Development and Characterization of Monoclonal Antibodies and Aptamers against Major Antigens of *Mycobacterium avium* subsp. *paratuberculosis*"الية

John P. Bannantine,¹* Thomas J. Radosevich,¹ Judith R. Stabel,¹ Srinand Sreevatsan,² Vivek Kapur,³ and Michael L. Paustian¹

National Animal Disease Center, USDA-ARS, Ames, Iowa,¹ and Veterinary Population Medicine Department² and Departments of Microbiology and Biomedical Genomics,³ University of Minnesota, St. Paul, Minnesota

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Specific antibodies, available in unlimited quantities, have not been produced against *Mycobacterium avium* subsp. *paratuberculosis*, the bacterium that causes Johnne’s disease (JD). To fill this gap in JD research, monoclonal antibodies (MAbs) against *M. avium* subsp. *paratuberculosis* were produced from BALB/c mice immunized with a whole-cell extract of *M. avium* subsp. *paratuberculosis*. A total of 10 hybridomas producing MAbs to proteins ranging from 25 to 85 kDa were obtained. All MAbs showed some degree of cross-reactivity when they were analyzed against a panel of whole-cell protein lysates comprising seven different mycobacterial species. The MAbs were characterized by several methods, which included isotype analysis, specificity analysis, epitope analysis, reactivity in immunoblot assays, and electron microscopy. The identities of the antigens that bound to two selected MAbs were determined by screening an *M. avium* subsp. *paratuberculosis* lambda phage expression library. This approach revealed that MAb 9G10 detects MAP1643 (isocitrate lyase) and that Mab 11G4 detects MAP3840 (a 70-kDa heat shock protein), two proteins present in high relative abundance in *M. avium* subsp. *paratuberculosis*. The epitopes for Mab 11G4 were mapped to the N-terminal half of MAP3840, whereas Mab 9G10 bound to the C-terminal half of MAP1643. Aptamers, nucleic acids that bind to specific protein sequences, against the hypothetical protein encoded by MAP0105c were also generated and tested for their binding to *M. avium* subsp. *paratuberculosis* as well as other mycobacteria. These detection reagents may be beneficial in many JD research applications.

The genus *Mycobacterium* comprises a diverse group of animal and human pathogens as well as saprophytes, many of which are ubiquitous in the environment. *Mycobacterium avium* subsp. *paratuberculosis* is a member of the *Mycobacterium avium* complex (MAC) and an animal pathogen that is highlighted by the large financial burden that it places on the dairy industry due to Johnne’s disease (JD). Figures extrapolated from the 1996 NAHMS dairy survey suggest that the cost of this disease was over $200 million per year (25). The growing recognition of *M. avium* subsp. *paratuberculosis* infection in wildlife species is of considerable concern, since it may affect our ability to control or eradicate JD from domesticated animals (10, 11).

Despite the research difficulties and economic consequences of JD, very few reports have described specific, antigen-based detection reagents for *M. avium* subsp. *paratuberculosis*. With the exception of a single study published 10 years ago (24), the scientific literature is silent on the subject of *M. avium* subsp. *paratuberculosis* monoclonal antibodies (MAbs) and their use in JD research. Very recently, single-chain antibodies were selected by cloning heavy and light chains from sheep with JD (6). This effort has resulted in two very promising recombinant antibodies; however, the *M. avium* subsp. *paratuberculosis* proteins that these antibodies react with remain unknown. The overall lack of detection reagents for *M. avium* subsp. *paratuberculosis* is in stark contrast to the availability of detection reagents for other bacterial pathogens of cattle, such as *Brucella* or *Mycobacterium bovis*, for which scores of MAbs are available to researchers (7, 9, 19, 21, 23, 32).

Against this background, recent changes have modified the JD research landscape. Within the United States, a national consortium, entitled the Johnne’s Disease Integrated Program (JDIP; www.jdip.org), has identified the high research priorities and the knowledge gaps necessary to combat JD. Similar JD research consortiums have also recently formed in Europe and New Zealand. One of the priorities identified by JDIP is the development of specific detection reagents such as MAbs for *M. avium* subsp. *paratuberculosis*. More than just their obvious application for the diagnosis of JD, MAbs are critical reagents in cell biology and pathogenesis studies, including studies of macrophage-pathogen interactions, studies that use Luminex and magnetic bead technologies, as well as histopathology studies. MAbs that detect specific *M. avium* subsp. *paratuberculosis* proteins are ideal for incorporation into diagnostic assays such as those already developed for *Campylobacter* (8) and *Escherichia coli* (16). Furthermore, MAbs have application in the histopathological examination of infected tissues, typically the lamina propria of the intestine, where acid-fast staining has historically been used to demonstrate the presence of *M. avium* subsp. *paratuberculosis*, albeit with a low sensitivity and specificity (30).

The results of this study have identified and characterized...
novel MAbs against \textit{M. avium} subsp. \textit{paratuberculosis} with potential use in several JD-related research applications. We demonstrate here the specificity, subcellular location, and utility by electron microscopy for each MAb developed. In addition, we have identified the corresponding \textit{M. avium} subsp. \textit{paratuberculosis} proteins detected by two of these MAbs.

\section*{MATERIALS AND METHODS}

\textbf{Myobacterial antigens.} The National Animal Disease Center’s mycobacterial culture collection served as the source of all strains used in this study (Table 1). \textit{M. avium} subsp. \textit{paratuberculosis} ATCC 19698 is the type strain; \textit{M. avium} subsp. \textit{paratuberculosis} Linda is a human isolate; and all other \textit{M. avium} subsp. \textit{paratuberculosis} strains tested are cattle isolates, including K-10, the sequenced strain (20). All myobacteria were cultivated in Middlebrook 7H9 medium supplemented with oleic acid-albumin-dextrose-catalase (Hardy Diagnostics, Santa Maria, CA). For the cultivation of \textit{M. avium} subsp. \textit{paratuberculosis}, mycobactin J (2 mg/liter; Allied Monitor, Fayette, MO) was added to the Middlebrook-oleic acid-albumin-dextrose-catalase medium. The whole-cell-sonicated extracts of mycobacterial species and isolates were prepared for use as antigens in immunoadsorbs, as described previously (31). The sonicated extracts were centrifuged at 50,000 \( \times g \) for 1 h. The pellet was resuspended in an equal volume of phosphate-buffered saline (PBS; 150 mM NaCl, 10 mM NaPO4, pH 7.4) and was thereafter used as the membrane-enriched fraction. The supernatant was collected and used as the cytosol-enriched fraction. All samples were assayed for protein content (Bio-Rad Laboratories [Richmond, CA] protein assay) and were stored at \(-20^\circ\text{C}\).

Expression clones producing recombinant \textit{M. avium} subsp. \textit{paratuberculosis} proteins were constructed by using the detailed methods described previously (4) and briefly mentioned below. All recombinant fusion proteins contained maltose-binding protein (MBP) as the tag for use in affinity purification. The MBP fusion was produced by cloning the \textit{M. avium} subsp. \textit{paratuberculosis} gene of interest into the pMAL-c2 expression vector (New England Biolabs, Beverly, MA). The entire reading frame or partial reading frame was amplified with AmpliTaq-Gold DNA polymerase (Applied Biosystems, Branchburg, NJ) and purified \textit{M. avium} subsp. \textit{paratuberculosis} K-10 genomic DNA as the template. The upstream and downstream oligonucleotides for each amplification are listed in Table 2. The vector and amplification product were each digested with XbaI and HindIII and purified from 1% agarose gels with Gene Clean (Bio101). Ligation of these products yielded in-frame fusions after overnight ligation at 16°C, the products were transfomed into competent E. coli DH5a cells (Invitrogen). Constructs from selected transformants in each experiment were authenticated by DNA sequencing. Each fusion protein was overexpressed and purified by maltose affinity chromatography by using an amylose resin supplied by New England Biolabs. The detailed methods used for the induction and affinity purification of MBP/MAP fusion proteins have been described previously (4).

\begin{table}[h]
\centering
\caption{Oligonucleotide primers used to amplify MAP1643, MAP3840, and MAP10105c}
\begin{tabular}{lllll}
\hline
Primer name & Sequence & Location within gene \footnote{a} & Location\footnote{b} & Reference or source \hline
MAP1643F & AATCTCTTACGATACCTGACAGAGGTACCAGAG & 10 to 32 & \\
MAP1643R & GCCATCGTCGTCCATGCGCGGTGTAG & 2266 to 2287 & \\
MAP3840F2 & ATCCTCTTACGATACCTGACAGAGGTACCAGAG & 1012 to 1041 & \\
MAP3840R2 & GCCATCGTCGTCCATGCGCGGTGTAG & 1153 to 1174 & \\
MAP3840R & ATCCTCTTACGATACCTGACAGAGGTACCAGAG & 1 to 24 & \\
MAP3840F & GCCATCGTCGTCCATGCGCGGTGTAG & 1849 to 1872 & \\
MAP3840F2 & ATCCTCTTACGATACCTGACAGAGGTACCAGAG & 859 to 882 & \\
MAP3840R & GCCATCGTCGTCCATGCGCGGTGTAG & 856 to 876 & \\
MAP3840R2 & ATCCTCTTACGATACCTGACAGAGGTACCAGAG & 163 to 183 & \\
218-4 & CTTCTCTTACGATACCTGACAGAGGTACCAGAG & 1837 to 1856 & \\
218-9 F & CTTCTCTTACGATACCTGACAGAGGTACCAGAG & 1609 to 1629 & \\
218-9 R & GCCATCGTCGTCCATGCGCGGTGTAG & 2987 to 2966 & \\
\hline
\end{tabular}
\footnote{a} Underlined nucleotides represent restriction endonuclease cut sites. The XbaI recognition sequence is TCTAGA, and AAGCTT is the HindIII recognition site.
\footnote{b} The numbers represent the nucleotide position within the respective gene. The gene is indicated within the primer name, except that 218-4 F, 218-4 R, 218-9 F, and 218-9 R target MAP10105c.
\end{table}
tein lysate (0.1 mg total) was loaded into the single, long lane and the gel was subjected to electrophoresis. Blotting was then carried out as described immediately above. The complete panel of MAbs was evaluated on preparative immunoblots placed in a slot-blot device (Bio-Rad), such that individual culture supernatants could be loaded into independent slots on the same blot. This method enabled the most direct comparison of the antigen sizes detected by the respective MAbs.

Aptamer selection against recombinant MAP0105c. An aptamer library that consisted of a randomized 40-mer DNA sequence flanked by two known 28-mer primer binding sites (5′-TGTGCTCTGTTCTTATGCAGAAGTGC-N60-AT TTCTCCTACTGGGATAGTTGGATAT-3′, where N60 represents 40 random nucleotides with equimolar amounts of A, C, G, and T) was synthesized (Integrated DNA Technology, Inc., Coralville, IA). Recombinant MBPs were used in immunoblot analysis to determine if the location of antibody described under “Mycobacterial antigens” above. The primers for these trun-
cated terminal halves of each were produced as a fusion with MBP by the method of MAP1643 (AceAb) and MAP3840 (DnaK) as well as the N-terminal and C-terminal halves of MAP0105c, respectively, served as targets for combinatorial library selection. The aptamer library was enriched for candidates unique to each protein by use of a counter SELEX protocol and standard lateral flow chromatography methods, as described previously (29). In brief, the aptamer library was exposed to MBP prior to exposure to 218-4 or 218-9 so as to exclude any candidates that bound to the MBP affinity tag. After six rounds of the counter SELEX protocol with each protein, the aptamer library was screened for cross-reactivity. All selected candidates appeared to bind to 218-4 and 218-9 alone. However, aptamers selected against each of these molecules cross-reacted. Thus, a second round of the counter SELEX protocol was applied, whereby aptamers exposed to 218-4 were subsequently exposed to 218-9. These manipulations were expected to remove any cross-reacting aptamers. After two additional rounds of the counter SELEX protocol, 50 clones from libraries derived from the two proteins were cloned and sequenced. Several candidate aptamers were identified for specificity analysis. Aptamers with no or no cross-reactivities between the two proteins were identified and were selected for use in further studies. Dot blots with the aptamers were performed as follows. A nitrocellulose membrane strip (5 by 5 in.; PROTRAN; Schleicher & Schuell Inc., Keene, NH) was cut and marked with a pencil for orientation. Positive and negative controls consisted of a 1-μl aliquot of 10 μM any biotin-
ylated oligonucleotide spotted on the nitrocellulose membrane strip and cross-linked under UV light for 5 min (positive control) as well as 1 μl of purified BSA (0.05 mg/ml; negative control). Test dots of 1 μl of an E. coli cell lysate suspension (E. coli negative control), 1 μl of 1 mg/ml MBP-LacZ (MBP negative control), 1 μl of 1 mg/ml MBP-218-4, and 1 μl of 1 mg/ml MBP-218-9 were also spotted on the strip and allowed to air dry. The strips were processed for immunoblot analysis as described in the preceding section.

Epitope mapping of selected recombinant proteins. The full-length proteins of MAP1643 (AceAb) and MAP3840 (DnaK) as well as the N-terminal and C-terminal halves of each were produced as a fusion with MBP by the method described under “Mycobacterial antigens” above. The primers for these truncated and full-length constructs are shown in Table 2. These recombinant proteins were used in immunoblot analysis to determine if the location of antibody binding was at the N-terminal or the C-terminal half of each protein.

Electron microscopy. All fixation and staining procedures were conducted at room temperature. Mycobacterial bacilli were fixed for 2 to 4 h in 2.5% glutar-
alddehyde in 0.1 M cacodylate buffer, pH 7.4. Fixed cells were washed in the same buffer, they were incubated with goat

FIG. 1. Immunoblot analysis of M. avium subsp. paratuberculosis whole-cell lysates with hybridoma culture supernatants containing MAbs. Ten hybridoma culture supernatants were loaded onto independent lanes and slots and analyzed in parallel on a preparative slot immunoblot containing M. avium subsp. paratuberculosis homogenates separated by SDS-PAGE. Antibodies bound to M. avium subsp. paratuberculosis proteins ranging in size from 25 kDa to 95 kDa. Lanes: 1, MAb 11F6; 2, MAb 5A10; 3, MAb 13A4; 4, MAb 4B6; 5, MAb 12C9; 6, MAb 11G4; 7, MAb 9G10; 8, MAb 14D4; 9, MAb 14G3; 10, MAb 14G11. Protein size standards are indicated in kilodaltons in the left and right margins.

RESULTS

MAbs against M. avium subsp. paratuberculosis whole-cell homogenates. To obtain MAbs against M. avium subsp. paratuberculosis proteins, 6-week-old female BALB/c mice were immunized with a sonicated protein lysate of M. avium subsp. paratuberculosis K-10, as described in Materials and Methods. Ten hybridomas were identified by using this immunization regimen. By immunoblot analysis, the hybridomas reacted with a variety of proteins of different sizes from approximately 25 kDa to 85 kDa, as shown in Fig. 1. However, the MAbs designated 11F6 and 9G10 each reacted with a protein of a similar size at approximately 85 kDa (Fig. 1, lanes 1 and 7), and MAbs 13A4 and 11G4 also reacted with a similarly sized protein at approximately 66 kDa (Fig. 1, lanes 3 and 6). MAb 5A10 initially reacted with a single band in the 45-kDa region; however, a subsequent tissue culture supernatant obtained from this hybridoma showed no reactivity (Fig. 1, lane 2), indicating that this hybridoma had stopped secreting antibody. The rest of the culture supernatants reacted strongly with a single, well-defined band (Fig. 1, lanes 1, 3 to 7, and 10) or two bands (Fig. 1, lanes 8 and 9). Because MAb 5A10 was not a stably secreting hybridoma, only the remaining nine MAbs were used in further experiments. A preliminary characterization of each stable MAb was performed by defining the isotype and antigen size. The isotype specificity of each MAb is presented in Table 3, along with the estimated size of the M. avium subsp. paratuberculosis proteins to which they bind.

Identification of M. avium subsp. paratuberculosis antigens that bind to selected MAbs. As shown in Fig. 1, several MAbs were obtained from mice immunized with a whole-cell homoge-
nate of M. avium subsp. paratuberculosis. However, the M. avium subsp. paratuberculosis antigens that react with these MAbs are unknown. Therefore, four of the MAbs were used to screen an M. avium subsp. paratuberculosis lambda phage expression library developed previously (5). No positive plaques were obtained with MAbs 12C9 and 14G3; however, positive plaques were obtained when the library was screened with MAbs 11G4 and 9G10. DNA sequencing of the subcloned lambda phage inserts revealed open reading frames for MAP3840 (dnaK) and MAP1643 (aceAb) that reacted with MAbs 11G4 and 9G10, respectively. In order to
conclusively demonstrate that these two MAbs reacted with the identified gene products, the MAP3840 and MAP1643 coding sequences were cloned and expressed in *Escherichia coli*. The purified recombinant fusion proteins representing MAP3840 and MAP1643 were analyzed by immunoblotting, which showed that these gene products were detected by the MAbs (Fig. 2). AceAb is a probable isocitrate lyase enzyme that is involved in the glyoxylate cycle (14). DnaK is the 70-kDa heat shock protein (34).

Mapping multiple MAbs to MAP3840 and MAP1643. Once the identities of the antigens that reacted with MAbs 9G10 and 11G4 were discovered, further experimentation quickly revealed that additional independently isolated MAbs, 13A4 and 11F6, also detected MAP3840 and MAP1643, respectively (Table 3 and Fig. 2). One-dimensional sodium dodecyl sulfate (SDS)-PAGE separation of the fractionated lysates, followed by excision and mass spectroscopy of prominent Coomassie blue-stained bands, showed that both the MAP3840 and the MAP1643 gene products were present in high relative abundance in *M. avium* subsp. *paratuberculosis* (data not shown). Therefore, because of the antigenicity and high relative abundance of the MAP1643 and the MAP3840 gene products, it was not surprising to obtain multiple MAbs to these proteins. To determine if these MAbs detected the same epitopes or distinct epitopes within the same protein, the N-terminal and C-terminal halves of each protein were cloned and purified from the recombinant *E. coli* cells. These proteins, along with the corresponding full-length proteins, were then analyzed by immunoblotting with each of the respective MAbs. Both MAb 11F6 and MAb 9G10 bound to the C-terminal half of AceAb, as shown in Fig. 2. Furthermore, MAb 11G4 detected the N-terminal half of DnaK, but MAb 13A4 detected only the full-length protein (Fig. 2). These data suggest that MAbs 11G4 and 13A4 may bind to distinct epitopes within DnaK; however, because MAbs 11F6 and 9G10 both bound to the C-terminal half of AceAb, it remains inconclusive if the epitope is shared or distinct.

**Specificities of antimycobacterial MAbs.** Antibodies were next screened by immunoblotting with whole-cell lysate preparations of nine mycobacterial species and subspecies, includ-
FIG. 3. Evaluation of MAbs against whole-cell homogenates from several mycobacterial species. Immunoblot analysis shows that the reactivity of each MAb is observed with more than just M. avium subsp. paratuberculosis lysates. (A) Lanes: 1, M. silvaticum; 2, M. scrofulaceum; 3, M. abscessus; 4, M. avium subsp. paratuberculosis K-10; 5, M. avium (strain TMC702); 6, M. bovis (strain 95-1315); 7, M. phlei; 8, M. bovis BCG; 9, M. avium subsp. paratuberculosis ATCC 19698; 10, M. avium subsp. avium (strain TMC715); 11, M. avium subsp. paratuberculosis (Linda); 12, M. intracellulare; 13, M. kansasi. (B) Lanes: 1, M. silvaticum; 2, M. scrofulaceum; 3, M. abscessus; 4, M. avium subsp. paratuberculosis K-10; 5, M. avium subsp. avium (strain TMC702); 6, M. bovis (strain 95-1315); 7, M. phlei; 8, M. avium subsp. paratuberculosis ATCC 19698; 9, M. avium subsp. avium (strain TMC715); 10, M. avium subsp. paratuberculosis (strain Linda); 11, M. intracellulare; 12, M. kansasi. Kilodalton size standards are indicated in the left margin, and the MAb used is indicated in the right margin.

FIG. 4. Localization of antigens in fractionated M. avium subsp. paratuberculosis cell lysates. Equal amounts (0.5 µg/lane) of cell lysates from membrane-enriched M. avium subsp. paratuberculosis K-10 (lanes M) and cytoplasmic enriched fractions of M. avium subsp. paratuberculosis K-10 (lanes C) were loaded onto SDS-polyacrylamide gels and analyzed by immunoblotting with selected MAbs, which are indicated beneath each blot. Three MAbs detected proteins in the cytoplasmic enriched fraction, and four MAbs detected proteins present in the membrane-enriched fraction. Kilodalton size standards are indicated in the left margin.

for MAbs 9G10 and 14G11 was obtained by using this MAb. MAb 14D4 showed the most unexpected immunoblot reactivity, with bands of widely varying sizes detected among the different mycobacterial species (Fig. 3). Surprisingly, MAb 14D4 was also the only antibody that did not detect either of the M. avium subsp. avium isolates but reacted with the more distantly related mycobacteria, such as M. phlei and M. bovis. While all antibodies showed some degree of cross-reactivity with other mycobacterial species, MAb 12C9 showed strong reactivity with the two M. avium subsp. paratuberculosis bovine isolates (Fig. 3, lanes 5 and 9) and weaker reactivity with Crohn’s disease isolate Linda (Fig. 3, lane 11). The 4B6 antibody detected a protein that was the most conserved among the mycobacteria, as a band of similar size was observed in every species and subspecies tested (Fig. 3).

Location of M. avium subsp. paratuberculosis antigens that bind to MAbs. Antigen localization was determined by immunoblot analysis of the MAbs against membrane-enriched and cytosol-enriched fractionated lysates, prepared as described in Materials and Methods. Note that MAbs 12C9, 14D4, 14G3, and 14G11 all bound to an unidentified M. avium subsp. paratuberculosis protein that is primarily localized in the cell membrane fraction (Fig. 4), whereas MAbs 4B6, 9G10, and 11G4 (Fig. 4) and MAbs 11F6 and 13A4 (data not shown) all detected proteins that were present predominantly in the cytoplasmic fraction. The protein detected by MAb 14G3 may form a dimer complex in the membrane-enriched fraction, as a protein band approximately twice the size of the monomer was also detected (Fig. 4).

Detection of M. avium subsp. paratuberculosis bacilli by immunoelectron microscopy with the MAbs developed in this study. Each of the MAbs was next evaluated to determine reactivity levels with mycobacterial bacilli by immunoelectron microscopy. Of all the MAbs tested, MAbs 14D4 and 9G10 showed the most immunogold labeling, which indicates antibody binding to M. avium subsp. paratuberculosis (Fig. 5). Although MAb 4B6 reacted strongly with all mycobacteria tested by immunoblotting, no reactivity by immunoelectron microscopy was observed, suggesting that either the processing for microscopy damaged the epitope or the epitope is perhaps masked by another protein(s). None of the labeling patterns...
were distinct enough to confirm the subcellular locations of the antigens to which they bind, although MAb 14D4 seemed to label mostly at the periphery of the bacilli (Fig. 5). This labeling pattern is consistent with what was observed by immunoblotting of the fractionated lysates probed with MAb 14D4 (Fig. 4).

Development of aptamers to the \textit{M. avium} subsp. \textit{paratuberculosis} hypothetical protein encoded by MAP0105c. In an attempt to obtain a more specific reagent to detect \textit{M. avium} subsp. \textit{paratuberculosis}, aptamers were screened to identify those that bind to the MAP0105c gene product recombinantly produced in \textit{E. coli}. Aptamers are short nucleic acid sequences that bind to specific protein epitopes with a high affinity (27). MAP0105c is a gene reported to be unique to \textit{M. avium} subsp. \textit{paratuberculosis} (2). In that study, MAP0105c was designated gene 218, because the project was published prior to annotation of the \textit{M. avium} subsp. \textit{paratuberculosis} K-10 genome (20).

Three aptamers, designated 43, 93, and 94, were obtained following repeated screening and enrichments with the recombinant protein. Immunoblot analysis with these aptamers (Fig. 6A) and dot blot analyses of aptamers to MAP0105c (Fig. 6B) were conducted to confirm the binding specificity. The antigenic epitopes recognized by these aptamers were further examined by immunoblotting and dot blotting of whole-cell sonicated extracts from various \textit{M. avium} subsp. \textit{paratuberculosis} strains and other mycobacterial species. The results showed that the aptamers selectively recognized the MAP0105c gene product from \textit{M. avium} subsp. \textit{paratuberculosis} K-10, distinguishing it from other \textit{M. avium} subsp. \textit{paratuberculosis} strains and related mycobacterial species.
showed binding to the protein of the correct size, but reactivity was also seen in most of the mycobacteria analyzed (Fig. 6A). This cross-reactivity with other mycobacteria prompted a reexamination of MAP0105c by BLAST analysis. This analysis still suggested that the nucleotide sequence of MAP0105c is present only in M. avium subsp. paratuberculosis and not other bacteria, including mycobacteria; however, BLAST analysis with the translated sequence did show hits in Streptomyces (30% identity), Frankia (22% identity), and Rhodococcus (28% identity). MAP0105c was also produced as N-terminal and C-terminal halves (designated 218-4 and 218-9, respectively), and dot blot analysis with these truncated proteins shows that all three aptamers detected the N-terminal half (Fig. 6B). Furthermore, all aptamers reacted more strongly with the non-denatured recombinant protein than with the denatured recombinant protein.

DISCUSSION

The predominant difficulties in working with M. avium subsp. paratuberculosis—the slow growth, the underdeveloped technology for genetic modification, and the intramacrophage location during infection, combined with a lack of knowledge regarding the 1,810 M. avium subsp. paratuberculosis hypothetical and unknown proteins—present challenges that require unique approaches. The production of MAbs, such as those produced in this study, is one critical tool currently lacking in JD research. The absence of these reagents has blocked the progress of unique research approaches directed at controlling this disease.

All MAbs and aptamers produced in this study cross-reacted with one or more species of mycobacteria. This result is not surprising, given the high degree of genetic similarity that M. avium subsp. paratuberculosis shares with other members of the MAC complex (26), and highlights the challenges encountered in the development of subspecies-specific detection reagents for this pathogen. However, what is surprising is that MAb 14D4 did not react with M. avium subsp. avium, which is most closely related to M. avium subsp. paratuberculosis, and yet this same MAb reacted with the more distantly related species M. bovis and even M. phlei. These findings highlight the need to broadly test any new detection reagent across a large number of mycobacterial species. Furthermore, even if specificity is demonstrated within the mycobacterial genus, additional tests with species outside the genus may be necessary.

In an effort to obtain a more specific detection reagent for M. avium subsp. paratuberculosis, aptamers that bind to the MAP0105c gene product were obtained. Nucleic acid similarity searches and PCR surveys have previously suggested that this gene is present uniquely in M. avium subsp. paratuberculosis (2). The three aptamers identified in these studies all detected the N-terminal half of MAP0105c. However, aptamer 94 bound to nearly all mycobacteria tested (Fig. 6A), suggesting that MAP0105c has conserved epitopes. Because the aptamers clearly reacted with the E. coli-expressed fusion protein representing MAP0105c (Fig. 6B), we are confident that they bind specifically to the native MAP0105c protein produced by M. avium subsp. paratuberculosis. The unexpected cross-reactivity prompted a BLAST analysis of the nonredundant protein database with MAP0105c, which shows that the nucleic acid sequence is present uniquely in M. avium subsp. paratuberculosis; however, the translated sequence has similarity to a hypothetical protein from Streptomyces avermitilis, with a 30% amino acid identity, and a hypothetical protein from Frankia species (22% identity). Nonetheless, there is still no bioinformatic evidence to explain the cross-reactivity with other mycobacterial species observed in this study (Fig. 6A). Taken together, these results suggest that MAP0105c does have conserved epitopes and that at least sections of the gene product should not be considered M. avium subsp. paratuberculosis specific.

To identify the corresponding antigens, four MAbs were chosen and used to screen an M. avium subsp. paratuberculosis lambda phage expression library. It is interesting to note that only MAbs 11G4 and 9G10, both of which detected proteins present in the cytoplasm of M. avium subsp. paratuberculosis, were identified during the screening of the expression library. The other two MAbs, 12C9 and 14D4, used in the screening experiments reacted with proteins in the mycobacterial cell membrane fraction (Fig. 4). It is likely that the membrane proteins detected by MAbs 12C9 and 14D4 are not readily cloned or expressed or are underrepresented in the lambda phage library. An alternative strategy that could be used to identify these membrane proteins is to combine affinity purification with the MAbs to capture the native M. avium subsp. paratuberculosis protein and analyze the antibody-antigen complex by tandem mass spectroscopy. This method would enable limited sequence identification of the peptides from the captured antigen, thus overcoming cloning and expression obstacles.

Heat shock proteins, which belong to families of widely conserved proteins found in prokaryotes and eukaryotes, are commonly immunodominant antigens recognized following infection with many bacterial pathogens (1, 17, 18, 35). The M. avium subsp. paratuberculosis DnaK, encoded by MAP3840, appears to be immunodominant as well, since two of nine immortalized B-cell cultures secreting antibody to this protein were obtained. While this cytoplasmically located antigen is not unique to M. avium subsp. paratuberculosis, it is present in high relative abundance in mycobacterial bacilli cultured in Middlebrook 7H9 medium, which may also account for the identification of more than one MAb. The same is also true for AceAb, encoded by MAP1643.

Although aceAb is considered a metabolic gene encoding the isocitrate lyase enzyme used in the glyoxylate cycle, it has been shown to be upregulated in M. avium subsp. avium-infected macrophages (28), implicating it in virulence as well. In M. tuberculosis H37Rv, the isocitrate lyase gene actually consists of two overlapping genes (aceAa at 1,104 bp and aceAb at 1,197 bp) that share a single base pair at the 3’ end of aceAa and the 5’ end of aceAb but is a single 2,300-bp gene in M. tuberculosis CDC1551 (12). In M. avium subsp. paratuberculosis, aceAb appears to be a single open reading frame 2,289 bp in length sandwiched by two hypothetical genes, MAP1642 and MAP1644 (20).

As an initial step in defining the antigenic structure of DnaK and AceAb, the epitopes were mapped to either the N-terminal or the C-terminal halves of the proteins. Both MAbs 11F6 and 9G10 detected the C-terminal half of AceAb, suggesting that this half may contain more B-cell epitopes or perhaps a
single dominant epitope. In contrast, MAB 11G4 detected the N-terminal half of DnaK, while MAB 13A4 did not react with either half of DnaK and detected only the full-length protein. These data suggest that MABS 11G4 and 13A4 recognize distinct epitopes. The exact reason why MAB 13A4 detects only the full-length protein is unclear; however, one possibility is that the epitope is at the center of the protein and that by producing the two halves, the epitope is no longer intact. A more likely possibility is that the MAB detects a conformational or discontinuous epitope that is disrupted when only one half of the protein is represented.

From this study, four MABS that react with proteins present in the membrane fraction of M. avium subsp. paratuberculosis were identified. Thus, these proteins may even be surface exposed and, hence, immune targets for the host. Although these potential surface proteins remain to be identified, the MABS are nonetheless useful in many applications. Pathogenesis studies should include MABS that bind to surface molecules because they may block infection of cultured epithelial cells (3) or facilitate uptake and entry into macrophages (15). The results from these studies would determine if the proteins are important in adherence or invasion of epithelial cells that line the bovine or ovine intestine. More practically, these novel MABS may be used to purify and concentrate M. avium subsp. paratuberculosis from environmental samples, such as water or bulk milk tank samples, by immunomagnetic separation technologies (22, 33). Confident identification of M. avium subsp. paratuberculosis in tissues from Crohn’s disease patients might also be obtained with these MABS. Furthermore, the MABS developed in this study can be used to identify the potential surface proteins on M. avium subsp. paratuberculosis, making them strong candidates for subunit vaccines. Finally, they also provide a way to check the quality of fractionated protein preparations, such as membrane-enriched or cytoplasm-enriched lysates used in proteomic studies.

It is important to have MABS against proteins that are located on the cell surface or cell membrane for ease of bacillus detection in downstream applications. While MABS to a cytoplasmic protein may be important in studies highly focused on particular proteins, they may not be as effective at detecting bacilli in diagnostic or general research settings. Not all MABS are used solely for detection purposes, however. Further delineation of the epitopes recognized by both antibodies as well as T cells will be important in understanding the immunopathological conditions caused by infection with M. avium subsp. paratuberculosis. The MABS described here may be extremely useful reagents for such studies.

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REFERENCES


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