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Characterisation of *Mycoplasma capricolum* P60 surface lipoprotein and its evaluation in a recombinant ELISA

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1 ABSTRACT

2	This paper reports the identification and characterization of a 60 kDa surface protein
3	antigen (P60) of Mycoplasma capricolum subspecies capricolum (Mcc), and describes its
4	diagnostic application. Genomic localization and presence in P60 of conserved functional
5	domains suggested a structural and functional relationship with the immunodominant antigen
6	P48 of Mycoplasma agalactiae, a basic membrane protein. A rP60-ELISA was developed,
7	and it resulted in a high specificity for Mcc infections after evaluation with 125 goat sera.
8	The comparison with an existent ELISA based on whole Mcc cell lysates showed that the two
9	assays have comparable sensitivities, but the rP60-ELISA has the significant advantage of a
10	greater specificity. Results indicate that P60 is a potential marker of Mcc infection, especially
11	useful in areas where the presence of Mycoplasma capricolum subspecies capripenumoniae
12	is also reported.
13	
14	KEYWORDS: Mycoplasma capricolum subspecies capricolum; contagious agalactia;
15	ELISA; basic membrane proteins; P60.
16	
17	INTRODUCTION
18	Mycoplasma capricolum subsp. capricolum (Mcc) (Leach et al., 1993) is a highly
19	invasive pathogen belonging to the Mycoplasma mycoides cluster, (Cottew et al., 1987;
20	Bradbury, 2001) together with the closely related subspecies Mycoplasma capricolum subsp.
21	capripneumoniae, the causative agent of contagious caprine pleuropneumonia (Bonnet et al.,
22	1993). Mcc is responsible for sporadic outbreaks of arthritis or polyarthritis, mastitis,
23	keratoconjunctivitis, pneumonia, and septicemia in goats (Cottew, 1985; Bolske et al., 1988,
24	Damassa et al., 1992), and more rarely in sheep (Jones et al., 1983). Mcc infections are often
25	associated with high morbidity, and clinical signs may be rapidly followed by death (Cottew,

26	1985; Madanat et al., 2001). Despite the low frequency of symptomatic infections, Mcc is
27	detected in geographically diverse situations (Perreau, 1979) and persists for long periods in
28	healthy animals (Cottew and Yeats, 1981). Identification of Mcc in carriers is therefore
29	needed for controlling the spread of this pathogen.
30	There is no widespread standard protocol for diagnosis of small ruminant
31	mycoplasmoses; clinical signs are not specific (Rosendal, 1994), and combined approaches
32	are often required for species identification (Lambert 1987). Also, members of the M.
33	mycoides cluster share genomic and antigenic features (Bonnet et al., 1993; Le Grand et al.,
34	2004), complicating diagnosis (Rosendal, 1994; Woubit et al., 2004). Although direct PCR-
35	based diagnostic methods for the <i>M. mycoides</i> cluster have been developed (Dedieu et al.,
36	1995; Woubit et al., 2004), dedicated serological methods are still lacking, and the ones
37	which are currently available suffer from many drawbacks (Bergonier et al., 1997). At
38	present, antibodies specific to Mcc are detected in blood or milk by the complement-fixation
39	test (CF) or by ELISA (Lambert et al., 1998). These indirect methods rely on whole cell
40	preparations as antigens, and are therefore particularly vulnerable to potential cross-
41	reactivity, especially with Mycoplasma capricolum subspecies capripneumoniae. Therefore,
42	the need for a simple and sensitive indirect test with the advantage of a greater specificity
43	becomes apparent. Recently, our group developed two dedicated specific recombinant
44	ELISAs based on <i>M. agalactiae</i> (<i>Ma</i>) and <i>M. bovis</i> (<i>Mbo</i>) P48 proteins (Rosati et al., 2000;
45	Robino et al., 2005), two major surface antigens belonging to the basic membrane protein
46	family (Bmp). In this paper we report identification and characterisation of Mycoplasma
47	capricolum subspecies capricolum P60, a basic membrane protein (Bmp) sharing structural
48	and genetic similarities with the Ma and Mbo P48 genes. We also report evaluation of its
49	diagnostic potential in a recombinant ELISA (rP60-ELISA).

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51 MATERIALS AND METHODS

52	Bacterial strains and plasmids. California kid ^T , Y-goat ^T , PG45 ^T , and PG2 ^T were used as
53	reference strains of Mcc, M. mycoides subsp. mycoides Large Colony (MmmLC), Mbo, and
54	Ma, respectively. Strains were obtained in 1988 from E. A. Freundt (Institute of Medical
55	Microbiology, University of Aarhus, Denmark). Three field isolates of Mcc were originally
56	obtained from geographically distinct outbreaks of goat arthritis and mastitis, and tested for
57	the presence of the mcs4 a/b genes, which are genetic markers of the M. capricolum species
58	(Ushida et al., 2003). Two field isolates of MmmLC were also used. Escherichia coli strain
59	BL 21 was used as host for cloning and expression studies. Plasmids pCR2-TopoTA
60	(Invitrogen, Paisley, UK) and pGEX-2T (Pharmacia, Uppsala, Sweden), were used as cloning
61	and expression vectors, respectively (Sambrook et al., 1989).
62	
63	Identification and sequencing of Mcc p60. The presence of a gene related to Ma p48 was
64	investigated in Mcc by nucleotide-nucleotide BLAST search using Ma p48 as query sequence
65	(Altschul et al., 1997), and by submitting the consensus sequences of the selected lipoprotein
66	associated motifs (SLAs, Calcutt et al., 1999, Rosati et al., 1999) SLA-1 and SLA-2 to
67	ScanProsite (EXPASY). Once identified, the p60 Mcc gene was amplified from the Mcc
68	strains CK and TO5812 using two primers obtained from the Mcc DNA sequence for
69	CONTIG MCABF (Bork et al., 1995): Myc1CK
70	(TTATAAAGGAGAGTTGAAAATGAAAA), and Myc3CK
71	(TATCAGCCAACATCTGGAATTA). Full length $p60$ genes obtained from the two strains
72	were cloned into pCR2TopoTA and double strand sequenced. The ABI PRISM Big Dye
73	Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems) was used for
74	sequencing, using universal M13 primers and sequence generated primers. At least two
75	positive clones were double-strand sequenced after each cloning event. The Mcc p60

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nucleotide sequences generated during this study were deposited in the GenBank database
 under accession numbers DQ988842 (strain CK^T), and DQ988843 (field isolate TO5812).

79 Site directed PCR-mediated mutagenesis and cloning. Standard overlap extension PCR 80 adapted to Mycoplasma (Robino et al., 2005) was used to selectively mutate UGA codons 81 into UGG. Briefly, 6 mutagenic primers were used to generate three overlapping fragments 82 (A, B, C) in a first PCR run (Figure 1, 1). The three fragments were joined using primers 83 CKW6F and CKW9R in a second PCR run (Figure 1, 2). Fragment D, containing a frame 84 coding for a C-terminal-located region of the protein, was thus generated. Fragment D was 85 also amplified with the same primers bearing restriction sites for *BamHI* (sense) and *EcoRI* 86 (antisense) at the 5'-termini to facilitate cloning in pGEX-2T. To generate the full length 87 product M (Figure 1, 4), fragment D amplified without restriction sites was joined to the 88 other 6 fragments generated (Figure 1, 3) using the outermost primers CKF and CKW10R, 89 carrying restriction sites for BamHI and EcoRI. Both fragment D and fragment M were 90 digested with the appropriate restriction enzymes, purified, and cloned into the pGEX-2T 91 expression vector, in frame with the glutathione S-transferase (GST) gene. Two plasmid 92 preparations from two PCR-positive transformed clones were sequenced in order to confirm 93 the induced point mutations.

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Expression and purification of recombinant P60. Early log phase bacterial cultures were
induced for 90 min with 1 mM IPTG (isopropyl-thio-β-D-galactopyranoside) under constant
agitation. Total cell lysates were obtained by sonication and proteins were solubilized using
1% sarkosyl and 2% triton X-100. The fusion proteins containing fragment D and M were
purified by affinity chromatography using glutathione sepharose 4B. Purity and yield of the

- recombinant proteins were evaluated by SDS-PAGE and by the Bradford method (Bradford,
 1976), respectively.
- 102



125	ELISAs were carried out as previously described (Rosati et al., 2000) with some
126	modifications. Briefly, microplates were coated overnight uncovered at 37 °C with 100
127	ng/well of the GST/Mcc rP60 fusion protein (odd columns) and 34 ng/well of the GST as
128	negative control (even columns). After three washes, plates were blocked with 2.5% bovine
129	casein for 1 h, and washed as before. Sera diluted 1/20 in PBS containing 1.25% bovine
130	casein were incubated at 37 °C for 1 h. After four washes, a peroxidase labeled anti-
131	goat/sheep IgG monoclonal antibody (Sigma, Saint Louis, Missouri, USA) was added, and
132	plates were incubated as above. After a final wash, reaction was developed with ABTS (2,2'-
133	azino-bis-3-ethylbenzothiazoline-6-sulfonic acid; Chemicon, Temecula, CA, USA), and read
134	after 15 min at 405 nm. ELISA net absorbances were obtained for each serum sample by
135	subtracting the absorbance measured against GST from the absorbance measured against the
136	fusion protein. Cut-off was evaluated using a subset of well characterized sera in dose
137	titration experiments, and a positive reaction was defined as having a reactivity of >20% of
138	the positive control serum enclosed in each plate. Box plots of the percentage of reactivity for
139	each group tested were obtained using the R software Version 1.7.1 (Fleiss, 1981; Ihaka and
140	Gentleman, 1996). A subset of serum samples (n=73) from groups A, B, C, D and E was
141	tested with the Mcc whole cell ELISA (wc-ELISA) described by Lambert and co-workers
142	(Lambert et al., 1998). Results were expressed as International Units/ml (UI/ml), as described
143	(Lambert <i>et al.</i> , 1998).
144	Significance of discordant results obtained by testing the same sera with wc-ELISA and rP60
145	ELISA was investigated by McNemar's $\chi 2$.

146

147 **RESULTS**

148 Identification and characterization of *Mcc* P60. The immunodominant antigen P48 of *Ma*149 is a conserved surface membrane protein with a high immunogenicity, and forms the basis of

150	a consolidated diagnostic recombinant ELISA for ovine contagious agalactia. In order to
151	search for P48 immunologically related proteins in other pathogenic mycoplasma species,
152	including Mcc, the presence of crossreactive proteins was investigated by western blotting.
153	Specifically, 8 rabbit sera raised against 8 different mycoplasma species were challenged
154	with purified rP48 (Figure 2). A strong reactivity was observed for Ma (as expected) and Mcc
155	only, indirectly suggesting the presence in Mcc of a protein immunologically related to Ma
156	P48 (Figure 2). A lower level of reactivity was also observed with the MmmLC and F38
157	hyperimmune sera; these results remain to be investigated further.
158	A nucleotide-nucleotide BLASTn search was performed using Ma p48 as query
159	sequence, but despite immunological crossreactivity, we did not observe significant
160	homologies with nucleotide sequences available in the GenBank for Mcc. Ma p48 is located
161	immediately upstream of p59, the ATP binding cassette gene of a putative ABC transporter
162	operon (Rosati et al., 1999; Rosati et al., 2000). In view of the adjacent positions occupied by
163	the two genes in the Ma genome, the $p59$ sequence was used to conduct a new BLASTn
164	search. This time BLASTn revealed a significant homology (453 bits, Expect = 1e-125)
165	between <i>Ma p59</i> and <i>Mcc</i> California Kid ^T ATP-binding protein CcmA (accession number
166	ABC01656). Upstream of this gene, a nucleotide sequence coding for a putative lipoprotein
167	weighing about 20 kDa (accession no. Z33368, 7) was identified as an open reading frame
168	coding for a truncated Bmp containing exclusively the selective lipoprotein associated motif
169	SLA-1 (Calcutt et al., 1999), but lacking the SLA-2 motif (Rosati et al., 1999). This is in
170	agreement with the findings of Calcutt and co-workers (Calcutt et al., 1999). The same Mcc
171	sequence was identified by submitting the consensus sequences of the selected lipoprotein
172	associated motifs SLA-1 and SLA-2 to ScanProsite. However, an additional analysis of
173	sequence Z33368 revealed that downstream of the stop codon truncating the ORF at
174	nucleotide position +601, producing a protein prematurely interrupted at position +201 with

respect to the methionine start codon, further amino acid homologies could be identified inassociation with a SLA-2 motif.

177 Full-sequence analysis conducted on the *Mcc* CK type strain cultured in our 178 laboratories and in the field isolate TO5812 revealed the presence of an open reading frame 179 (orf) of 1644 bp, lacking the stop codon truncating the protein at amino acid +201. Moreover, 180 partial sequencing of p60 in 3 MmmLC and in 2 additional Mcc strains confirmed the absence 181 of a stop codon at the same position. The 1644 bp orf identified in *Mcc* encodes for a basic 182 protein with a theoretical pI of 8.81 and a putative Mw of 60 kDa, as calculated with the 183 Compute pI/Mw tool (Expasy). The protein has a typical leader peptide of 20 residues, which 184 is putatively cleaved by a bacterial protease at the recognition site VISC, upstream of the 185 cysteine residue representing the putative acylation site to which palmitate binds. The levels of nucleotide and amino acid identity between *Mcc* CK^T P60 and TO5812 186 187 P60 were 97.9% and 97.5%, respectively. A low level of amino acid identity (about 15%) 188 was obtained when comparing Mcc P60 to Ma P48. Full length P60 is expressed both in the 189 *Mcc* CK type strain and in three field strains of *Mcc* obtained from three geographically 190 distinct outbreaks, as demonstrated by western blotting with the hyperimmune antiserum 191 directed against the recombinant fragment D (Figure 3, lanes 2, 3). The same hyperimmune antiserum did not show any reactivity with MmmLC Y-goat^T and with Mycoplasma mycoides 192 193 subsp. capri (Figure 3, lanes 4, 5). 194

195 Cloning and expression of *Mcc* P60. Ten UGA codons where successfully mutated to UGG 196 by site-directed PCR-mediated mutagenesis. Sequence analysis confirmed the base changes 197 and that D and M were correctly inserted into the pGEX-2T vector in frame with the

198 glutathione S-transferase (GST) gene.

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Evaluation of cross-reactivity between *Ma* P48 and *Mcc* P60. A hyperimmune antiserum

against Ma rP48 and against total protein preparations of Ma PG2^T, Mbo PG45^T, Mcc CK^T, a

field isolate of Mcc, MmmLC Y-goat^T, a field isolate of MmmLC, and Mycoplasma mycoides

subspecies *capri*. As a result, anti-recombinant P48 antiserum reacted selectively with native

Ma P48 but not with whole Mcc protein extracts. However, low cross reactivity was observed

when the purified recombinant Mcc P60 protein was probed with anti-recombinant Ma P48

developed in rabbit against purified Ma rP48 was tested by western blotting for reactivity

rP60-ELISA and wc-ELISA. Sera collected from animals positive to *Mcc* (group A), from animals negative to *Mycoplasma* (group B), and from animals positive to mycoplasmas other than *Mcc* (groups C, D, and E), were tested by ELISA using *Mcc* rP60 as capture antigen (rP60 ELISA). A boxplot of the absorbance values obtained is shown in Figure 4. With the exception of 1 group E serum, only sera from *Mcc* infected animals (group A) produced a positive reaction with rP60. A subset of serum samples (N= 73) was also tested with the wc-ELISA, and results were compared to those obtained by rP60 ELISA (Table 1). All group A sera of the subset tested positive by wc-ELISA and all but one were positive by rP60 ELISA, whereas only one serum was positive by rP60 ELISA and was negative by rP60 ELISA, and the difference between these discordant results was statistically significant (13 vs 1, McNemar's $\chi^2 = 10.3$, d.f. =1, P < 0.01). We therefore concluded that the probability of obtaining a false positive by wc-ELISA was greater than the probability of obtaining a false

222 positive by rP60 ELISA. In conclusion, the two assays have a comparable sensitivity, but the

rP60 ELISA has the significant advantage of a greater specificity.

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(data not shown).

225 **DISCUSSION**

226 The characterization of mycoplasma surface proteins has long been a challenging 227 goal. In the last decade, several variable surface proteins (VSPs) involved in evasion of the 228 host immune response have been described in pathogenic mycoplasmas (Yogev *et al.*, 1991; 229 Nussbaum et al., 2002). However, because of their intrinsic variable nature, these proteins are 230 unsuited to use as markers of infection or for development of related immunogenic products. 231 Among invariable antigens, the basic membrane proteins (Bmps) have shown a great 232 potential for the development of specific and sensitive serological tests. One of these is Ma 233 P48, which forms the basis for a recombinant ELISA, now validated and commercially 234 available, for detection of contagious agalactia in sheep (Rosati et al., 2000). 235 Here we report the characterisation of Mcc P60, a protein sharing positional and 236 functional relationships with Ma P48, and demonstrate its application as a candidate antigen 237 in the development of a sensitive and specific serological test for detection of *Mcc* infections 238 in goats. Nucleotide and aminoacid sequence analyses revealed a striking similarity of P60 to a protein described as P20 in Mcc CK^T by Bork and co-workers (1995). Interestingly, this 239 240 similarity extends to nucleotides following an in-frame TAA stop codon which prematurely 241 interrupts translation of the p20 gene. This stop codon occurs at nucleotide position + 601, leading to expression of a 20 kDa protein in Mcc CK^T (ATTC27343). Conversely, in this 242 243 study we detected an A to G transition at nucleotide position + 602, resulting in a TGA codon 244 instead of a stop codon in all the *Mycoplasma mycoides* cluster strains evaluated, including 245 $Mcc \ CK^T \ ATCC27343$. We speculate that the TGA codon observed at nucleotide position + 246 601 is conserved within the *Mycoplasma mycoides* cluster, and that the TAA stop codon described in *Mcc* CK^T ATCC27343 could have arisen in the strain used by Bork and co-247 workers (1995) during prolonged *in vitro* cultivation. Indeed, *Mcc* CK^T ATCC27343 cultured 248 249 in our laboratory encodes the full length version of the protein (P60).

250 In spite of the immunological crossreactivity seen by western blotting (Figure 2), a 251 low level of amino acid identity was observed between Ma P48 and Mcc P60 along the whole 252 sequence (about 15%). Analogy between the two proteins relies, however, in presence of two 253 consensus sequences for the Bmp functional domains SLA-1 and SLA-2, which are 254 conserved in this protein family. The elevated divergence observed in other protein regions 255 might reasonably be explained by the absence of tight functional constraints and by 256 immunological escape, given the surface localization. The hypothesis that the two proteins 257 might be functionally and structurally related is also supported by the finding that p48 and 258 *p60* have the same genetic location in the genomes of *Mcc* and *Ma*, being both located within 259 a structurally conserved ABC transporter operon and upstream of a conserved protein 260 sequence. The presence of the SLA-1 and SLA-2 domains might be responsible for the 261 crossreactivity observed by western blotting when probing recombinant P60 with a rabbit 262 serum developed against recombinant P48. The reason remains unclear, however, why the 263 native Mcc P60 could not be detected within total cell lysates of Mcc probed by western 264 blotting with anti-recombinant P48 (Fig. 4b). It should be pointed out that this apparent lack 265 of reactivity could be due to low P60 abundance below the detection limits of this assay and 266 deserves further investigation.

267 P60 is conserved in size and is stably expressed in all the *Mcc* strains tested in this 268 work, as demonstrated by reactivity with a rabbit hyperimmune antiserum (Figure 3). 269 Moreover, experiments of colony blotting performed using the same hyperimmune antiserum 270 suggest the absence of clonal variability (data not shown). Comparison of the results obtained 271 by western blotting and ELISA with other mycoplasmas confirmed that P60 is specifically 272 recognized only by sera of goats infected by *Mcc* (Figure 4). The extremely low positivity 273 rate observed with sera from goats infected by other mycoplasmas (1/74) suggests the 274 suitability of rP60 as a specific marker of infection. In fact, the rP60-ELISA has a level of

275	sensitivity comparable to that of the wc-ELISA, but it has the significant advantage of a
276	higher specificity when challenged with sera from goats with infections caused by other
277	mycoplasmas (Figure 4), as demonstrated by the chi-square. This is especially relevant when
278	considering the lack of ELISA crossreactivity with the closely related Mccp subspecies,
279	which renders rP60-ELISA an additional specific and reliable tool for developing Mcc
280	diagnostic strategies in areas were both Mcc subspecies are present. Moreover, the
281	availability of a sensitive and highly specific serological test for detection of Mcc infections
282	in small ruminants could represent a practical and cost-effective approach for surveillance
283	and control programs, since Mcc infection is not always accompanied by visible symptoms.
284	
285	Conclusion
286	We developed the first recombinant ELISA for diagnosis of Mycoplasma capricolum
287	subspecies capricolum based on the use of P60, a basic membrane protein structurally and
288	functionally related to the basic membrane proteins P48 of <i>M. agalactiae</i> and <i>M. bovis</i> ,
289	respectively. This antigen could supplement the p48-based ELISA test already developed for
290	Contagious Agalactia, and might lead to the development of a multi-antigen test for diagnosis
291	and control of contagious agalactia syndromes associated with ovine and caprine
292	mycoplasmas.
293	
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Table 1

Cluster	Group	Pathogen	Geographic origin	rP60-ELISA			wc-ELISA		
				N. of	Pos	Neg	N. of	Pos	Neg
1		17	T /T 1	sera	1.1	1	sera	10	0
1	А	Мсс	France/Italy	12	11	1	12	12	0
2	В	None	Scotland/Italy	14	0	14	14	0	14
	С	Ма	Italy	15	0	15	15	5	10
3	D	MmmLC	Italy	18	0	18	18	0	18
	Е	Mccp	UK	14	1	13	14	8	6

Sera used for comparison of rP60-ELISA with wc-ELISA

Mcc, *Mycoplasma capricolum* subsp. *capricolum*; *Ma*, *Mcoplasma agalactiae*, *MmLC*, *Mycoplasma mycoides* subsp. *mycoides* Large Colony; *Mccp*, *Mycoplasma capricolum* subsp. *capripneumoniae*. rP60 ELISA, recombinant *Mcc* P60-based ELISA; wc ELISA, *Mcc* whole-cell proteins-based ELISA.

Figure 1

Strategy used for introducing multiple distant point mutations. Eighteen primers (CKF, CKW1F/R, CKW2F/R, CKW3-4R, CKW4F, CKW5F/R, CKW6F/R, CKW7F/R, CKW8F/R, CKW9F/R, CKW10R) containing the desired mutations were used to generate seven overlapping fragments (E, F, G, H, I, D, and L). Purified fragments were joined in M using primer CKF and CKW10R in a second PCR run. Mutated nucleotides in primers and in PCR products are shown as vertical bars.

Figure 2

Western blotting showing reactivity of rP48 (P48) and GST-rP48 fusion protein (GSTP48) with 8 rabbit hyperimmune antisera raised against 8 different *Mycoplasma* species. M: molecular weight markers (weights are indicated on the left); 1, *M. capricolum* subspecies *capripneumoniae* F38; 2, *M. ovipneumoniae*; 3, *M. capricolum* subspecies *capricolum*; 4, *M. arginini*; 5, *M. putrefaciens*; 6, *M. mycoides* subspecies *capri*; 7, *M. mycoides* subspecies *mycoides* large colony; *Ma* purified GST-rP48 and rP48, respectively. Arrows indicate GST-rP48 and rP48. Strips were cut from a membrane obtained by blotting a single-well gel loaded with 4 µg of recombinant protein preparation.

Figure 3

Western blotting performed to investigate presence and size of P60 in the *Mycoplasma mycoides* cluster using a rabbit antiserum raised against *M. capricolum* P60. 1, rP60 and rP60-GST fusion protein (0.5 μ g); 2-5, total cell lysates of *Mcc* CK, a *Mcc* field isolate, *M. mycoides* subspecies *mycoides* large colony Y-goat^T, and *M. mycoides* subspecies *capri*, respectively; M, molecular weight markers. The amount of mycoplasma proteins loaded were the same in each lane (about 50 μ g).

Figure 4

Boxplot of absorbance values obtained by rP60-ELISA: A-E: *Mcc* naturally infected goats; *Mycoplasma capricolum* subsp. *capricolum* (*Mcc*) seronegative goats; *M. agalactiae* positive sheep; *M. mycoides* subspecies *mycoides* large colony naturally infected goats, and *M. capricolum* subspecies *capripneumoniae* positive goats, respectively. Optical densities are expressed as percent of positivity respect to the positive control. Differences in optical density between the groups of sera were statistically significant (P<0,05).









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