Immunogenicity and Reactivity of Novel Mycobacterium avium subsp. paratuberculosis PPE MAP1152 and Conserved MAP1156 Proteins with Sera from Experimentally and Naturally Infected Animals

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Received 23 July 2010/Returned for modification 13 September 2010/Accepted 9 November 2010

Mycobacterium avium subsp. paratuberculosis causes Johne's disease (JD) in ruminants. Development of genetic tools and completion of the M. avium subsp. paratuberculosis genome sequencing project have expanded the opportunities for antigen discovery. In this study, we determined the seroreactivities of two proteins encoded at the 5′ and 3′ regions of the MAP1152-MAP1156 gene cluster. MAP1152 encodes a PPE protein, and MAP1156 encodes a diacylglycerol acyltransferase involved in triglyceride metabolism and classified in the uncharacterized protein family UPF0089. Recombinant MAP proteins were overproduced and purified from Escherichia coli as maltose-binding protein (MBP) fusions. Immuno blotting analysis indicated that both MAP1152 and MAP1156 displayed reactivity against sera of mice and rabbits immunized with live M. avium subsp. paratuberculosis cells and against samples from naturally infected cattle. In immunoblot assays, MAP1156 yielded a stronger positive signal than MAP1152 against sera from cattle with JD. An enzyme-linked immunosorbent assay for the recombinant proteins was developed and used to test preclassified positive and negative serum samples from naturally infected and noninfected cattle. Samples, with one exception, displayed no seroreactivity against the MBP-LacZ fusion protein (P > 0.05), the negative-control antigen. MAP1152 displayed seroreactivity against all positive sera but no seroreactivity to the negative sera (P < 0.01). MAP1156 displayed stronger and more variable reactivity than MAP1152, but significant differences were observed between noninfected and infected cattle (P < 0.05). Otherwise, degrees of reactivity followed the same trend as the positive reference antigen. In conclusion, both proteins are immunogenic in mice and rabbits, and M. avium subsp. paratuberculosis-infected cattle mount a humoral response to both MAP1152 and MAP1156 cross-reactive epitopes. These findings have potential applications to diagnostics, vaccine production, and elucidation of the immunopathogenesis of JD.

Mycobacterium avium subsp. paratuberculosis, one of the slowest-growing mycobacteria (28), is the etiologic agent of Johne’s disease (JD) in ruminants (11, 24). JD is a chronic enteritis with significant economic impact and worldwide distribution (23, 51, 53, 57). A JD regression model estimates that losses to the dairy industry range from $40 to $227 per inventoried cow per year (24, 40). JD has lower prevalence in beef herds, but this disease still has a negative impact on trade (38, 42, 60). Concerns for human health have also been raised, since M. avium subsp. paratuberculosis has the potential to be a zoonotic and/or food-borne pathogen, as evidenced by its possible linkage to Crohn’s disease (6, 8, 9, 21).

The physiology and pathogenesis of M. avium subsp. paratuberculosis have been reviewed (24, 61). Neonates and juvenile animals are the most susceptible to infection. Disease progression is classified into four stages: silent infection and subclinical, clinical, and advanced clinical disease (61). Despite the progress made in the analysis of mechanisms of pathogenesis, a diagnostic test of high sensitivity and specificity for detection of subclinically infected animals has not been developed (15, 19, 27, 33, 34, 39, 50). In this situation, most diseased animals escape detection, especially during early infection. Likewise, current vaccines against JD are highly regulated, have poor efficacy, and interfere with diagnostic tests against bovine tuberculosis (5, 10, 20, 23, 55).

The information obtained from the completed M. avium subsp. paratuberculosis genome sequencing project ushered in the development of new tools for diagnosis and disease control (29). In the context of our study, approximately 1% of the M. avium subsp. paratuberculosis genome encodes members of the PE (Pro-Glu) and PPE (Pro-Pro-Glu) protein families, so denominated by their characteristic motifs at their N-terminal domains. These genes were initially discovered in the Mycobacterium tuberculosis genome, which dedicates approximately 10% of its coding capacity to these elements. Cole et al. hypothesized that the PE and PPE families may have immunological importance, being the main source of antigenic variation (14, 52, 56). This quantitative difference in coding capacity...
MMT1152 and MAP1156 coding sequences were amplified from M. avium subsp. paratuberculosis K-10 genomic DNA and cloned into the pMAL-c2 translational fusion expression vector using the primers 5′-AATGAAACGGCTTTCGAGTGTCG-3′ and 5′-GCCGAACTT TCTATTGCGCTTGCCGGAATG-3′ for MAP1152 and 5′-ATCTCTCTAG AATGAAACGGCTTTCGAGTGTCG-3′ and 5′-GCCGAACTTTTGCCG GTCGAG-3′ for MAP1156. Both primer pairs amplified the corresponding full-length coding sequence. The vector and amplification products were each digested with XbaI and HindIII. Following overnight ligation at 4°C, the products were transformed into E. coli DH5α and selected on LB agar plates containing 0.1 mg/ml ampicillin. Drug-resistant colonies were screened by PCR using the amplification primers, and plasmid DNA for sequencing analysis was produced from positive colonies to confirm each clone. E. coli protein lysates from verified clones were prepared as previously described (47).

Proteins used in this study were expressed and purified as recombinant maltose-protein lysates from verified clones were prepared as previously described (47).

This study focused on the MAP1152-MAP1156 gene cluster, as the Tn5367 transposon insertion in the colony morphology M. avium subsp. paratuberculosis strain K-10 mutant with an attenuated phenotype in bovine macrophages (31), has now been mapped ca. 0.6 kb upstream from MAP1152. To evaluate the potential role of this gene cluster in M. avium subsp. paratuberculosis immunobiology, we performed further bioinformatic analysis and determined the activities of MAP1152 and MAP1156 against sera from mice and rabbits immunized with live M. avium subsp. paratuberculosis and against samples from naturally infected cattle.

### MATERIALS AND METHODS

Cloning, expression, and purification of M. avium subsp. paratuberculosis proteins in Escherichia coli. MAP1152 and MAP1156 coding sequences were amplified from M. avium subsp. paratuberculosis K-10 genomic DNA and cloned into the pMAL-c2 translational fusion expression vector using the primers 5′-AATGAAACGGCTTTCGAGTGTCG-3′ and 5′-GCCGAACTTTTGCCGGTCGAG-3′ for MAP1152 and 5′-ATCTCTCTAGAATGAAACGGCTTTCGAGTGTCG-3′ and 5′-GCCGAACTTTTGCCGGTCGAG-3′ for MAP1156. Both primer pairs amplified the corresponding full-length coding sequence. The vector and amplification products were each digested with XbaI and HindIII. Following overnight ligation at 4°C, the products were transformed into E. coli DH5α and selected on LB agar plates containing 0.1 mg/ml ampicillin. Drug-resistant colonies were screened by PCR using the amplification primers, and plasmid DNA for sequencing analysis was produced from positive colonies to confirm each clone. E. coli protein lysates from verified clones were prepared as previously described (47).

Proteins used in this study were expressed and purified as recombinant maltose-binding protein (MBP) N-terminal fusions (e.g., LaZ, MAP1152, and MAP1156; referred to here by these short names, with the understanding that all recombinant proteins used in the experiments were fusion products). These MBP-tagged recombinant proteins were overexpressed by induction of 1.0-liter LB broth cultures with 0.3 mM isopropyl-β-D-thiogalactopyranoside (Sigma Chemical Company, St. Louis, MO) for 2.5 h with shaking at 37°C. E. coli cells were harvested by centrifugation at 4,000 × g for 15 min and suspended in column buffer, and the cell suspension was subjected to a freeze-thaw cycle at −20°C and sonicated under conditions described previously (1). The resulting crude extracts were purified by affinity chromatography with an amyllose resin (New England Biolabs). Purified protein yields were determined from eluted fractions with a tool. This version has the ability to record pixel gray values using the default measurement scale (1 pixel = 1 pixel). Each spot was measured identically by using a defined window area. Values were exported into a spreadsheet for further analysis. The background statistics were calculated by determining the means and standard deviations of the bands that had the least signal intensity within each output graph. Each intensity score was normalized to this calculated background intensity.

**ELISA**. An enzyme-linked immunosorbent assay (ELISA) was developed to quantify the activities of MAP1152 and MAP1156 proteins with a subset of serum samples from cattle with known exposure to M. avium subsp. paratuberculosis (Table 1). Antibody conjugate (HRP-conjugated rabbit anti-bovine IgG) was applied (0.1 ml/well) at room temperature. The ELISA was performed as per the instructions provided with the HerdChek ELISA kit (Idexx Laboratories, Westbrook, ME). Briefly, sera were diluted 1:25 in either BSA-PBST or the buffer supplied by Idexx containing Mycobacterium phlei antigen for clarification. Diluted serum was applied (0.1 ml) to each well and incubated for 30 min at room temperature. Plates were washed five times with PBS, and secondary antibody conjugate (HRP-conjugated rabbit anti-bovine IgG) was applied (0.1 ml/well) and incubated for 30 min at room temperature. After additional washing steps, 0.1 ml tetramethylbenzidine (TMB) was added, and the subsequent reaction was stopped with the supplied SDS Stop solution as the appropriate color developed. Absorbance was read at 650 nm with a Molecular Devices Vmax kinetic microplate reader and translated with the xChrom software from Idexx. The sample-to-positive (S/P) ratios for each antigen were calculated based on optical density (OD) values, as follows: [OD of serum sample − OD of negative-control serum]/[OD of positive-control serum − OD of negative-control serum], as described for the Idexx HerdChek assay. Statistical analysis of ELISA results was performed using SAS 9.2 for Windows (SAS Institute Inc., Cary, NC). To compare average absorbances of all seropositive cattle samples to

### TABLE 1. Cattle serum samples used in the study

<table>
<thead>
<tr>
<th>Serum sample</th>
<th>Original classification (Idexx test)</th>
<th>Type of infection</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cow 183</td>
<td>+</td>
<td>Natural (JD)</td>
<td>NADC</td>
</tr>
<tr>
<td>Cow 2075</td>
<td>+</td>
<td>Natural (JD)</td>
<td>NADC</td>
</tr>
<tr>
<td>Cow 184</td>
<td>+</td>
<td>Natural (JD)</td>
<td>NADC</td>
</tr>
<tr>
<td>Cow 805</td>
<td>+</td>
<td>Natural (JD)</td>
<td>NADC</td>
</tr>
<tr>
<td>Cow 45</td>
<td>+</td>
<td>Natural (JD)</td>
<td>NADC</td>
</tr>
<tr>
<td>Cow 193</td>
<td>−</td>
<td>Experimental, with M. avium hominisissus</td>
<td>NADC</td>
</tr>
<tr>
<td>Cow 2291</td>
<td>−</td>
<td>Experimental, with M. avium hominisissus</td>
<td>NADC</td>
</tr>
<tr>
<td>Cow 47</td>
<td>+</td>
<td>Natural (JD)</td>
<td>NADC</td>
</tr>
<tr>
<td>Positive controlb</td>
<td>+</td>
<td>Natural (JD)</td>
<td>Idexx Laboratories</td>
</tr>
<tr>
<td>EDNA</td>
<td>+</td>
<td>Natural (JD)</td>
<td>NADC</td>
</tr>
<tr>
<td>Cow 308</td>
<td>+</td>
<td>Natural (JD)</td>
<td>NADC</td>
</tr>
<tr>
<td>2010-07</td>
<td>+</td>
<td>Natural (JD)</td>
<td>Nebraska dairy</td>
</tr>
<tr>
<td>Negative controld</td>
<td>−</td>
<td>None</td>
<td>Idexx Laboratories</td>
</tr>
<tr>
<td>J5-90</td>
<td>−</td>
<td>None</td>
<td>Nebraska beef herd</td>
</tr>
<tr>
<td>Cow 559</td>
<td>−</td>
<td>None</td>
<td>NADC</td>
</tr>
<tr>
<td>3438-08</td>
<td>−</td>
<td>None</td>
<td>Nebraska dairy</td>
</tr>
</tbody>
</table>

a NADC, National Animal Disease Center, Ames, IA.
b Positive-control serum provided with the Idexx kit, derived from a single naturally infected Holstein cow (Idexx Technical Service).
c Dairy or beef cattle of the University of Nebraska Lincoln Veterinary Diagnostic Center, Lincoln, NE.
d Negative-control serum provided with the Idexx kit, derived from a single Holstein cow residing in a herd that tested negative for paratuberculosis by whole-herd testing over multiple years (Idexx Technical Service).
FIG. 1. Genomic map of PE, PPE, and UPF genes in *M. avium* subsp. *paratuberculosis* K-10 (MAP). Genes encoding PE (shown as bars inside of the circular chromosome), PPE (bars crossing the circular chromosome), and UPF (bars outside the circle) protein family members are shown. No PGRS protein-coding sequences were found. (Inset) MAP1152-MAP1156 genomic region, indicating genes encoding PPE proteins MAP1152, MAP1153, and MAP1155 (black boxes), the proximal (MAP1152) and distal (MAP1156) ORFs in the published genome sequence (29) and comprises MAP1514, encoding a PE protein, and six PPE genes. The MAP1152-MAP1156 region of interest for this study is the second major cluster and is located 1.21 Mb in the clockwise direction. This region encodes the PPE proteins MAP1152 (40.8 kDa), MAP1153 (45.8 kDa), and MAP1155 (32.3 kDa) (Fig. 1, inset). This region also encodes a putative open reading frame (ORF) of unknown function (MAP1154; 11.8 kDa) and MAP1156 (50.7 kDa), a member of the uncharacterized protein family (UPF0089) (http://pfam.sanger.ac.uk/family/PF03007). The *M. avium* subsp. *paratuberculosis* genome encodes nine UPF0089 family genes, and MAP1156 is the only member that is immediately adjacent to a PPE gene (Fig. 1). This cluster does not encode a PE protein sequence.

It is tempting to speculate that genes in the MAP1152-MAP1156 region are organized in a functional unit, since ORFs further upstream and downstream are transcribed from the complementary strand with short (e.g., <200-bp) intergenic regions. However, more stringent predictions indicate that only MAP1152 and MAP1153 are organized in a true operon with an estimated probability that a pair of genes is in the same operon (pOp) value of 0.842 (http://www.microbesonline.org/operons/gnc262316.html) (44, 45). Nonetheless, the genes in this cluster may comprise more than one operon.

The proximal (MAP1152) and distal (MAP1156) ORFs in the cluster were selected for immunological tests of humoral immunity in infected and noninfected animals. MAP1152 encodes a typical PPE protein of 416 amino acids with a predicted molecular mass of 40.8 kDa (Table 2). Protein structural analysis predicts for the best model three trans-membrane helices (48; http://www.predictprotein.org), consistent with a surface or membrane localization, as shown for other PPE proteins (7, 25, 32, 36, 43). MAP1156 is a protein of 464 amino acids with a predicted molecular mass of 50.7 kDa. Protein structural analysis for the best fit model predicts one trans-membrane helix, suggesting surface localization (48). Both MAP1152 and MAP1156 have homologous sequences in both *M. avium* subsp. *paratuberculosis* and other mycobacterial genomes. Further bioinformatic analysis of the ORFs in the cluster is presented in Table 2.

### RESULTS

Bioinformatic analysis of the MAP1152-MAP1156 gene cluster. Nine PE and 37 PPE protein genes are scattered around the *M. avium* subsp. *paratuberculosis* chromosome (Fig. 1). The major PPE cluster is at 1.66 Mb in the clockwise direction in the published genome sequence (29) and comprises MAP1514, encoding a PE protein, and six PPE genes. The MAP1152-MAP1156 region of interest for this study is the second major cluster and is located 1.21 Mb in the clockwise direction. This region encodes the PPE proteins MAP1152 (40.8 kDa), MAP1153 (45.8 kDa), and MAP1155 (32.3 kDa) (Fig. 1, inset). This region also encodes a putative open reading frame (ORF) of unknown function (MAP1154; 11.8 kDa) and MAP1156 (50.7 kDa), a member of the uncharacterized protein family (UPF0089) (http://pfam.sanger.ac.uk/family/PF03007). The *M. avium* subsp. *paratuberculosis* genome encodes nine UPF0089 family genes, and MAP1156 is the only member that is immediately adjacent to a PPE gene (Fig. 1). This cluster does not encode a PE protein sequence.

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### TABLE 2. Characterizations of ORFs MAP1152 to MAP1156

<table>
<thead>
<tr>
<th>ORF</th>
<th>Size (no. of aa, mass)</th>
<th>H37Rv homolog&lt;sup&gt;b&lt;/sup&gt;/E-value&lt;sup&gt;c&lt;/sup&gt;</th>
<th>Domain, motif&lt;sup&gt;d&lt;/sup&gt;</th>
<th>Comment(s)&lt;sup&gt;d&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAP1152</td>
<td>416, 40.7</td>
<td>Rv1808 (PPE32)/8.0 E−78</td>
<td>PPE, GxxSVPxxW</td>
<td>Three MH</td>
</tr>
<tr>
<td></td>
<td>454, 45.7</td>
<td>Rv1809 (PPE33)/1.0 E−84</td>
<td>PPE, GxxSVPxxW</td>
<td>Coding sequence starts 7 bp downstream from MAP1152; three MH</td>
</tr>
<tr>
<td>MAP1154</td>
<td>117, 11.7</td>
<td>Rv1810/8.0 E−19</td>
<td>DUF732 superfamily</td>
<td>Hypothetical protein; no MH</td>
</tr>
<tr>
<td>MAP1155</td>
<td>320, 32.2</td>
<td>Rv1807 (PPE31)/4.0 E−24</td>
<td>PPE, GxxSVPxxW</td>
<td>Attenuating mutation in <em>M. tuberculosis</em> homolog (49); two MH</td>
</tr>
<tr>
<td>MAP1156</td>
<td>464, 50.6</td>
<td>Rv1425/0.0</td>
<td>UPF0089</td>
<td><em>M. tuberculosis</em> homolog encodes enzyme with low TGS activity (16); possibly one MH</td>
</tr>
</tbody>
</table>

<sup>a</sup> Data are based on National Center for Biotechnology Information (NCBI) database output. Sizes are reported as the number of amino acids (aa) and as molecular mass (in kilodaltons).

<sup>b</sup> Data entries based on the Pfam database (http://pfam.sanger.ac.uk/family). Most homologous *M. tuberculosis* proteins are not necessarily orthologs (22).

<sup>c</sup> E-values (determined using the Blastp suite) are formatted as described in the BLAST help manual (http://www.ncbi.nlm.nih.gov/blast/blast_help.shtml).

<sup>d</sup> MH, membrane helices (determined via the PredictProtein server [http://www.predictprotein.org] for protein analysis [PHDhtm output]).
Seroreactivity of recombinant proteins by immunoblot analysis. Purified recombinant proteins MAP1152 and MAP1156 were subjected to SDS-PAGE and immunoblot analyses. Equal amounts of both proteins were examined by SDS-PAGE to verify that their migration corresponded with their molecular size (Fig. 2, SDS-PAGE). Both fusion proteins migrated to the expected positions between the 75-kDa and 100-kDa protein markers, with MAP1156 (90.6 kDa) located slightly higher than MAP1152 (82.8 kDa). Likewise, LacZ (42 kDa) migrated to a position below the 50-kDa marker. These data indicate that the MBP method resulted in protein preparations of the necessary purity and yield to carry out further testing. MAP1156 did show multiple bands, in contrast to the discrete single bands observed for MAP1152 and LacZ. Immunoblot quality control analysis was also performed, using a monoclonal antibody developed to the MBP affinity tag. All three MBP fusion proteins were detected by this antibody (Fig. 2, MBP mAb). The additional bands observed in the MAP1156 preparation likely represent degradation products with the same N terminus, as the fast-migrating bands reacted also with the MBP monoclonal antibody.

The immunogenicity of the recombinant proteins was tested by immunoblotting using immune mouse (C57BL/6) or rabbit (New Zealand White) serum from animals immunized with a live preparation of M. avium subsp. paratuberculosis, as described previously (2). The mouse serum displayed little to no reactivity to MAP1152 but strong reactivity to MAP1156, with the most intense band migrating between the 50- and 75-kDa markers (Fig. 2, mouse panel, lane 4). The rabbit immune serum showed strong reactivities to both proteins (Fig. 2, rabbit 273). Reactivity against the LacZ antigen carrying the MBP tag was used as a negative control. The mouse serum displayed no MBP-LacZ reactivity (Fig. 2, mouse panel, lane 4), and only a weak reaction was observed with the rabbit serum (Fig. 2, rabbit panel, lane 4). Thus, the MBP tag yielded no to minimal reactivity in these immunoblot assays.

Immunoblot assays were also performed with sera from five cattle naturally infected with M. avium subsp. paratuberculosis (Fig. 3A, 183, 2075, 184, 805, and 45) naturally infected with M. avium or M. bovis (B). Size standards, reported in kDa, are indicated to the left. Assignments for the blots were as follows: lane 1, protein size standards; lane 2, MAP1152; lane 3, MAP1156; lane 4, LacZ.

We also followed the reactivity of the proteins against serum samples taken at different time points during natural infection. Samples corresponded to bleeds taken 9 to 14 months apart, corresponding to disease progression from subclinical to clinical infection. Results obtained with these samples (Fig. 4) indicated that MAP1152 did not react with any of the serum samples (Fig. 4, upper panel, lanes 1 to 4), while MAP1156 (Fig. 4, middle panel, lanes 1 to 4) and M. avium subsp. paratuberculosis K-10 whole-cell extract (Fig. 4, lower panel) displayed increasing reactivities with samples from the subclinical (Fig. 4, lanes 1 and 2) and clinical stages (Fig. 4, lanes 3 and 4).
Both proteins reacted with the anti-MBP monoclonal antibody control (Fig. 4, lane 5), although MAP1152 yielded a weaker reaction.

Seroreactivity of recombinant protein with sera from M. avium subsp. paratuberculosis-infected and noninfected cattle by ELISA. As the ELISA technology is readily adaptable to diagnostic applications, we also determined the reactivities of MAP1152 and MAP1156 by this method. In addition, this assay is generally performed to evaluate the antigen-antibody reaction in the absence of denaturing agents. Thus, both linear and conformational epitopes may contribute to the overall reactivity. Due to limiting amounts of serum samples, the ELISA was performed using archived serum samples which were previously evaluated with the Idexx test at the University of Nebraska—Lincoln Veterinary Diagnostic Laboratory (Table 1).

Each sample was tested in triplicate against LacZ (negative-control antigen) and on three different days in duplicate (day 3) or triplicate (days 1 and 2) to evaluate reproducibility and performance against MAP1152, MAP1156, and a standard M. avium subsp. paratuberculosis antigen control (the Idexx antigen, a proprietary mixture of M. avium subsp. paratuberculosis antigens) included in the Idexx test kit (see Table S2 in the supplemental material). Each antigen showed low reactivity and low variability as indicated by the error bars in Fig. 5. With the M. avium subsp. paratuberculosis infection results in a humoral response directed against epitopes present in MAP1152, MAP1156, and the Idexx antigen. However, absorbance values obtained using MAP1152 and MAP1156 as the capture antigens were lower than those attained with the Idexx capture antigen. This performance is not surprising, because these results were obtained with the standardized Idexx test protocol.

Comparative analysis of the reactivity of each serum-antigen combination was also carried out (Fig. 6). Reactivity trends were similar for both MAP1152 and MAP1156, as all samples with higher absorbance readings for MAP1152 also yielded higher values for MAP1156. The Idexx antigen followed a similar trend, except for the positive control, as all three M. avium subsp. paratuberculosis antigens yielded similar absorbance values. In contrast, three seropositive samples (EDNA, 308, and 2010-07) yielded significantly higher absorbance values for the Idexx antigen than for MAP1152 and MAP1156. No samples were expected to yield above-background absorbance readings with LacZ, the negative antigen control carrying the MBP tag. However, the reactivity of seropositive samples against LacZ was also more variable, as indicated by the error bars in Fig. 5. With the M. avium subsp. paratuberculosis capture antigens we were able to differentiate, in the combined analysis, between the groups of seropositive and seronegative samples. Thus, M. avium subsp. paratuberculosis infection results in a humoral response directed against epitopes present in MAP1152, MAP1156, and the Idexx antigen. However, absorbance values obtained using MAP1152 and MAP1156 as the capture antigens were lower than those attained with the Idexx capture antigen. This performance is not surprising, because these results were obtained with the standardized Idexx test protocol.
is indicated (see inset for pattern key). The reaction to each antigen
(0.010 mg) was evaluated by ELISA against sera from cattle naturally in-
fected with M. avium subsp. paratuberculosis and sera from culture-
negative cattle. Each serum was diluted 1:25 in Idexx dilution buffer.

FIG. 6. Individual responses of serum samples from infected and
noninfected cattle to recombinant antigens. Antigen (0.010 mg) reac-
tivity was evaluated by ELISA against sera from cattle naturally in-
fected with M. avium subsp. paratuberculosis and sera from culture-
negative cattle. Each serum was diluted 1:25 in Idexx dilution buffer.
Each column represents mean absorbance (triplicate measurements
against LacZ; average measurements on three different days in dupli-
cate or triplicate for other antigens, as indicated in Table S2 of the
supplemental material) per antigen, ± standard errors of the means
from noninfected (−) or infected (+) cattle, as evidenced from the
original classification of serum samples. The reaction to each antigen
is indicated (see inset for pattern key).

or negative based on the P value obtained for the comparison
against the negative-control serum for the corresponding test
antigen. This analysis indicated that the nonspecific MBP-
LacZ antigen control identified all samples, except EDNA, as
seronegative; in contrast, antigens MAP1152 and MAP1156
misclassified only the seropositive sample 2010-07 as seroneg-
avative (see Table S4). Thus, overall, all M. avium subsp. para-
tuberculosis antigens yielded a classification of serum samples
consistent with the original test.

DISCUSSION

Development of effective strategies for the control of JD
remains one of the most challenging issues in animal health
(15, 19). Advances in M. avium subsp. paratuberculosis genom-
ics and molecular genetics provide an integrated rational ap-
proach to solve this problem (1, 3, 29). In this context, the
search for new diagnostic tests can be most effective if com-
bled with novel approaches to vaccination and knowledge of
what the test indicates regarding the underlying mechanisms of
disease pathogenesis. Targeting of the MAP1152-MAP1156
gene cluster was based on the identification of an attenuating
mutation possibly related to the expression of this cluster and
a potential role of the encoded proteins as B- or T-cell anti-
gens. An attenuated mutant may serve as a candidate live
attenuated vaccine strain and the protein as a subunit vaccine
or diagnostic indicator; all relevant aspects are combined into
an integrated approach.

In this study, we demonstrated that both MAP1152 and
MAP1156 encode reactive B-cell epitopes, a result predicted
from the surface localization implied by in silico analysis (Table
2). This finding is also consistent with prior experimental
evidence on other PE/PPE proteins. For example, the M. tuber-
culosi s protein Rv2430c (PE25) was identified as a strong B-
cell antigen (12), and the seroreactivity of MAP3420 c was
demonstrated in cattle (36). In contrast, antigens MAP1518
(Map41; ortholog of Rv1808 [PPE32]) and MAP3184 (Map39;
ortholog of Rv3135 [PPE50]), the M. avium strain 104 MaPE
protein, and the cell wall-associated M. tuberculosis protein
Rv3873 (PPE68) serve as T-cell antigens (35, 37, 41).

MAP1152 and related PPE proteins MAP1153 and
MAP1155 are members of the ancestral PE sublineage IV
(22). The genes encoding these proteins belong to an ancestral
cluster that underwent duplication events from ancestral
ESAT-6 clusters but without a concomitant duplication of the
ESAT-6 genes and, thus, these paralogs are no longer associ-
ated with the ESAT-6 genes. PE/PPE genes are usually orga-
nized in operons encompassing at least several PE and/or PPE
members (46, 58). Biochemical evidence indicates that PE and
PPE function in pairwise combinations of interacting proteins
exposed to the cell surface (18, 46, 54), with the larger-sized
PPE proteins providing a pocket for the PE partner (54).
However, MAP1152 is organized in a cluster devoid of coding
sequences for PE proteins. Because the probability of PPE
proteins participating in pairwise associations decreases for
unlinked PE and PPE genes (46), the function of MAP1152
may or may not require a PE partner. Instead, MAP1152 may
play additional roles in the mechanisms of pathogenesis, as
shown for other PE/PPE proteins. For example, M. tuberculosis
transposon mutants of the PE/PPE genes Rv1807 (PPE31),
Rv3872 (PPE35), and Rv3873 (PPE68) are attenuated in mice
(49). Likewise, a transposon mutant in the M. avium PPE gene
homologous to Rv1787 (PPE25) displayed impaired growth in
macrophages, reduced virulence in mice, and failed to prevent
phagosome acidification (26, 30). Thus, a group of PE and PPE
proteins may be necessary for intracellular survival.

MAP1156 is also a B-cell antigen, with stronger reactivity
than MAP1152 in Western blot assays, a property also consis-
tent with its reactivity with immune mouse and rabbit sera and
inferred surface localization. MAP1156 belongs to the unchar-
acterized protein family UFP0089. M. tuberculosis encodes 15
members of this family, which includes proteins with triacyl-
glycerol synthase (TGS) activity (16). The M. tuberculosis ORF
Rv1425 is the closest homolog to MAP (Table 2), but this ORF
has been shown not to possess significant TGS activity, at least
under the conditions tested. One possible role consistent with
a strong humoral reaction is that this ORF “hitchhiked” with
M. avium subsp. paratuberculosis into a coexpression unit that
modulates the immune response. Microorganisms of the M.
tuberculosis complex possess a large number of PE-PGRS pro-
teins that are associated with immunoregulatory roles (4, 17).
However, as indicated above, the M. avium subsp. paratubercu-
losis evolutionary lineage separated prior to the further ex-
pansion of the ESAT-6 region V that gave rise to the PE-
PGRS and PPE-MPTR sublineage V PE/PPE proteins (22).
Thus, the absence of PE-PGRS proteins may require the re-
cruitment of other proteins, for example, MAP1156, to play
this immunomodulatory role. Future experiments will be di-
rected to identify T-cell epitopes in both MAP1152 and
MAP1156. These tests are indispensable for determining the
major roles of these antigens in immunopathogenesis. For
example, it is possible that the PPE protein MAP1152, the weaker B-cell antigen in Western immunoblotting analyses, may elicit a predominant T-cell response early in infection, with MAP1156 exerting a countermodulating B-cell response, most favorable for *M. avium* subsp. *paratuberculosis* to maintain a chronic infection. This hypothesis is consistent with the increasing MAP1156 seroreactivity observed with serum samples withdrawn as JD progressed from the subclinical to clinical stage (Fig. 4). However, a more detailed study of linear and conformational epitopes in these proteins, especially for MAP1152, should be undertaken, as conformational epitopes may not be reactive in Western immunoblot assays.

The B-cell reactivities of both MAP1152 and MAP1156 in Western blot assays and the ELISA with serum samples from *M. avium* subsp. *paratuberculosis*-infected cattle are likely associated with private rather than cross-reactive or shared epitopes from related *M. avium* subsp. *paratuberculosis* proteins. In this context, the closest paralog to MAP1152 is MAP1518, with 47% identity. Likewise, the closest paralog to MAP1156 is MAP1969c, with 38% identity (see Table S5 in the supplemental material). The low degree of reactivity of MAP1152 in the immunoblot assays against sera from *M. bovis*-infected animals may be explained in a similar manner, as the closest homolog (Mb1837) shares only 50% identity. In contrast, the low reactivity of MAP1156 against the *M. bovis* serum, and of MAP1152 and MAP1156 against *M. avium* hominis suis serum, may be associated with low expression levels in these microorganisms. Otherwise, the corresponding proteins are highly homologous, with 86 to 99% identity (see Table S5) and, thus, likely to be highly cross-reactive, as most epitopes are shared. Moreover, the MAP1152-MAP1156 cluster organization is conserved between *M. avium* subsp. *paratuberculosis* and *M. avium* 104 (a sequenced isolate of *M. avium* subsp. *hominis suis*), with both genomes possessing highly homologous genes within this region. However, sequence divergence with *M. avium* 104 occurs upstream from MAP1152 that could affect gene regulation. Nonetheless, to substantiate these findings for the development of diagnostic tests, it will be necessary to test a larger group of cattle infected with *M. bovis*, *M. avium* subspecies, and other environmental species, such as *Mycobacterium kansasii*.

Interestingly, MAP1152, MAP1156, and the Idexx antigen yielded similar absorbance values against the standardized Idexx positive-control bovine serum included in the Idexx kit, which is from a single naturally infected Holstein cow (Table 1). However, the other three seropositive clinical samples reacted more strongly with the Idexx antigen (Fig. 6). As indicated above, these results may be due to methodological aspects, as the overall assay optimization was based on the Idexx protocol. Alternatively, or by confounding effects, the increased reactivity in these samples against the Idexx antigen may in part reflect the presence of cross-reactive antibodies against the various *M. avium* subsp. *paratuberculosis* proteins present in the Idexx antigen.

In summary, *M. avium* subsp. *paratuberculosis*-infected cattle mount a humoral response to both MAP1152 and MAP1156. Further research is needed to determine the values of these recombinant proteins as diagnostic capture antigens, subunit vaccines, markers of disease progression, and their suitability for the development of tests for diagnosis of infected from vaccinated animals (DIVA), coupled with the development of live attenuated deletion mutant marker vaccines (13, 59).

**ACKNOWLEDGMENTS**

This work was supported by funds from the Johnne’s Disease Integrated Program (J.P.B. and R.G.B.) and USDA-ARS (I.P.B.), USDA grant CSREES-NRI 2004-35204-14231 (R.G.B. and C.J.C.), the BARD program grant IS-3673-05C (R.G.B.), USDA Animal Health Project NEB141-141 (R.G.B.), and the Department of Veterinary and Biomedical Sciences at the University of Nebraska (D.R.S., D.S.M., and R.G.B.). We thank Malory Becker for her assistance to A.L.P. in preparation of materials and reagents. We thank Steve Kachman for assistance with SAS analysis.

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