGTCACCGTTAATTAC), A1-U1 (see above) and A1-U2 (1985).
(5' GCCCTGCAAGACTTTTGTA) (Ransom Hill Bioscience). The DNA sequence and deduced amino acid sequence data were analysed using the GCG Sequence Analysis package (Deveraux et al., 1984). Protein sequencing of the N terminus of CbMip was carried out by the Biochemistry Bioanalysis service at Washington State University.

PCR amplification. All PCR was carried out in a DNA Thermocycler (Perkin–Elmer) using a GenAmp kit (Perkin–Elmer). The PCR reaction contained 200 μM of each nucleotide dATP, dGTP, dTTP and dCTP, 1 pM each of primers, 50 mM KCl, 10 mM Tris/HCl (pH 8.3), 1.75 mM MgCl₂, 1 ng genomic DNA ml⁻¹ or 10 pg plasmid DNA ml⁻¹ as a template and 2.5 units Taq DNA polymerase per 100 μl solution. The amplification protocol consisted of 30 cycles of 0.5 min at 94°C, 1 min at 42°C and 0.5–1 min at 72°C. PCR products were separated in a 1.5% agarose gel and purified using GeneClean Kit II.

Primers A1-R1 and A1-U1 were used for amplifying the cbmip gene from various C. burnetii isolates. Immunological detection of CbMip by LpMip-specific antibodies. E. coli strain XL1-blue carrying an appropriate plasmid was incubated in LB broth with ampicillin and 1 mM IPTG at 37°C overnight, pelletted and lysed in 1 x Laemmli buffer (Laemmli, 1970). For isolation of L. pneumophila proteins, strain 130b was grown on buffered charcoal–yeast extract agar medium (Cianciotto et al., 1989) for 3 d at 37°C. The bacteria were soaked with 4 ml PBS per plate for 2 h at room temperature (RT), collected, centrifuged and suspended in 1 x Laemmli buffer. After separation by SDS-PAGE (15% separation gel), the proteins were transferred to a nitrocellulose membrane in transfer buffer (Ausubel et al., 1989) for 2 h at 250 mA. Immunological reactions and washes were conducted at 26°C with gentle shaking. The membrane was soaked in blocking solution [9.5% (w/v) powdered milk in 20 mM Tris/HCl, pH 7.4, 0.87% (w/v) NaCl (TBS)] for 1 h and washed in 0.05% Tween 20 in TBS (TBST). Proteins were reacted with LpMip-specific antibodies (1:1000) in blocking solution for at least 1 h. After three washes with TBST, horseradish-peroxidase-conjugated goat anti-rabbit antibodies (Sigma) diluted 1:1000 were added, incubated for 1 h, washed and signals visualized by adding a 4-chloro-1-naphthol solution containing 0.03% (w/v) hydrogen peroxide in TBS.

In vitro transcription and translation of the cbmip gene. To express the cbmip gene, plasmids were purified by CsCl gradient centrifugation and transcribed and translated in vitro using an E. coli extract (Promega). Proteins were labelled with [³⁵S]methionine (DuPont NEN) and separated by SDS-PAGE (15%) using a standard protocol (Ausubel et al., 1989). The gel was dried and exposed to X-ray film.

Overexpression and purification of CbMip protein. Bacterial cells (E. coli strain Top10) carrying pYMA1.14–1 were grown in 5 ml SOC containing ampicillin at 37°C at 300 r.p.m. to an OD of ~0.6, and induced with 1 mM IPTG. At each time point after induction, a 0.5 ml sample was taken, pelleted and suspended in 1 x Laemmli buffer. To examine the solubility of the overproduced protein, 50 ml of the induced cell culture was harvested and resuspended in 10 ml 20 mM sodium phosphate buffer (pH 7.0) containing 500 mM NaCl, and sonicated for a total of 2 min. Bacterial cell debris was separated from soluble proteins by centrifugation at 9000 g for 15 min and the pellet resuspended in 10 ml 0.5% Triton X-100 containing 10 mM EDTA to solubilize membrane proteins. The Triton-containing suspension was further centrifuged under the same conditions to separate Triton-soluble and -insoluble proteins. As a control, the plasmid carrying cbmip in the opposite orientation to the trc promoter of pTrcB (pYMA1.14–2) was subjected to the same process. Protein samples were resolved by SDS-PAGE (15%) and stained with Coomassie Brilliant Blue G-250 (Neuhoff et al., 1985).

Attempts to purify the recombinant protein using a nickel-containing column (Invitrogen) were unsuccessful since the recombinant CbMip protein appeared to be processed. Consequently, gel filtration and ion exchange chromatography were employed (Reiland, 1970). Total protein extracts containing CbMip were passed through a Bio-Gel P10 column (Bio-Rad). Major fractions containing CbMip, as determined by SDS-PAGE, were pooled and further purified by loading partially purified CbMip on a CM-Sepahex C25 (Sigma) column equilibrated with 10 mM sodium phosphate buffer (pH 7.0). CbMip was eluted with a linear gradient of 10 mM sodium phosphate buffer containing 0–0.5 M NaCl (pH 7.0) at 4°C and monitored by absorbance at 280 nm. The major peak containing CbMip eluted at ~0.15 M NaCl.

Enzyme assay. The assay for PPIase activity of CbMip was conducted using the method of Kofron et al. (1991). In brief, purified CbMip protein at concentrations of 0, 0.03, 0.06, 0.12, 0.3, 0.6, 0.9 and 1.2 μM was incubated in 1 ml 35 mM HEPES buffer (pH 7.8) containing 0.25 mg ml⁻¹ α-chymotrypsin at 0°C; the reaction was initiated by adding 10 μl succinyl-Ala-Phe-Pro-Phe-p-nitroanilide (Bachem). Activity of PPIase was calculated according to Harrison & Stein (1990). Inhibition assays at 100 nM CbMip were carried out under the same conditions in the presence of various concentrations of rapamycin (Wyeth-Ayerst) dissolved in absolute ethanol. The colour change resulting from hydrolysis of the substrate was monitored at 590 nm.

RESULTS

Isolation of clones containing the cbmip gene

Approximately 2500 plaques were screened by LpMip-specific antibodies and three were positive. After in vivo excision, plasmid DNAs were analysed by physical mapping. All three clones contained the same 5.3 kb EcoRI DNA fragment and the plasmid was designated
was a putative ribosome-binding site (RBS), AGGAGA. It was a potential termination signal similar to those in the ribosome-binding site of E. coli (Doolittle, 1982). At the 3' end of this sequence there was a D-loop structure with a free energy of -41.5. Hydrophobicity analysis (Kyte & Doolittle, 1982) suggested that except for the 21 amino acid leader peptide (Fig. 3a), the protein was highly hydrophilic. Codon usage of the cbmip gene was biased compared to highly expressed E. coli proteins but within the range of most C. burnetii proteins (Hoover & Vodkin, 1991).

### Amino acid sequence identity and similarity between CbMip and Mip/Mip-like proteins of Legionella and Chlamydia as well as FKBP

When the deduced amino acid sequence of the ORF was compared to that of Mip of L. pneumophila (LpMip), an overall 46% identity was detected by the GAP program (Fig. 3b). The two proteins exhibit no gap in the alignment of their entire sequences and the molecular masses of the proteins are very close. Sequence identity of CbMip with the larger, 27 kDa, Chlamydia trachomatis Mip-like protein (CtMip) was lower (30% identity). Furthermore, a search of protein databases using the FASTA program revealed amino acid sequence conservation of the C terminus of this ORF with respect to those of prokaryotic and eukaryotic FKBP (Mozier et al., 1990; Standaert et al., 1990; Nelson et al., 1991; Pahl & Keller, 1992; Sampson & Gotchlich, 1992). For instance, the 140 amino acids of CbMip at the C-terminal region shared >35% identity to FKBP from a variety of sources (data not shown). Computer analysis using the MOTIFS program showed that, with very few exceptions, all Mip/Mip-like proteins and FKBP had two signature patterns: (1), 12-13 amino acids at the N terminus of FKBP, (L,I,V,M,C)XYXGX(L,F)X[2,3]GXF (where amino acids in parentheses means any one of the amino acids may be present and X[2,3] means that any 2 or 3 amino acids may be present); and (2), 17-18 amino acids at the C terminus of FKBP, (A,G)YGX[2](S,A,G,R)X[2,3] (G,P)XIX[5]L(L,V,F). CbMip had an identical pattern at amino acids 153-166, VNYEGRLINGTVFD, and amino acids 208-226, AYGEQGAPGVIGPNEALIF (Fig. 3b). Among the amino acids that form the signature patterns, four were shown to be involved in binding to FK506 (Hacker & Fischer, 1993), indicative of functional conservation. In LpMip, Asp-162 was shown by site-directed mutagenesis (Ludwig et al., 1993), indicative of functional conservation. In LpMip, Asp-162 was shown by site-directed mutagenesis (Ludwig et al., 1993), indicative of functional conservation.

### Expression of cbmip by E. coli

To examine whether the cbmip promoter was functional in E. coli, plasmids containing the cbmip gene in either orientation relative to the lac promoter of the vector were transcribed in vitro and translated (IVTT) using an E. coli extract. The IVTT data suggested that the cbmip gene had its own promoter within the 1.7 EcoRI–ClaI fragment because a protein was still produced with the pUC19 (pYMA1.6) (data not shown).

The cbmip gene was overexpressed in E. coli (pYMA1.14-1)
Fig. 3. DNA sequence and deduced amino acid sequence of the cbmip gene (a) and sequence comparison (b). (a) The potential promoter region (−10 and −35) is underlined and the potential RBS is bold. The dyad symmetry sequence at the 3' end of the gene is indicated by opposite arrows. The arrow pointing down shows the putative leader sequence.
Fig. 4. Overexpression and purification of CbMip protein. Bacterial cultures were harvested 2 h after induction with 1 mM IPTG. Proteins were resolved by SDS-PAGE (15%) and stained with Coomassie Brilliant Blue. Lanes: M, protein markers with molecular mass indicated on the left in kDa; 1 and 2, whole cell lysates of E. coli harbouring pYMA1.14-2 and pYMA1.14-1, respectively; 3, 1 µg purified CbMip protein.

(Fig. 4). The expression was detected 1 h after induction and reached maximal levels at 3 h after induction. In contrast, when the cbmip gene in pYMA1.14-2 (same as pYMA1.14-1, but in opposite orientation) was overexpressed in E. coli, no band corresponding to CbMip was apparent. After separation by successive gel-filtration and ion-exchange chromatography, a protein band with a molecular mass of 24 kDa was obtained (Fig. 4). Western blotting analysis using LpMip-specific antibodies confirmed that this protein was CbMip (Fig. 2, lane 5). The overproduced CbMip protein was soluble as it was purified from the supernatant fraction of cell extracts.

PPIase activity of the recombinant CbMip

The purified CbMip exhibited PPIase activity (Fig. 5a), comparable to that reported for other FKBP (Sampson & Gotchlich, 1992; Standaert et al., 1990). A consistently higher level of activity was observed using CbMip which had been affinity-purified from all extracts containing pYMA1.35-1, providing additional evidence that the PPIase activity was due to CbMip (data not shown). Enzymic activity was inhibited by the immunosuppressive drug, rapamycin. Less than 20% relative activity, compared to that in the absence of rapamycin, remained when the drug concentration was 500 nM (Fig. 5b).

Processing of the CbMip precursor and possible export of CbMip in E. coli

A potential N-terminal signal peptide of CbMip was identified by computer analysis of the DNA-deduced amino acid sequence and the cleavage site predicted to be

Fig. 5. PPIase activity of CbMip. (a) PPIase activity at various concentrations of CbMip. (b). Inhibition of PPIase activity of CbMip (100 nM) by rapamycin. The relative activity is calculated by comparing the enzymic activity in the absence or presence of rapamycin (Wyeth–Ayerst). One-hundred percent activity ($K_{	ext{cat}}$) of 100 nM CbMip is 0.092 s⁻¹. Data shown in the figure are from three experiments with SE ≤ 0.02.

(2867)
between amino acids Ala and Ala at positions 21 and 22 (Fig. 3a). N-terminal amino acid sequencing of CbMip confirmed this prediction. The first seven amino acids of CbMip purified from lysates of cells carrying pYMA1.14-1 was determined to be ATPLKTE. This confirmed this prediction. The first seven amino acids of CbMip suggested secretion of the protein. Furthermore, the size of recombinant CbMip matched with that of LpMip (Fig. 1), suggesting that CbMip was processed to generate a mature protein. To further examine its possible surface export, CbMip was expressed in E. coli, and detected by Western blotting was likely an exported, mature protein.

DISCUSSION

In this study a mip analogue was cloned from C. burnetii and its nucleotide sequence determined. The predicted amino acid sequence of the gene product was shown to have a high degree of identity and similarity to those of L. pneumophila and Chl. trachomatis Mip/Mip-like proteins. Mip/Mip-like proteins belong to the prokaryotic and eukaryotic FKBP family based on their amino acid sequence similarities and PPIase activity (Hacker & Fischer, 1993). The prokaryotic FKBP families appear to fall into two categories. The larger (≥ 24 kDa) FKBP-like proteins or Mip/Mip-like proteins of L. pneumophila and Chl. trachomatis are membrane-associated and/or secreted, while those present in bacteria generally not considered to be intracellular pathogens are smaller (≤ 12 kDa) and appear to be cytosolic proteins (Sampson & Gotchlich, 1992). A possible exception to this general finding is a report that E. coli encodes a 28849 Da FKBP-like protein with 28–34 % identity to known Mip-like proteins (Horne & Young, 1994). By PCR amplification we also demonstrated that the cbmip gene was present in all C. burnetii isolates tested, including isolates from cases of acute and chronic Q fever. Mip/Mip-like proteins have been shown to be important for L. pneumophila and Chl. trachomatis infections (Cianciotto et al., 1990b, 1995a; Cianciotto & Fields, 1992; Lundemose et al., 1992). With its high sequence similarity and similar enzyme activity to Mip/Mip-like proteins, CbMip may be a C. burnetii virulence factor.

Mip/Mip-like proteins (≥ 24 kDa) have been identified in at least three intracellular bacterial pathogens, i.e. L. pneumophila, Chl. trachomatis and C. burnetii. Whether these organisms adopt a similar mechanism of resistance to host killing is not clear, but following entry into the host cell, they grow in different cellular compartments (Weiss et al., 1991). For instance, both L. pneumophila and Chl. trachomatis reside in a phagosome, while acidification of the phagosome by lysosomal fusion is a necessary event that initiates active metabolism and proliferation of C. burnetii (Hackstadt & Williams, 1981). In contrast, these organisms have developed similar strategies for the early steps of infection, in which Mip proteins may play a central role. Indeed, LpMip and CrMip have both been
shown to affect some earlier stage of host–parasite interaction of *L. pneumophila* and *Cbl. trachomatis*. Unfortunately, the early steps of *C. burnetii* host interaction are not clear due to a lack of information on cell-surface recognition, attachment and entry processes. For example, it is still not known whether *C. burnetii* is passively phagocytosed into host cells or whether factors from the pathogen are involved (Baca & Paresky, 1983; Williams et al., 1989).

Because of its exposure to the cell surface, LpMip was shown to be involved in interaction with host cells (Engleberg *et al.*, 1989). ChMip appears to be processed to a mature protein by cleavage of the signal peptide, as demonstrated by N-terminal amino acid sequencing. Moreover, TnpbA mutagenesis suggests that ChMip is an exported protein in *E. coli*. Whether ChMip is actually secreted by *C. burnetii* is currently being investigated. Of interest is the recent observation that viable *C. burnetii* cells incubated in host-cell-free medium at low pH rapidly synthesize and export several proteins, one of which is similar in molecular mass to ChMip (Redd & Thompson, 1995). The synthesis and secretion of proteins by *C. burnetii* subjected to low pH (*in vitro*) suggests that this might occur as the organism is being taken in by endocytosis. If ChMip is secreted, one could speculate that it would interact with host components both during uptake and intracellular growth. Identification of ChMip would appear to support the argument that infection of host cells by *C. burnetii* is an active process, in that it requires the presence of specific virulence components.

While the significance of the observation is not known, it is worth noting that ChMip, like LpMip, is a very basic protein. Predicted pls for LpMip and ChMip are 9.8 (Engleberg *et al.*, 1989) and 10.7, respectively. It will be interesting to see if the basic nature of these secreted proteins is related to a common feature of their different intracellular niches.

Although Mip/Mip-like proteins have been studied in great detail (Hacker & Fischer, 1993), how they function during host–parasite interaction is still unknown. The recent finding of significant homology to FKBP genes provides some clues as to the physiological function of Mip-related proteins. FKBP genes exhibit PPIase activity which may mediate folding of proteins (Fischer & Schmid, 1990; Tropschug *et al.*, 1990). The enzymic activity of both Mip-related proteins and FKBP genes is inhibited by binding to FK506 or rapamycin (Fretz *et al.*, 1991), but the direct target for FK506 has been shown to be calcineurin (Fruman *et al.*, 1992; O'Keefe *et al.*, 1992), a calcium- and calmodulin-dependent phosphatase that is required for the activation of the cytoplasmic nuclear factor of activated T cells. It will be interesting to see whether impairing host FKBP function leads to facilitated uptake by host macrophages or the intracellular survival of the parasite. Given the potential secretory feature of Mip/Mip-like proteins, one cannot exclude the possibility that such proteins are able to bind to the natural ligand of host FKBP, thus deregulating the host immune system.

**ACKNOWLEDGEMENTS**

The software cited is part of the VADMS® Center, a campus-wide computer resource at Washington State University. This work was supported by grant AI20190 from the National Institutes of Health (NIAID).

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Received 14 March 1995; revised 26 June 1995; accepted 10 July 1995.