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Research Article

Proteome analysis of the plasma membrane of Mycobacterium tuberculosis

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Abstract

The plasma membrane of Mycobacterium tuberculosis is likely to contain proteins that could serve as novel drug targets, diagnostic probes or even components of a vaccine against tuberculosis. With this in mind, we have undertaken proteome analysis of the membrane of M. tuberculosis H37Rv. Isolated membrane vesicles were extracted with either a detergent (Triton X114) or an alkaline buffer (carbonate) following two of the protocols recommended for membrane protein enrichment. Proteins were resolved by 2D-GE using immobilized pH gradient (IPG) strips, and identified by peptide mass mapping utilizing the M. tuberculosis genome database. The two extraction procedures yielded patterns with minimal overlap. Only two proteins, both HSPs, showed a common presence. MALDI–MS analysis of 61 spots led to the identification of 32 proteins, 17 of which were new to the M. tuberculosis proteome database.

We classified 19 of the identified proteins as ‘membrane-associated’; 14 of these were further classified as ‘membrane-bound’, three of which were lipoproteins. The remaining proteins included four heat-shock proteins and several enzymes involved in energy or lipid metabolism. Extraction with Triton X114 was found to be more effective than carbonate for detecting ‘putative’ M. tuberculosis membrane proteins. The protocol was also found to be suitable for comparing BCG and M. tuberculosis membranes, identifying ESAT-6 as being expressed selectively in M. tuberculosis. While this study demonstrates for the first time some of the membrane proteins of M. tuberculosis, it also underscores the problems associated with proteomic analysis of a complex membrane such as that of a mycobacterium. Copyright © 2002 John Wiley & Sons, Ltd.

Keywords: genome; proteome; Mycobacterium tuberculosis; membrane; peptide mass mapping

Introduction

A third of the world’s population is considered to be infected with Mycobacterium tuberculosis, which leads to nearly 8 million new patients and 3 million deaths due to tuberculosis every year. Multi-drug-resistant strains of the pathogen, emerging in association with HIV, have added a frightening dimension to the problem (Raviglione et al., 1995; Snider and Castro, 1998). It has long been realized that successful tuberculosis control strategies would evolve from exploring and exploiting the biology of M. tuberculosis (Young and Duncan, 1995; Cole et al., 1998). Identification and characterization of subcellular proteins of the microbe is important to understanding their function, especially where the genomic data is not predictive or, quite often, not even suggestive (Domenech et al., 2001; Jungblut et al., 2001). Covalent modifications to amino acid sequences can occur co- or post-translationally, and neither event is dictated, at least not in a manner that is fully understood, by the nucleotide sequences of genes (Jensen, 2000). Other types of processing events, such as
proteolytic cleavage, may need to occur before a protein is rendered fully functional. Furthermore, proteins can function as multimeric complexes, hence identifying the interacting partners involved in these complexes is essential to understanding biological processes. Consequently, a systematic and comprehensive study of the proteins of the pathogen is required in the quest for novel drug targets, diagnostic probes or vaccines (Monahan et al., 2001; Covert et al., 2001; Betts et al., 2000; Rosenkranz et al., 2000a,b). Proteome analysis, involving a combination of 2D electrophoresis, mass spectrometry, and bioinformatics, has now emerged as a robust and efficient strategy for rapid identification of proteins (Jungblut et al., 1999).

The prokaryotic cell membrane is rich in proteins comprising several essential enzymes, receptors and transporters (Brennan and Nikaido, 1995; Sigler and Hofer, 1997). Being lipid in nature, it also provides a hydrophobic environment for certain biochemical reactions. Immunogenicity of membrane proteins, as reported with certain pathogens, has been attributed to their inherent hydrophobicity and lipid modification (Deres et al., 1989; Akins et al., 1993; Frankenburg et al., 1996). Bioinformatic analysis of the Mycobacterium tuberculosis genome predicts >65 lipoproteins of ‘cell envelope’ origin, some of which were identified previously as ‘secreted’ proteins, or enzymes involved in cell wall biogenesis. Besides these, there are 17 conserved MmpL and MmpS proteins, and >600 other ‘putative’ membrane proteins. The latter differ in the number of transmembrane hydrophobic segments, and include proteins belonging to the major facilitator and ATP-binding cassette (ABC) superfamilies (Tekiaia et al., 1999). These proteins undoubtedly play a role in the uptake and effects of various metabolites, peptides, drugs and antibiotics. Nonetheless, the real location, expression patterns and function of most of these proteins remain unexplored (Young and Garbe, 1991; Lee et al., 1992).

The aim of our study is to characterize mycobacterial membrane proteins. Upon extraction with Triton X114 (Bordier, 1981), they partition into detergent- and water-rich phases, the former being classified as ‘integral’ and the latter as ‘peripheral’ membrane proteins (IMP and PMP; Mehrotra et al., 1999). In both BCG (Mehrotra et al., 1999) and Mycobacterium tuberculosis H37Rv (unpublished) the IMP pool was found to contain, besides a range of unidentified proteins, three of the known ‘immunodominant’ ones: the 19 and 38 kDa lipoproteins and the 33/36 kDa ‘proline-rich’ protein. Similarly, both the PMP pools showed the presence of the 16 kDa α-crystallin heat-shock protein. Of particular interest are the results of human T cell proliferation assays, which showed a significantly higher T cell activating potency of IMP over PMP or cytosol. These results focused our attention on IMP and we applied a protocol based on ‘continuous-elution SDS–PAGE’ for purification of its constituents (Mehrotra et al., 1997). Purified fractions were compared in human T cell proliferation assays, which revealed a greater T cell stimulatory potency of certain low molecular weight IMPs than the others (Mehrotra et al., 1999).

There is thus enough evidence to suggest that identification of Mycobacterium tuberculosis membrane proteins, and monitoring changes in their expression profiles under relevant conditions of growth, would be of considerable importance for designing novel and effective interventions against tuberculosis. However, despite some recent progress in this direction (Molloy et al., 2000), proteome analysis of the cell membrane remains a challenge, due mainly to problems encountered during the resolution of membrane-associated proteins by the available 2D electrophoresis protocols (Santoni et al., 2000). In this paper we describe the results of our proteomic analysis of the membrane of Mycobacterium tuberculosis H37Rv using 2D electrophoresis and peptide mass mapping. Proteins for this purpose were obtained by extraction of membrane vesicles with either Triton X114 or carbonate (Fujiki et al., 1982). We have also tried to ascertain the suitability of the protocols used for proteomic comparisons between mycobacterial membranes.

Materials and methods

Isolation and fractionation of mycobacterial cell membranes

The membranes of Mycobacterium tuberculosis H37Rv and Mycobacterium bovis BCG (Pasteur) were isolated as described previously (Mehrotra et al., 1995; Mehrotra et al., 1999). In brief, 3–4 week old bacterial cultures (in Lowenstein–Jensen medium) were harvested and probe-sonicated in a buffer containing protease inhibitors (50 mM Tris, 10 mM MgCl₂, 1 mM EGTA, 1 mM PMSF, 0.02% NaN₃, pH 7.4). The sonicates were centrifuged, initially at 23,000 × g
to remove cell wall debris and later at 150 000 × g to obtain the membrane sediment. The sediment was resuspended in sonication buffer and membrane vesicles were morphologically characterized by transmission electron microscopy (Mehrotra et al., 1995). Proteins from washed vesicles were extracted using either of the following protocols. In the first protocol, the membrane sediment was resuspended in sonication buffer at a concentration of 10 mg protein/ml, to which precondensed Triton X114 (Bordier, 1981) was added, at a final concentration of 2%. The suspension was then stirred (1 h, 4°C) to obtain the extract in a single phase. Residual insoluble matter was removed by centrifugation at 150 000 × g and the phases were allowed to separate at 37°C in a water bath. The upper (aqueous) and lower (detergent) phases were collected by centrifugation (1000 × g) and ‘back-washed’ three times. Protein in the pooled detergent phase was recovered by precipitation with 5 volumes of chilled acetone. Dried sediment was resuspended in distilled water and stored as lyophilized aliquots. In the second protocol, membrane components were extracted with carbonate using the recommended procedure (Fujiki et al., 1982). In brief, the membrane pellet was suspended in 100 mM sodium carbonate (pH 11.5) to give a final protein concentration of 1 mg/ml. It was stirred for 30 min at 4°C and centrifuged at 150 000 × g for 1 h at 4°C. Sediment (membrane ‘stripped’ of the peripheral proteins) was resuspended in distilled water and stored in lyophilized aliquots. All protein estimations were done by the modified Lowry method (Markwell et al., 1978).

Two-dimensional polyacrylamide gel electrophoresis (2D-PAGE)

A solubilization buffer (7 M urea, 2 M thiourea, 4% CHAPS, 0.3% DTT, 2% carrier ampholytes 3–10 and 40 mM Tris, pH 9.6) recommended for iso-electric focusing (IEF) of membrane proteins (Friso and Wikstrom, 1999) was used. 1 mg lyophilized protein was solubilized in 500 µl this buffer by vortexing (30 min). This was followed by centrifugation (12 000 rpm × 10 min) to remove the insoluble matter. 150 µl (~300 µg protein) or 450 µl (~900 µg protein) clear supernatant was applied, respectively, to immobilized pH gradient (IPG) strips of 7 cm or 17 cm length (Bio-Rad), using the method of ‘in-gel rehydration’ (Gorg et al., 2000). IEF was performed at 20°C in an IEF cell (Bio-Rad) using the following four-step program for 7 cm IPG strips: (a) 0–250 V in 1 h; (b) 250 V constant for 1 h; (c) 250–3000 V in 4 h; and (d) 3000 V constant until 15 kVh. In the case of the 17 cm strips, the applied voltage gradient was as follows: (a) 0–250 V in 1 h; (b) 250 V constant for 2 h; (c) 250–3000 V in 5 h; (d) 3000 V constant until 50 kVh. The current limit was set at 50 µA/strip. In each case, the program led to a ‘steady state’.

After IEF, IPG strips were equilibrated sequentially (Gorg et al., 2000) in solutions ‘A’ (0.05 M Tris–HCl, pH 8.8, containing 6 M urea, 30% glycerol, 2% SDS, 1% DTT) and ‘B’ (0.05 M Tris–HCl, pH 8.8, containing 6 M urea, 30% glycerol, 2% SDS, 4% iodoacetamide, 0.005% bromophenol blue). Later, each strip was loaded on top of a vertical SDS–polyacrylamide gel (12% T, 1.08% C, 1 mm thickness) and sealed in place with 1% low-melting agarose dissolved in electrode buffer. Molecular mass markers were loaded in a separate well by the side of the strip. Electrophoresis was performed using Laemmli’s (1970) buffer system at a constant current of 20 mA (for 7 cm gels) or 40 mA (for 17 cm gels) until the indicator dye (bromophenol blue) approached the bottom edge of the gels. Proteins were stained with Coomassie brilliant blue R250. Images were acquired by an imaging densitometer (GS710, Bio-Rad).

Peptide mass mapping

For in-gel digestion, sample preparation was performed as described by Shevchenko et al. (1996). Briefly, the Coomassie blue stained spot was excised from the gel, washed, in-gel reduced, S-alkylated with iodoacetamide and digested with bovine trypsin (sequencing grade, Roche Molecular Biochemicals) at 37°C overnight. Peptides were extracted, dried in a SpeedVac and resolubilized in 8 µl 0.1% TFA. ZipTips (Millipore) were used to desalt the samples. Peptide mass mapping was performed on 0.5 µl tryptic digest mixture using α-cyano-4-hydroxycinnamic acid (CHCA, Sigma). The samples were analysed by MALDI–MS on a Voyager DE STR (PerSeptive Biosystems, Framingham, MA, USA) equipped with a nitrogen laser (337 nm). The instrument was operated in the delayed extraction mode with a delay time of 150 ns. Each mass spectrum was
an average of 250 laser shots. Close external calibration was performed with a mixture of des-arg-1 bradykinin (904.468), angiotensin-I (1296.685), neurotensin (1672.917), and fragment 18–39 of adrenocorticotropic hormone (2465.199). To search the *Mycobacterium tuberculosis* ORF database ‘TubercuList’ ([http://genolist.pasteur.fr/TubercuList](http://genolist.pasteur.fr/TubercuList)), monoisotopic masses were assigned, using a local copy of the MS-Fit3.2 part of the Protein Prospector package (University of California, Mass Spectrometry Facility, San Francisco, CA). The parameters were set as follows: no restriction on the isoelectric point of proteins, a maximum mass error of 100 ppm and only one incomplete cleavage allowed per peptide.

**Results**

**2D resolution patterns of *M. tuberculosis* membrane proteins**

Despite using a widely accepted protocol for membrane solubilization, a portion of the sample remained insoluble and formed sediment upon centrifugation. With this limitation, the visibility of spots after Coomassie blue staining was best at the applied protein concentrations. Lesser amounts produced poorly visible spots and greater amounts led to an increase in streaking and smearing. Silver staining might have detected more spots, but was not used since it could have posed problems during protein identification by MALDI–MS. The reproducibility of the 2D patterns was confirmed and considered final when two consecutive runs produced identical patterns.

2D resolution patterns of the detergent (Triton X114) soluble membrane proteins of *M. tuberculosis* are shown in Figures 1 and 2. With the use of a pH 3–10 IPG strip (Figure 1), proteins in the mass range of 35–80 kDa tended to focus sharply in the neutral-to-basic region of the gel. However, separation was not so clear in the acidic region, particularly of proteins of 15–35 kDa. Similar results were obtained with a pH 4–7 IPG

![Figure 1](http://genolist.pasteur.fr/TubercuList)
Figure 2. 2D-GE of Triton X114 soluble membrane proteins of M. tuberculosis H37Rv. Proteins were separated using pH 4–7 IPG strips and SDS–PAGE on 12.5% gels. Spots 1–10 were processed for protein identification.

strip (Figure 2), wherein relatively larger proteins (35–80 kDa) focused mostly towards neutral pH and smaller ones (1535 kDa) appeared mostly unresolved. In addition, this gel also showed good resolution of certain high abundance, low molecular mass (<15 kDa) proteins in the acidic region.

2D profiles of the carbonate-extracted membrane sample (Figures 3 and 4) appeared different from those of the detergent soluble sample. With either pH 3–10 (Figure 3) or pH 4–7 (Figure 4) IPG strips, proteins of 25–40 kDa appeared grossly unresolved in the acidic region of gel, though the smaller (<15 kDa) proteins focused sharply. Several proteins of a relatively higher molecular mass (>20 kDa) also tended to focus sharply in the basic region of gel.

Protein identification by peptide mass mapping

Sixty-one protein spots (marked in Figures 1–4) isolated from M. tuberculosis membranes were picked for identification; 20 of these were from the detergent-soluble samples (Figures 1 and 2) and 41 were from the carbonate extracted samples (Figures 3 and 4). Selection was generally based on clarity and the ease with which the spots could be picked. For individual spots, the number of peptides giving matches in the genome database were in the range 3–18 and the coverage 8–60%.

Although 8% sequence coverage may be considered low, all five peptides of this particular protein (Rv0822c, Table 1) come from the N-terminal domain. Its molecular mass as estimated from the 2D gel analysis was about 15 kDa (Figure 2, spot 4) whereas the predicted mass is 72 911 Da. This probably indicates proteolysis of this protein, causing liberation of an N-terminal domain that was well covered by the peptides detected by mass spectrometry.

Peptide mass mapping of the selected spots led to the identification of 32 proteins, 15 of which...
originated from the detergent soluble samples and 19 from carbonate extracted membrane samples (Tables 1–3). Only two proteins were common to both preparations (Rv2031c, Table 2 and Rv0251c, Table 3). In all, 17 proteins (eight in Table 1, three in Table 2 and six in Table 3) were considered ‘new’ to the *M. tuberculosis* proteome database, since they had not been reported previously.

The identified proteins were classified into three categories: (a) putative membrane proteins (*n* = 14, Table 1); (b) proteins with known membrane associations (*n* = 5, Table 2); and (c) other proteins (*n* = 13, Table 3). The criteria used for this classification were published reports, annotations in the genome database (http://genolist.pasteur.fr/TubercuList), and predictions for transmembrane regions, signal sequences or lipid attachment sites by two relevant prediction servers TMPRED (http://www.ch.embnet.org/software/TMPRED_form.html) and PSORT (http://psort.nibb.ac.jp). Nineteen proteins (60% of all those identified) met the criteria to be described as ‘membrane-associated’ (Tables 1 and 2). ‘Grand average of hydropathy’ (GRAVY) scores for all proteins were obtained using ProtParam (http://us.expasy.org/tools/protparam.html), in which a score >−0.4(...
mean score for cytosolic proteins) indicates probability for membrane association — the higher the score greater the probability (Kyte and Doolittle, 1982). By this criterion alone, 25 (78%) proteins could be considered ‘hydrophobic’ since only seven (two in Table 2, and five in Table 3) showed a GRAVY score of < − 0.4.

Detergent solubilization appeared to perform better than carbonate extraction in isolating membrane proteins. By the most stringent criteria applied in this study (Table 1), 9/15 (60%) proteins identified from the detergent-soluble samples and only 5/19 (26%) proteins from the carbonate-extracted membrane qualified as ‘membrane-bound’. Further, the analysis of detergent-soluble, but not carbonate-extracted, membrane samples also revealed three lipoproteins of the bacillus (Rv1270c, Rv1368 and Rv0934).

The observed mass and charge of several proteins were different from those predicted by the genome, which is a common feature of most proteomic analyses, probably reflecting the effect of protein ‘maturation’ events including co- or post-translational modifications. Likewise, many proteins appeared as more than one spot representing their multiple ‘charge’ and/or ‘mass’ forms. In this respect, a significant observation was the presence of multiple forms of the FadA2 protein (Rv0243). The database predicts the mass of this protein as 46 075 Da and the pI as 6.64. However the expressed mature protein appeared to have three charge forms (Figure 1, spots 4–6) and one mass form (Figure 1, spot 9),

Figure 4. 2D-GE of carbonate-extracted membrane of M. tuberculosis H37Rv. Proteins were separated using pH 4–7 IPG strips and SDS–PAGE on 12.5% gels. Spots 1–26 were processed for protein identification
Table 1. Putative membrane proteins

<table>
<thead>
<tr>
<th>Fig. No.; spot No.</th>
<th>Protein</th>
<th>Peptides matched/sequence covered</th>
<th>Size (Da), pI</th>
<th>Functional category*/description</th>
<th>Predicted TM/LP/SS*</th>
<th>GRAVY score@</th>
<th>Previous proteomic detections#</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Rv0270</td>
<td>16/36%</td>
<td>59 909, 6.76</td>
<td>1/Probable FadD2</td>
<td>TM = 272–290a</td>
<td>−0.071</td>
<td>[i]</td>
</tr>
<tr>
<td>1</td>
<td>Rv2682c</td>
<td>9/21%</td>
<td>67 886, 6.34</td>
<td>7/Dxs, probable 1-deoxyxylulose 5-phosphate synthase</td>
<td>TM = 367–387*, 503–519b</td>
<td>0.024</td>
<td>[i]</td>
</tr>
<tr>
<td>1</td>
<td>Rv0243</td>
<td>7–15/21–40%</td>
<td>46 075, 6.64</td>
<td>1/FadA2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>Rv1770</td>
<td>10/25%</td>
<td>45 964, 6.52</td>
<td>10/Unknown</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>Rv1872c</td>
<td>18/34%</td>
<td>45 333, 10.15</td>
<td>7/IdD2, probable oxidoreductase</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>Rv1368</td>
<td>7/40%</td>
<td>26 848, 9.15</td>
<td>3/Hypothetical. N-terminal signal sequence and lipid attachment site. Homologous to Rv170c</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Rv0934</td>
<td>4/18%</td>
<td>38 207, 5.02</td>
<td>3/Mycobacterial equivalent of PsS, prokaryotic membrane lipoprotein, lipid attachment site at N-terminus</td>
<td></td>
<td>0.066</td>
<td>[ii, iii]</td>
</tr>
<tr>
<td>2</td>
<td>Rv0822c</td>
<td>5/8%</td>
<td>72 911, 6.08</td>
<td>10/Similar to membrane bound regulatory protein from B. subtilis lipoprotein</td>
<td></td>
<td>−0.278</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Rv1270c</td>
<td>6/27%</td>
<td>24 871, 5.21</td>
<td>3/Similar to M. bovis 27 kDa lipoprotein</td>
<td></td>
<td>0.014</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Rv2159c</td>
<td>12/37%</td>
<td>36 363, 7.82</td>
<td>8/Unknown</td>
<td></td>
<td>−0.050</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Rv2461c</td>
<td>3–5/17–37%</td>
<td>21 644, 4.54</td>
<td>7/ClpP, ATP-dependent clip protease proteolytic subunit</td>
<td></td>
<td>0.039</td>
<td>[iv]</td>
</tr>
<tr>
<td>4</td>
<td>Rv3099c</td>
<td>5/21%</td>
<td>30 465, 5.02</td>
<td>8/Unknown</td>
<td></td>
<td>−0.073</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Rv3417c</td>
<td>5–7/17–23%</td>
<td>55 894, 4.74</td>
<td>0/groEL-1</td>
<td></td>
<td>0.110</td>
<td>[i]</td>
</tr>
<tr>
<td>4</td>
<td>Rv0440</td>
<td>4–5/13–17%</td>
<td>56 755, 4.56</td>
<td>0/groEL-2</td>
<td></td>
<td>−0.091</td>
<td>[ii, iii]</td>
</tr>
</tbody>
</table>

* Functional categories: 0, virulence, detoxification, adaptation; 1, lipid metabolism; 2, information pathways; 3, cell wall and cell processes; 7, intermediary metabolism and respiration; 8, unknown; 9, regulatory proteins; 10, conserved hypotheticals.

† TM, transmembrane/hydrophobic regions; LP, lipoprotein; SS, signal sequence.

* Using the software TMPRED (http://www.ch.embnet.org/software/TMPRED_form.html).

+ Using the software PSORT (http://psort.nibb.ac.jp).

@ According to Kyte and Doolittle (1982).

# [i] Jungblut et al. (1999); [ii] Rosenkrands et al. (2000a); [iii] Rosenkrands et al. (2000b); [iv] Covert et al. (2001).
Table 2. Proteins with known membrane associations

<table>
<thead>
<tr>
<th>Fig. No.; spot No.</th>
<th>Protein</th>
<th>Peptides matched/sequence covered</th>
<th>Size (Da), pI</th>
<th>Functional category*/description</th>
<th>Evidence for membrane association*</th>
<th>GRAVY score®</th>
<th>Previous proteomic detectionsº</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fig. 2; 5</td>
<td>Rv2031c</td>
<td>4–5/31–37%</td>
<td>16 218, 4.75</td>
<td>0/HSP16, α-crystallin homologue</td>
<td>[a,b,c]</td>
<td>−0.520</td>
<td>[ii, iii]</td>
</tr>
<tr>
<td>Fig. 3; 1</td>
<td>Rv1876</td>
<td>3–5/30–43%</td>
<td>18 329, 4.23</td>
<td>7WfrA, bacterioferritin. Also similar to bfrB, Rv3841</td>
<td>[d]</td>
<td>−0.455</td>
<td></td>
</tr>
<tr>
<td>Fig. 4; 11</td>
<td>Rv1309</td>
<td>4/15%</td>
<td>33 883, 5.15</td>
<td>7/AtgP, ATP synthase γ chain</td>
<td>[e]</td>
<td>−0.267</td>
<td></td>
</tr>
<tr>
<td>Fig. 4; 16–17</td>
<td>Rv1310</td>
<td>14–16/43–46%</td>
<td>53 097, 4.60</td>
<td>7/AtgD, ATP synthase β chain</td>
<td>[e]</td>
<td>−0.168</td>
<td></td>
</tr>
<tr>
<td>Fig. 4; 25–26</td>
<td>Rv1308</td>
<td>5–9/9–21%</td>
<td>59 305, 4.78</td>
<td>7/AtgA, ATP synthase α chain</td>
<td>[e]</td>
<td>−0.207</td>
<td>[i]</td>
</tr>
</tbody>
</table>

* As in Table 1.
*a [a] Young and Garbe (1991); [b] Lee et al. (1992); [c] Mehrotra et al. (1999); [d] Pessolani et al. (1994); [e] Futai et al. (1989).

® As in Table 1. Scores < −0.4, suggesting greater probability for cytosolic origin, are underlined.

º As in Table 1.

Table 3. Other proteins

<table>
<thead>
<tr>
<th>Fig. No.; spot No.</th>
<th>Protein</th>
<th>Peptides matched/sequence covered</th>
<th>Size (Da), pI</th>
<th>Functional category*/description</th>
<th>GRAVY score®</th>
<th>Previous proteomic detectionsº</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fig. 2; 2, 4</td>
<td>Rv0251c</td>
<td>5–8/48–59%</td>
<td>17 774, 5.04</td>
<td>0/Probably HSP20 family</td>
<td>−0.473</td>
<td></td>
</tr>
<tr>
<td>Fig. 3; 2–3</td>
<td>Rv2744c</td>
<td>4–5/22–31%</td>
<td>29 255, 5.77</td>
<td>7/35 kDa antigen. CDS is split into two ORFs in M. leprae</td>
<td>−0.464</td>
<td>[i]</td>
</tr>
<tr>
<td>Fig. 3; 4–5</td>
<td>Rv0055c</td>
<td>4/15%</td>
<td>30 977, 5.62</td>
<td>10</td>
<td>−0.458</td>
<td>[i]</td>
</tr>
<tr>
<td>Fig. 3; 6.</td>
<td>Rv2296</td>
<td>6/26%</td>
<td>33 347, 6.98</td>
<td>7/Hydrolase, similar to e.g. HALO_XANAU, haloalkane dehalogenase</td>
<td>−0.228</td>
<td>[i]</td>
</tr>
<tr>
<td>Fig. 3; 7.</td>
<td>Rv1479</td>
<td>8/35%</td>
<td>40 755, 6.36</td>
<td>9/MoxR, highly similar to MoxR homologues of M. tuberculosis, Rv3692, Rv3164c and M. ovum</td>
<td>0.051</td>
<td>[i]</td>
</tr>
<tr>
<td>Fig. 3; 10–12</td>
<td>Rv0242c</td>
<td>6–10/19–30%</td>
<td>46 797, 6.38</td>
<td>1/FabG4, probably 3-O xyloacyl-[acyl carrier protein] reductase</td>
<td>0.069</td>
<td>[i]</td>
</tr>
<tr>
<td>Fig. 4; 4–6</td>
<td>Rv0798c</td>
<td>4–6/25–38%</td>
<td>28 822, 4.67</td>
<td>0/29 kDa antigen, Cfp29</td>
<td>−0.141</td>
<td>[ii, iii]</td>
</tr>
<tr>
<td>Fig. 4; 7–9</td>
<td>Rv0831c</td>
<td>3–5/21%</td>
<td>30 177, 4.85</td>
<td>8</td>
<td>−0.212</td>
<td></td>
</tr>
<tr>
<td>Fig. 4; 14–15</td>
<td>Rv0685</td>
<td>6–12/26–46%</td>
<td>43 567, 5.12</td>
<td>2/Tuf elongation factor Tu (ef-tu). ATP/GTP-binding motif A</td>
<td>−0.288</td>
<td>[ii, iii]</td>
</tr>
</tbody>
</table>

* As in Table 1.
*a As in Table 1. Scores < −0.4, suggesting greater probability for cytosolic origin, are underlined.
º As in Table 1.

the latter being significantly smaller than the predicted size (Table 1).

Four heat-shock proteins were also found to be present in the membrane fractions. Among those present in both detergent-soluble and carbonate-extracted samples were an α-crystallin homologue (Rv2031c, Table 2) and HSP20 (Rv0251c, Table 3). Two proteins of the HSP60 family,
Proteome of M. tuberculosis cell membrane

Proteomic comparison of M. tuberculosis and BCG membranes

We were interested to know whether the proteome analysis protocol applied in this study was applicable to the identification of those proteins that are differentially expressed between mycobacterial cell membranes. The 2D protein profiles of the whole unfractionated membranes of M. tuberculosis and BCG that were obtained appeared quite similar (Figure 5). Peptide mass mapping of a low molecular mass protein (marked in Figure 5), which was expressed abundantly and selectively in the M. tuberculosis membrane, identified it as ESAT-6, which belongs to the family of ‘early secretory antigenic target’ proteins of the bacillus.

Discussion

Proteome analysis of the cell membrane is considered a daunting task, due mainly to problems encountered at two levels: (a) isolation of membrane which is free from ‘non-membrane’ constituents; and (b) solubilization of membrane proteins in a manner amenable to isoelectric focusing (Santoni et al., 2000). The existing databases of the mycobacterial proteome (http://www.ssi.dk/publichealth/tbimmun; http://www.mpiib-berlin.mpg.de/2D-PAGE/) and some recent reports (Monahan et al., 2001; Covert et al., 2001; Mattow et al., 2001a,b) have so far identified nearly 500 proteins, yet hardly any of them correspond to the ∼800 putative membrane proteins predicted from the genome. Against this backdrop, our work was planned as a case study on the application of proteomics to the membrane of M. tuberculosis H37Rv. The difference between our strategy and that of the previous studies is that we worked with isolated membrane fractions of the bacillus rather than the whole cell lysate. This fraction was further enriched for membrane proteins using two of the recommended protocols, involving extractions with either a detergent (Triton X114; Bordier, 1981) or carbonate (Fujiki et al., 1982). We also used a sample solubilization protocol specifically recommended for membrane proteins (Friso and Wikstrom, 1999). Another membrane solubilization protocol involving the use of sulphobetaine 3–10 and tributylphosphine (Molloy et al., 1998) was also tried, which gave similar results (not described here).

2D gel electrophoresis and peptide mass mapping of 61 spots from the two membrane samples of M. tuberculosis led to identification of

Figure 5. 2D-GE of whole cell membranes of M. tuberculosis H37Rv and BCG Pasteur. Isoelectric focusing was performed on pH 4–7 IPG strips and SDS–PAGE on 12.5% Laemmli gels. The marked spot expressed selectively in M. tuberculosis was processed for peptide mass mapping to be identified as ESAT-6.
32 proteins; 17 of these are ‘new’ to the mycobacterial protein database, as they bear no previous references. A set of parameters including published reports, annotations in the genome data, and software-based predictions for putative transmembrane/hydrophobic domains, signal sequences and lipid attachment sites were used for ascertaining the membranous nature of the identified proteins. Accordingly, 19 proteins qualified as ‘membrane-associated’, of which 14 could indeed be classified as ‘membrane-bound’, based on the stringency of the criteria met by them (Table 1). Three proteins of the latter category were lipoproteins (Rv0934, Rv1270c and Rv1368). Rv1270c and Rv1368 are members of the P4.24 family of lipoproteins, which show strong sequence conservation (http://genolist.pasteur.fr/TubercuList/mast/P4.24). This family also includes Rv1411c and Rv2945c. The third lipoprotein detected here, Rv0934, is the well-characterized 38 kDa antigen that is the ‘membrane-bound’ substrate binding component of the ABC transporter required for phosphate uptake (Braibant et al., 1999). We had previously identified this protein in the integral membrane protein pools of BCG (Mehrotra et al., 1999) and M. tuberculosis (unpublished) with the help of monoclonal antibodies. Previous proteomic analyses of M. tuberculosis have not detected any lipoprotein, although one study (Rosenkrands et al., 2000b) has detected the 38 kDa (Rv0934) and 19 kDa lipoproteins through staining with antibodies.

We have classified some of the proteins as membrane-associated, mainly on the basis of published reports, even though their structural attributes do not suggest a membrane origin. These observations point to that fact that structure alone may not be the deciding factor as far as the association of proteins with the cell membrane is concerned. The proteins may be bound to the membrane simply to fulfil their functional obligations. Consequently, they could become part of multimeric complexes involving membrane proteins and may not dissociate easily under the conditions of sample preparation. For instance, this could be true of FadA2 (Rv0243), which is involved in lipid metabolism — a biochemical process occurring in membranes — and Rv1872c, which is a probable lactate dehydrogenase. This enzyme generally interacts with membrane-bound components of the electron transfer chain of bacteria. Heat-shock proteins are also known to become associated with membrane proteins while working as molecular chaperones (Cordwell et al., 2001; Wissing et al., 2000). This could be the reason behind the observed presence of four HSPs (Rv2031c, α-crystallin; Rv0251c, HSP20; Rv3417c, groEL1; and Rv0440c, groEL2) in our membrane preparations. The α-crystallin homologue has already been reported to be membrane-associated in our studies (Mehrotra et al., 1999) and those of others (Young and Garbe, 1991; Lee et al., 1992). Other identified proteins that could be associated with the membrane in this way are bacterioferritin (bfrA, Rv1876) and ATP synthase (Rv1308, Rv1309, Rv1310). Bacterioferritin is a conserved, iron-rich protein previously described as the major membrane protein-II (MMP-II) of M. leprae (Pes-solani et al., 1994). Membrane association of ATP synthase is also well documented (Futai et al., 1989). Similar reasons could be used to explain the presence of some other, apparently cytosolic, proteins in the membrane. On the other hand, some truly cytosolic proteins may simply become entrapped within membrane vesicles formed during the sonication process and become difficult to remove by the extraction methods used (Friso and Wikstrom, 1999).

In view of the reports recommending one method or the other, it was important to compare the efficacies of the detergent (Triton X114) and carbonate extraction procedures in uncovering putative membrane proteins of the bacillus. At the outset, there was hardly any resemblance between the profiles revealed by the two procedures, in terms of either 2D patterns or identified proteins. Only two proteins, both HSPs (Rv2031c and Rv0251c), were commonly present in the two preparations. The results suggest a better efficacy of the detergent-based method in selecting membrane proteins. 60% of all identified proteins of the detergent extract qualified as ‘membrane bound’ (Table 1) whereas only 26% of proteins from the carbonate extracted sample did so. More importantly, the detergent-soluble but not carbonate-extracted sample displayed three lipoproteins of the bacillus, as elaborated above. These observations appear logical, since hydrophobic/lipophilic proteins, such as those from the membrane, are expected to partition selectively in a detergent-rich medium. The success of the carbonate-based strategy reported...
in some cases (Molloy et al., 2000; Fujiki et al., 1982) could depend on the complexity of the target membrane. The mycobacterial cell envelope (including the membrane) is considered unique in its composition and complexity (Barksdale and Kim, 1977; Brennan and Nikaido, 1995). Even within the genus, the envelope of ‘slow growers’, such as M. tuberculosis, is more complex than that of the ‘fast growers’. Many a ‘sticky’ and poorly defined molecule, such as lipoarabinomannans, arabinogalactans, phosphatidyl inositol mannosides, etc., and several others (mostly undefined), such as proteoglycolipids, glycolipids, phospholipids, sulpholipids and glycans, are present in the cell wall or membrane. These components, besides imposing problems on membrane solubilization, have most probably also contributed to the streaking and smearing seen in our 2D gels. Even in one-dimensional (1D) gels, where a strong detergent like SDS is used for sample solubilization, the smearing effect is observed (Lee et al., 1992; Mehrotra et al., 1999).

The reliability of the protocol for comparative analyses of mycobacterial membrane proteins was also an important consideration in this study. 2D protein profiles of both M. tuberculosis and BCG membranes appeared to be similar, reflecting the genomic similarities between these microbes (Gordon et al., 1999). The identity of a low molecular mass protein, which was expressed prominently in M. tuberculosis but not at all in BCG, was revealed as ESAT-6 by peptide mass mapping. The genome of M. tuberculosis H37Rv has five copies of a cluster of genes known as the ESAT-6 (early secretory antigenic target) loci. These clusters contain members of the ESAT-6 gene family (encoding secreted T cell antigens that lack detectable secretion signals), as well as genes encoding secreted, cell-wall-associated serine proteases, putative ABC transporters, ATP-binding proteins and other membrane-associated proteins (Tekaia et al., 1999). The multiple duplicates of the ESAT-6 gene of M. tuberculosis are also conserved in other mycobacteria, e.g. M. bovis, M. leprae, M. avium and the avirulent strain M. smegmatis. The protein in M. leprae appears in the cell wall fraction (Spencer et al., 2002). Thus there is ‘circumstantial’ evidence for the existence of this protein in the cell membrane. ESAT-6 is not expected to be present in BCG, since the corresponding gene locus (RD1) of M. tuberculosis is deleted in BCG (Gordon et al., 1999).

In conclusion, the knowledge of the proteome of M. tuberculosis is still in a descriptive phase and there is a long way to go before the complete definition of the proteins allows identification of candidate drug targets, diagnostic probes or components of a vaccine. Comparative proteomics of the highly conserved M. tuberculosis complex is a powerful approach to understand phenotypic differences such as virulence (Botts et al., 2000; Mattow et al., 2001b) and merits further application. The area of membrane proteomics is only just beginning to unfold. Clearly, progress in this area hinges not only on our ability to efficiently solubilize the membrane proteins but also on making them free from interfering substances (Santoni et al., 2000). Nonetheless, the approach using Triton X114-based extraction has shown promise in this as well as earlier (Wissing et al., 2000) studies. We have provided evidence for some of the ‘true’ membrane proteins of the bacillus and also detected some of those described as ‘unknowns’ or ‘hypotheticals’ in the genome database.

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Proteome of M. tuberculosis cell membrane

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