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P159 is a proteolytically processed, surface adhesin of *Mycoplasma hyopneumoniae*: defined domains of P159 bind heparin and promote adherence to and invasion of eukaryote cells

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Summary

*Mycoplasma hyopneumoniae*, the causative agent porcine enzootic pneumonia, colonises the respiratory cilia of affected swine causing significant economic losses to swine production worldwide. Heparin is known to inhibit adherence of *M. hyopneumoniae* to porcine epithelial cilia. *M. hyopneumoniae* cells bind heparin but the identity of the heparin-binding proteins is limited. Proteomic analysis of *M. hyopneumoniae* lysates demonstrated 27 kDa (P27), 110 kDa (P110) and 52 kDa (P52) proteins representing different regions of a 159 kDa (P159) protein derived from the mhp494 gene. These proteins were surface located and present at all growth stages. Following purification of 4 recombinant proteins spanning P159 (F1\textsubscript{P159}, F2\textsubscript{P159}, F3\textsubscript{P159}, and F4\textsubscript{P159}), only F3\textsubscript{P159} and F4\textsubscript{P159} bound heparin in a dose-dependent manner (Kd values 142.37 ± 22.01 nM; 75.37 ± 7.34 nM respectively). Scanning electron and confocal microscopic studies showed *M. hyopneumoniae* bound intimately to and entered porcine kidney epithelial-like cells (PK15 cells) but these processes were inhibited by excess heparin and F4\textsubscript{P159}. Similarly, latex beads coated with F2\textsubscript{P159} and F4\textsubscript{P159} adhered to and entered PK15 cells, but heparin, F2\textsubscript{P159}, and F4\textsubscript{P159} was inhibitory. These findings indicate that P159 is a post-translationally cleaved, glycosaminoglycan-binding adhesin of *M. hyopneumoniae*.
Introduction

*Mycoplasma hyopneumoniae,* the etiological agent of enzootic pneumonia (EP), ranks as one of the most economically significant diseases affecting swine production worldwide. The initial event in colonization of the respiratory tract by *M. hyopneumoniae* is binding to respiratory cilia (Blanchard *et al.*, 1992; Mebus and Underdahl, 1977; Tajima and Yagihashi, 1982). Colonization disrupts the mucociliary escalator through ciliostasis, loss of cilia, and epithelial cell death (DeBey and Ross, 1994). Acute inflammation of airways surrounding the site of infection leads to epithelial hyperplasia and infiltration of the lamina propria by inflammatory cells composed largely of neutrophils and mononuclear cells (Livingston *et al.*, 1972). Disease resolution occurs only after a prolonged period (if at all) and once infected, swine remain recalcitrant to reinfection (Kobisch *et al.*, 1993). Most cases of EP are chronic, and are often complicated by secondary bacterial infections which exacerbate morbidity and mortality (Ciprian *et al.*, 1988). *M. hyopneumoniae* also plays a major role in the porcine respiratory disease complex in countries where infections with porcine respiratory and reproductive syndrome virus complicate respiratory disease pathology (Thacker *et al.*, 2000). Collectively, these observations indicate that losses in swine production due to this pathogen are likely to be considerably underestimated.

Genome sequence information for several strains of *M. hyopneumoniae* has facilitated proteomic studies and provided insight into families of molecules likely to play a role in the disease process (Djordjevic *et al.*, 2004; Minion *et al.*, 2004; Vasconcelos *et al.*, 2005). These advances are significant given that overall poor growth on agar surfaces coupled with a lack of development of genetic tools to selectively mutate target genes has for many years hampered efforts to identify molecules that play fundamental roles in pathogenesis (Minion, 2002). The cilium adhesin, P97 is the only cell surface adhesin that has been extensively characterized in *M. hyopneumoniae* (Hsu and Minion, 1998; Minion *et
P97 is extensively cleaved post-translationally during growth in vitro and processing is strain-specific. Most cleavage products remain associated with the *M. hyopneumoniae* cell surface despite the absence of hydrophobic domains or other motifs that might act to anchor these fragments to the cell membrane (Djordjevic et al., 2004). Protein-protein interactions either with other *M. hyopneumoniae* proteins and/or with host-derived molecules may facilitate the localization of these cleavage fragments to the cell surface (Djordjevic et al., 2004). The p97 gene (mhp183) forms part of a two gene operon with p102 (mhp182) (Adams et al., 2005; Hsu and Minion, 1998). The *M. hyopneumoniae* genome contains six paralogs of p97 and six of p102 (Minion et al., 2004) many of which occur as two-gene operons containing a p97 and p102 paralog (Adams et al., 2005).

Attachment of *M. hyopneumoniae* to respiratory cilia is a necessary prerequisite for epithelial damage (DeBey and Ross, 1994). Monoclonal antibodies F1B6 and F2G5, which recognise the R1 cilium binding region in P97 (Zhang et al., 1995), are able to reduce adherence of *M. hyopneumoniae* to respiratory cilia by approximately 70%. Purified recombinant P97 inhibits adherence of *M. hyopneumoniae* cells to cilia in a dose-dependent manner (Zhang et al., 1995) and binding of recombinant P97 to porcine respiratory cilia is inhibited by sulfated glycosaminoglycans (Hsu et al., 1997). Consistent with these observations, P97 was recently shown to possess two heparin-binding domains (Jenkins et al., 2006). Heparin, dextran sulfate, chondroitin sulfate, laminin, mucin and fucoidan also inhibit the ability of *M. hyopneumoniae* to bind respiratory cilia (Zhang et al., 1994). The ability to bind glycosaminoglycans is likely to arm *M. hyopneumoniae* with the capability to bind a variety of important host molecules (Duensing et al., 1999; Menozzi et al., 2002; Patti et al., 1994; Wadstrom and Ljungh, 1999) that also possess glycosaminoglycan binding capabilities, and thus circumvents the need to evolve specific receptors that target these molecules (Jenkins et al., 2006). Although these experiments indicate that heparin-binding
surface proteins are likely to be important in pathogenesis, knowledge of heparin-binding surface proteins (apart from P97) of *M. hyopneumoniae* is lacking.

The observation that P97 is extensively modified by proteolytic cleavage suggests that other molecules secreted to the surface of *M. hyopneumoniae* may also be modified in a similar fashion. In this study we characterize a gene known as mhp494 (Minion *et al.*, 2004) that encodes a protein with a putative mass of 159 kDa (P159). We show that P159 undergoes post-translational proteolytic cleavage, generating a complex pattern of fragments that reside on the surface of *M. hyopneumoniae*. We examined the ability of *M. hyopneumoniae* cells to bind heparin and used a porcine epithelial-like cell line (PK15 cells) previously shown to bind *M. hyopneumoniae* (Zielinski *et al.*, 1990) to develop an assay to identify new adhesins and study pathogen adherence to these cells. We show that *M. hyopneumoniae* binds intimately to and enters PK15 cells and that these abilities are inhibited by pre-incubating *M. hyopneumoniae* with heparin. To understand the role that cleavage fragments of P159 play in binding heparin and adhering to and entering PK15 cells, latex beads coated with recombinant fragments spanning different regions of this molecule were constructed and examined in our assay. Our findings indicate that P159 is a novel glycosaminoglycan binding adhesin of *M. hyopneumoniae* and that regions within P159 play a role in adherence to, and entry of, PK15 cells.

**Results**

*Expression pattern of P159 in M. hyopneumoniae strain 232*

The deduced amino acid sequence of *p159* (GenBank accession number AAV27918, mhp494) comprised 1410 amino acids with a predicted pI of 8.42. *p159* is a novel gene and its location in the genome is unusual in that it forms part of two gene structure with a *p97* paralog identified here as *p216* (mhp493; Minion *et al.*, 2004). An ongoing comprehensive
peptide mass mapping study of *M. hyopneumoniae* has resolved three groups of protein spots (see boxed regions in Fig. 1A) with apparent molecular masses of 27 (P27), 52 (P52) and 110 (P110) kDa that represented different regions spanning P159. To confirm the identity of the P159 fragments, 2-D immunoblots of whole cell lysates of *M. hyopneumoniae* probed with a pool of antisera raised to recombinant fragments F1-P159-F4-P159 spanning P159 (see fig. 1C) identified P159 fragments shown in Fig. 1 (data not shown). TMpred analysis (www.ch.embnet.org/software/TMPRED_form.html) of P159 identified a single, putative transmembrane region (score 2150) between amino acids 9-29 (Fig. 1B). N-terminal sequence analysis of P27 identified a peptide sequence corresponding to the first 7 amino acids (MKKQIRN) of P159. Assuming P159 is a surface antigen (see later), this data suggests that the transmembrane domain is not removed when the P159 preprotein is secreted to the cell surface.

Based on peptide mass mapping and N-terminal sequence analyses, P27 (observed pI ~10) spans between amino acids 1-219 of the P159 sequence and cleavage at amino acid 220 would generate a protein fragment with a predicted mass of 24.5 kDa and a pI of 9.12 (Fig. 1B). Peptide mass matches of protein spots representing P52 and P110 spanned amino acids 978-1387 and 303-841 respectively (Fig. 1B) indicating that a cleavage event occurred between amino acids 220-302 and between amino acids 842-977. To generate the P110 fragment, cleavage events at amino acids 220 and 977 would generate a protein with a mass of 84.8 kDa (pI of 6.28); cleavage at amino acids 303 and 841 would generate a peptide of 60.5 kDa (pI of 8.81). Protein spots representing P110 migrate with a pI between 6-6.5 suggesting that two cleavage events probably occurred near amino acids 220 and 977. In either case, P110 has a predicted mass ranging between 61 and 85 kDa indicating that this protein fragment migrates aberrantly during SDS-PAGE. Amino acids 736-977 representing the predicted C-terminal region of P110 are enriched in acidic residues (predicted pI of 5.01)
and P159 fragments such as P110 that span this region are expected to migrate with a more acidic pI compared to P27 and P52 (pI 8.85). The presence of this region in P110 is likely to contribute to its aberrant migration during SDS-PAGE. Assuming the first cleavage scenario is correct, P52 would span amino acids 977-1410 generating a protein with a predicted mass of 49 kDa. This is largely consistent with the size and pI of P52 shown in Fig. 1A. Attempts to generate N-terminal sequence by Edman degradation for P110 and P52 cleavage fragments were unsuccessful. Collectively, these data suggest that P159 is rapidly processed during secretion to the cell surface (see later).

Purification and western blot analysis of P159 fragments

To examine the function(s) of regions within P159, four non-overlapping regions spanning the entire molecule (Fig. 1C) were cloned and expressed as poly-histidine fusion proteins in Escherichia coli: F1_{P159}, F2_{P159}, F3_{P159}, and F4_{P159} comprising amino acids 31-264, 265-519, 558-909 and 958-1405, respectively. F1_{P159}-F4_{P159} were readily expressed and purified by Nickel-NTA agarose affinity chromatography (Fig. 2, panels A-D). The central region of P159 representing P110 and spanning amino acids 265-909 was cloned as two separate fragments (F2_{P159} and F3_{P159}) because previous experience of cloning large mollicute genes in Escherichia coli typically resulted in an extremely poor protein yield and/or multiple translation products presumably due to the high A+T content of mycoplasmal genes (Notarnicola et al., 1990). Attempts to clone and express the entire p159 gene into E. coli were unsuccessful.

Rabbit antisera raised separately to purified recombinant fragments F1_{P159}-F4_{P159} (Fig. 1C) were used to further investigate the post-translational cleavage pattern of P159 and to determine their cellular location. Antiserum raised against F1_{P159} (which spans P27) reacted strongly with purified recombinant F1_{P159} (Fig. 2, panel A lane 2) but reacted poorly with P27.
in cell lysates of *M. hyopneumoniae* (Fig. 2, panel A, lane 1). Although the poly-histidine tag engineered into the N-terminus will contribute to the increased size of F1<sub>P159</sub> compared to P27, it is unlikely to account for the 4 kDa difference in apparent mass of these two proteins.

Of note, the N-terminal 22-kDa cleavage fragment of the cilium adhesin P97 was also not easily detected by immunoblotting (Djordjevic *et al.*, 2004). These data suggest that small cleavage fragments containing intact transmembrane domains may bind poorly to PVDF membrane. As expected both F2<sub>P159</sub> and F3<sub>P159</sub> antisera (which span P110) identified P110 (Fig. 2, panel B and C, lane 1). However these sera also detected a second protein with a predicted mass of approximately 68 kDa (P68) which probably represents an additional cleavage product of P159 so far undetected in our proteomic analyses (see also Fig. 2 panel E). Anti-F4<sub>P159</sub> serum (which spans P52) reacted with a *M. hyopneumoniae* protein equivalent in size to P52 (panel D, lane 1). Interestingly, anti-F4<sub>P159</sub> serum also strongly recognized a higher mass protein (> 118 kDa) when reacted with an affinity purified preparation of recombinant F4<sub>P159</sub> (Fig. 2, panel D, lane 2). Peptide mass mapping analysis of this higher mass protein matched the C-terminal 52 kDa region of P159 indicating that this represents an SDS-PAGE-stable, multimeric form of F4<sub>P159</sub> (data not shown). The higher mass form of F4<sub>P159</sub> was also recognized by commercial anti-poly-histidine antisera further supporting this interpretation (data not shown). Whether this multimeric form of P52 plays a role in the biology of *M. hyopneumoniae* remains unknown.

To examine the immunoblot profile of P159 during different stages of growth in *vitro*, synchronised cultures of *M. hyopneumoniae* collected between 8 h (early log phase) and 72 h (late stationary phase) post-inoculation were reacted with a pool of F1<sub>P159</sub>-F4<sub>P159</sub> antisera. A consistent pattern of three strongly staining fragments of masses 52, 68, and 110 kDa (representing P52, P68 and P110) were detected at all time points suggesting that P159 is processed in an identical fashion during early log (8 h), mid-log (16-28 h) and stationary
phases (40-72 h) of growth in vitro (Fig. 2 panel E). The P159 pre-protein was not detected suggesting that it is rapidly processed. Immunoblot profiles of whole cell lysates representing different strains of *M. hyopneumoniae*, when reacted with a pool of anti F1_{P159-F4_{P159}}, showed similar yet distinct patterns suggesting that strain-specific cleavage events occur (Fig. 2F).

Trypsin sensitivity and immuno-electron microscopy analysis of P159

To determine if P159 cleavage fragments are surface accessible, freshly cultured *M. hyopneumoniae* strain 232 cells were exposed to concentrations of trypsin ranging from 0-150 µg/ml. Exposure of intact *M. hyopneumoniae* cells to trypsin concentrations from 0.1-3 µg/ml showed a gradual loss of P68 and P110; these two proteins being almost completely digested at a trypsin concentration of 10 µg/ml. P52 was the most resilient fragment and was detectable at a trypsin concentration of 10 µg/ml but completely degraded with 50 µg/ml. There was no evidence of any P159 cleavage fragment at trypsin concentrations above 50 µg/ml (Fig. 3A). The digestion kinetics shown in Fig. 3A are similar to those of the cilium adhesin fragments that are known to reside on the cell surface (Djordjevic et al., 2004) indicating that processed P159 fragments are likely to also reside on the surface of *M. hyopneumoniae*. Control experiments using antisera raised against recombinant ribosomal protein L7/L12 (shown to reside in the cytosol; Burnett et al., unpublished results), pyruvate dehydrogenase subunits A and D and lactate dehydrogenase (previously shown to reside in the cytosol) were resistant to trypsin concentrations up to 300 µg/ml (data not shown; Djordjevic et al., 2004).

To confirm the surface location of P159 fragments, immuno-electron microscopy was conducted using F1_{P159-F4_{P159}} antisera. F2_{P159} and F4_{P159} antisera clearly showed that P159 fragments P110 and/or P68 and P52 recognized by these antisera reside on the surface of *M. hyopneumoniae*. **
hyopneumoniae strain 232 (Fig. 3C and 3E). Control sera collected prior to immunisation with recombinant fragments reacted poorly with *M. hyopneumoniae* cells (Fig. 3B and 3D). We were unable to generate reliable images using antisera raised against F1 and F3 proteins because of unacceptable levels of gold labeling with preimmune sera (data not shown).

*M. hyopneumoniae* binds heparin

Various glycosaminoglycans have been shown to interfere with the ability of *M. hyopneumoniae* to adhere to porcine cilia (Zhang *et al.*, 1994). Fig 4A shows that biotinylated heparin binds to the surface of freshly cultured cells of *M. hyopneumoniae* strain 232 in a dose dependent and saturable manner. *M. hyopneumoniae* strain 232 proteins ranging in mass from 15 to 150 kDa bind biotinylated heparin (Fig. 4B).

Domains within P159 bind heparin

With the aim of determining the function(s) of P159 and specifically determine if any of its cleavage fragments bind heparin, a panel of extracellular matrix (ECM) components (including fibronectin, laminin, collagen and fibrinogen) and various glycosaminoglycans (including heparin, heparan sulfate, mucin, chondroitin sulfate A and B and fucoidan), were tested for either their ability to bind directly to recombinant fragments of P159, or to interfere with binding to one of these components. Although none of the recombinant fragments bound any of the ECM proteins, F3 and F4 bound biotinylated heparin in a saturable and dose-dependent manner with saturation occurring between 15-20 µg/ml (0.5-1.5 µM) of biotinylated heparin. A 50-fold excess of unlabelled heparin was found to extinguish > 90% of the signal (Fig. 5) indicating that heparin occupies specific binding sites on both F3 and F4. Non-linear regression and one-site binding analyses were performed on the specific
binding data producing an estimate of the apparent dissociation constants for F3\textsubscript{P159}– and F4\textsubscript{P159}– biotinylated heparin complexes of 142.37 ± 22.01 nM (2.13 ± 0.44 µg/ml) and 75.37 ± 7.34 nM (1.13 ± 0.11 µg/ml) respectively. To further investigate the interaction of F3 and F4 with heparin, binding of these proteins to a heparin-agarose (Sigma-Aldrich, St. Louis, Missouri) column was investigated. Both F3\textsubscript{P159} and F4\textsubscript{P159} bound to the heparin-agarose column and were eluted with 10 mM Tris containing approximately 0.22 M NaCl and 0.32 M NaCl respectively (data not shown).

The kinetics of binding biotinylated heparin by F3\textsubscript{P159} and F4\textsubscript{P159} was examined in more detail. At concentrations between 1-250 µg/ml, heparin profoundly affected the ability of F3\textsubscript{P159} and F4\textsubscript{P159} to bind biotinylated heparin with concentrations > 500 µg/ml effectively blocking binding (Fig. 6A). Non-linear regression with one-site competition determined the 50% inhibitory concentration (IC\textsubscript{50}) for F3\textsubscript{P159} and F4\textsubscript{P159} to be 52.92 ± 1.03 µg/ml and 66.63 ± 1.02 µg/ml, respectively. Various glycosaminoglycans were tested for their ability to inhibit the binding of F3\textsubscript{P159} and F4\textsubscript{P159} to biotinylated heparin (Fig. 6B and C). Fucoidan, a highly sulfated fucose polymer, effectively inhibited the binding of both F3\textsubscript{P159} and F4\textsubscript{P159} to biotinylated heparin with IC\textsubscript{50} values of 96.28 ± 1.19 µg/ml and 36.23 ± 1.14 µg/ml, respectively. Heparan sulfate, chondroitin sulfate A, chondroitin sulfate B (Fig. 6), and mucin (results not shown) were unable to inhibit the binding of F3\textsubscript{P159} or F4\textsubscript{P159} to biotinylated heparin.

Adherence and invasion of PK15 cell monolayers by M. hyopneumoniae.

Radiolabelled M. hyopneumoniae strains J, 232 and 144L have previously been shown to adhere to a porcine kidney epithelial-like (PK15) cell line in a receptor-dependent manner and their adherence was blocked by either pre-treating PK15 cells with unlabelled M. hyopneumoniae or by pre-treating M. hyopneumoniae cells suspensions with trypsin
In our study we examined the ability of *M. hyopneumoniae* strain J cells to interact with PK15 cell monolayers by scanning electron microscopy. We showed that *M. hyopneumoniae* adheres intimately to the surface of PK15 cells with the mycoplasma often seen closely associated with microvilli on the surface of the monolayers (Fig. 7A). Furthermore, a proportion of the *M. hyopneumoniae* cells enter the PK15 cells and the microvilli appear to entrap the mycoplasma (Fig. 7A). *M. hyopneumoniae* cells were separately pre-incubated with recombinant fragments F1<sub>P159</sub>-F4<sub>P159</sub> prior to addition to PK15 cells to determine if regions within P159 influence the ability of mycoplasma cells to bind and/or enter the monolayers. When *M. hyopneumoniae* cells were pre-incubated with 1 µg of F4<sub>P159</sub> protein [and not F1<sub>P159</sub>, F2<sub>P159</sub> or F3<sub>P159</sub>, (data not shown)], an obvious decrease in adherence was observed (Fig. 7B). *M. hyopneumoniae* cells pre-incubated with a saturating concentration of heparin (500 µg/ml) also bound poorly to the surface of PK15 cell monolayers (Fig. 7C). Purified immunoglobulins (25 µg) from serum obtained from rabbits separately immunized with F1<sub>P159</sub>, F2<sub>P159</sub>, F3<sub>P159</sub> and F4<sub>P159</sub> proteins did not appear to affect the ability of *M. hyopneumoniae* to adhere to PK15 cells or the uptake and entry of latex beads (see later) coated with P159 recombinant fragments (data not shown).

To define domains within P159 that might play a role in adherence (and entry) into PK15 cells, a latex bead binding assay was used. Adherence was observed by a combination of double-immunofluorescence microscopy (Fig. 8) and scanning electron microscopy (Fig. 9). Latex beads separately coated with F2<sub>P159</sub>, F3<sub>P159</sub> and F4<sub>P159</sub> were found to adhere to PK15 cells within 2 h incubation at 37°C (Fig. 8). Furthermore, latex beads coated with F2<sub>P159</sub> and F4<sub>P159</sub> (but not F1<sub>P159</sub> or F3<sub>P159</sub>) were detected inside PK15 cells (Fig. 8 see arrows) between 2-22 h post-incubation and increasing numbers of internalized beads were detected over this time (results not shown). Latex beads alone (data not shown) or beads coated with recombinant F1<sub>P159</sub> protein (Fig. 8A) did not adhere to or enter PK15 cells.
To examine the specificity of binding of $F_{1P159} - F_{4P159}$-coated latex beads to PK15 cells, binding experiments using latex beads that had been separately pre-incubated with recombinant P159 fragments (1 µg each) were performed and examined by scanning electron microscopy. In preliminary experiments, pre-incubation with soluble $F_{2P159}$, $F_{3P159}$ and $F_{4P159}$ reproducibly decreased the attachment of $F_{2P159}$- (Fig. 10A), $F_{3P159}$- (data not shown) and $F_{4P159}$- (Fig. 10B) coated latex beads to PK15 cells. Similarly, when $F_{4P159}$-coated latex beads were pre-incubated with heparin they poorly bound to PK15 cell monolayers (Fig. 10C and D). The effect of pre-incubating $F_{2P159}$- and $F_{4P159}$-coated latex beads separately with heparin and with excess $F_{2P159}$ and $F_{4P159}$ proteins on their ability to adhere to and enter PK15 cells is summarized in Fig. 10D. Pre-incubation of $F_{2P159}$- and $F_{4P159}$ -coated latex beads with a saturating concentration of heparin inhibited binding to PK15 cells by 89 and 64% respectively (Fig. 10D). Significantly, heparin completely abolished entry of $F_{2P159}$- and $F_{4P159}$ -coated latex beads into PK15 cells (Fig. 10D). Pre-incubation of $F_{4P159}$ -coated latex beads with excess $F_{4P159}$ inhibited the binding and entry of $F_{4P159}$ -coated latex beads by 71% and 67% respectively and displayed the greatest ability of all the P159 recombinant proteins to inhibit the binding and invasion latex beads coated with recombinant P159 proteins (Fig. 10D).

Discussion

$mhp494$ encodes a protein with a predicted mass of 159 kDa (P159) and is unusual in that it forms part of a two gene structure with $mhp493$, a putative cilium adhesin paralog (Minion et al., 2004). MALDI-TOF mass spectrometric analyses of $M. hyopneumoniae$ proteins separated by 2-D gel electrophoresis identified proteins with masses of 27, 52 and 110 kDa that represented regions within P159. Immunoblotting studies using monospecific antisera raised to different regions of $mhp494$ readily identified these and other proteins.
(putative cleavage fragments) with masses between 27-110 kDa in whole cell lysates of *M. hyopneumoniae* harvested during early, mid, late exponential and stationary phases of growth indicating that P159 is extensively cleaved post-translationally. A high mass protein that might represent P159 was virtually undetectable by immunoblotting indicating that P159 is rapidly processed, probably by a proteolytic enzyme(s). Trypsin digestion studies confirmed that the majority of these cleavage fragments reside on the cell surface despite the absence of hydrophobic stretches of amino acids that might anchor these peptides to the cell membrane. The N-terminal sequence MKKQIRN (amino acids 1-7 in Mhp494) obtained from the N-terminal cleavage fragment P27 precedes the only significant transmembrane domain in P159 (amino acids 9-29; TMpred score 2150) consistent with a hypothesis that cleavage occurs simultaneously with or immediately after translation and secretion to the cell surface.

These observations bear a striking resemblance to those reported for the cilia adhesin P97 (mhp183); i) the P126 pre-protein is barely detectable by immunoblot and is extensively cleaved, generating fragments ranging in mass from 20-120 kDa (Djordjevic *et al.*, 2004), ii) the N-terminal cleavage fragment P22 contains the only significant transmembrane domain found in the molecule, yet many of the cilia adhesin cleavage fragments are present on the cell surface and iii) processing is strain-specific. These observations suggest that P159 and P126 pre-proteins are processed via the same pathway. Although the surface topography of *M. hyopneumoniae* is poorly understood we have now provided evidence that three high-mass surface proteins of *M. hyopneumoniae* P159 (this study; mhp494), P97 (mhp183) and P102 (mhp182) (Djordjevic *et al.*, 2004) are cleaved with fragments residing on the cell surface. No evidence for proteolytic processing was reported for two well characterized surface lipoproteins with masses of 65 kDa (Kim *et al.*, 1990) and 46 kDa (Futo *et al.*, 1995). These data suggest that surface molecules secreted via type II but not type I secretory pathways may be targeted for further proteolytic processing in *M.
*hyopneumoniae* but additional studies are needed to rigorously test this hypothesis. The
identity and specificity of the corresponding protease(s) that cleave these proteins remains
unknown. However, bioinformatic analysis of the *M. hyopneumoniae* genome identified five
proteins with aminopeptidase signatures (mhp209, Map; mhp462, PepA; mhp520, PepF;
mhp680, PepP; and mhp656, Gcp) and a further two with serine protease signatures (mhp287
and mhp292). One or several of these are suspected of playing a role in surface protein
processing.

BlastP analyses showed that mhp494 is a novel molecule with discrete regions
showing limited homology to proteins found in *Mycoplasma conjunctivae* and *M.
hyopneumoniae*. Specifically, two regions spanning amino acids 1004-1406 and 2-200 of
P159 showed 22% identity (41% similarity) and 25% identity (46% similarity) respectively
with LppT from *Mycoplasma conjunctivae* (Belloy et al., 2003). *lppT* is the second gene in a
two-gene operon with *lppS* which was reported to be an adhesin in this species (Belloy et al.,
2003). Furthermore, amino acids 1026-1165 displayed 26% identity (48% similarity) with
mhp182 (P102) and amino acids 10-209 and 17-191 showed 28% identity (51% similarity)
and 28% identity (44% similarity) with P102 paralogs mhp272 and mhp384 respectively.

Different strains of *M. hyopneumoniae* have been shown to adhere to PK15 cell
monolayers (Zielinski et al., 1990) but in that study adherence was monitored by counting
radiation emitted from radiolabelled adhering cells. Scanning electron microscopy studies
reported here show that *M. hyopneumoniae* strain J adheres intimately to PK15 cells
especially in regions where microvilli are prominent with a proportion of *M. hyopneumoniae*
cells entering the cell monolayers. We cannot determine if *M. hyopneumoniae* actively
invades the cells or if PK15 cells engulf the *M. hyopneumoniae* at this time. However, pre-
incubating *M. hyopneumoniae* cells with a saturating concentration of heparin almost
completely abolished binding to PK15 cells, underscoring the importance that heparin
binding proteins on the surface of *M. hyopneumoniae* play in adherence to eukaryote cells. Importantly, Zhang *et al.* (1994) showed that heparin significantly inhibited the ability of *M. hyopneumoniae* to adhere to preparations of porcine respiratory tract cilia. Collectively, these studies indicate that PK15 cell monolayers provide a useful model system for identifying adhesins in *M. hyopneumoniae*. To this end we showed that P159 recombinant fragments F2\textsubscript{P159} and F4\textsubscript{P159} (and to a limited extent F3\textsubscript{P159}) which span all but the N-terminal 27 kDa of P159 promote the ability of latex beads to bind to PK15 cells demonstrating that P159 is a novel eukaryote cell adhesin. Pre-incubation of F2\textsubscript{P159}− and F4\textsubscript{P159}−-coated latex beads with a saturating concentration of heparin significantly blocked the ability of these beads to adhere to, and completely abolished their entry into, PK15 cells. Recombinant fragments F3\textsubscript{P159} and F4\textsubscript{P159}, which span the C-terminal half of P159, were found to bind heparin in a dose-dependent, saturable and specific manner (Kd values of 142.37 ± 22.01 nM and 75.37 ± 7.34 nM respectively). F3\textsubscript{P159} and F4\textsubscript{P159} were also shown to bind to heparin-agarose showing that these P159 recombinant fragments bind both soluble and bound heparin. These values are comparable to other biologically significant heparin-protein binding interactions (Pethe *et al.*, 2000) and falls in the midrange of other reported constants for heparin-protein interactions (Pankhurst *et al.*, 1998). The ability of F2\textsubscript{P159} to promote the adherence of latex beads to PK15 cells despite an inability to bind heparin suggests that different regions within P159 use different mechanisms to bind eukaryote cells. Our data suggests that P159 cleavage fragments P110 and P52 each possess the ability to bind heparin and to adhere to and enter PK15 cells; the function of F1\textsubscript{P159} remains unknown. *M. hyopneumoniae* cells pre-incubated with an excess of F4\textsubscript{P159} protein were significantly affected in their ability to adhere to PK15 cells suggesting that the C-terminal region of P159 spanning P52 interacts with a receptor(s) on the surface of PK15 cells. Further processing events that affect the integrity of P110 and P52 may have important ramifications for their
biological function. Immunoblotting studies (Fig. 2) indicate that P68 resides within P110 and further studies are needed to examine the biological properties specific to this fragment.

It is becoming evident from this and previous studies (Djordjevic et al., 2004; Jenkins et al., 2006) that *M. hyopneumoniae* processes key surface proteins to generate domains with potentially important biological functions. Processing of surface proteins may provide *M. hyopneumoniae* with a means to regulate its surface architecture enabling it to adapt to various tissue environments within the host. Cytokines, growth factors, complement components, plasma lipoproteins, regulators of homeostasis, and various extracellular matrix components such as vitronectin and fibronectin have been shown to bind heparin (Bernfield et al., 1999; Jackson et al., 1991; Kim et al., 1990). Microbial pathogens bind heparin and related glycosaminoglycans as a means of recruiting a wide variety of mammalian heparin binding proteins to their surface, thus bypassing the need to evolve specific receptor molecules for these key mammalian proteins (Duensing et al., 1999). More importantly, the ability to recruit these proteins to the surface of microbial pathogens impacts on key aspects of microbial pathogenicity such as an increased capacity to invade epithelial cells and inhibition of chemokine-induced chemotaxis (Duensing et al., 1999).

The ability of a protein to bind glycosaminoglycans largely depends on electrostatic interactions between the negatively charged sulfate groups and positively charged regions of the protein; the role of different sugar moieties in the backbone of the glycosaminoglycan in protein binding is less well understood. Although the heparin-binding motifs, XBBXBX and XBBBXXBX (where B represent basic amino acids and X any other amino acids) have been known for many years (Cardin and Weintraub, 1989), more recent studies indicate that various combinations of clustered basic amino acids can bind heparin (Aoki et al., 2004). P159 is rich in lysine (K) and arginine (R) residues (15.6% and 13.9% of F3_{P159} and F4_{P159}.
sequences respectively are K and R), and further studies aim to more accurately delineate the heparin binding domains within regions of P159.

Fucoidan, a sulfated polysaccharide of non-mammalian origin, inhibited the interaction between heparin and $F_{3P159}$ and $F_{4P159}$. It is generally the case that heparin-binding proteins also interact with fucoidan due to its high sulfate density and branched, comb-like structure, which contrasts with the linear structure of mammalian glycosaminoglycans (Patankar et al., 1993). Chondroitin sulfate A and B and mucin did not competitively inhibit the ability of heparin to bind P159 fragments $F_{3P159}$ and $F_{4P159}$; heparan sulfate, a less sulfated version of heparin, only slightly inhibited these interactions. Chondroitin sulfate B is similar in structure to heparin and heparan sulfate in that it contains a backbone of iduronate residues yet failed to act as a competitive inhibitor. Collectively, these observations suggest that the degree of sulfation is a key component in $F_{3P159}$ and $F_{4P159}$ binding heparin.

In conclusion, evidence presented here indicates that P159 is a proteolytically processed, heparin binding surface protein of $M. hyopneumoniae$ and that the C-terminal half of P159 houses at least 2 heparin-binding domains located within $F_{3P159}$ and $F_{4P159}$ respectively. We show that i) $M. hyopneumoniae$ adheres intimately to the surface of PK15 cells where microvilli predominate, ii) heparin blocks the ability of this pathogen to adhere to PK15 cells and show for the first time that $M. hyopneumoniae$ can enter these cells, iii) regions within P159 are intimately involved in adherence to and entry into PK15 cells. Collectively our data suggests that $M. hyopneumoniae$ may possess the armory to invade epithelial cells, spread to other sites within the host and attract host molecules to its surface. In this regard it is not insignificant that $M. hyopneumoniae$ has been isolated in pure culture from the pericardial fluid of swine with clinical symptoms of pericarditis (Buttenschon et al., 1997). Despite possessing limited coding capacity, evidence of differences in strain virulence
(Vicca et al., 2003), cleavage of key surface proteins (Djordjevic et al., 2004), and our recent report that key surface proteins bind glycosaminoglycans (Jenkins et al., 2006) suggests that subtle changes in surface protein sequences may have significant ramifications for disease caused by *M. hyopneumoniae*.

**Experimental procedures**

*Experimental procedures*  

*Bacterial strains and growth conditions.*  

*M. hyopneumoniae* strain 232 (Zhang et al., 1995) was a kind gift from F. C. Minion. Two strain J isolates were used in these studies; NCTC 10110 was used for immunoblot experiments and a low passage isolate derived from ATCC 27715 was used for infection studies of PK15 cells. The ATCC 27715 strain was kindly provided by P. Valentin-Weigand, University of Veterinary Medicine Hannover, Germany. A description of *M. hyopneumoniae* strains Beaufort, Sue and C1735/2 and their source has been described previously (Scarman et al., 1997). *M. hyopneumoniae* was grown in 0.22 µm filter sterilized modified Friis broth (Friis, 1975) and harvested as described previously (Djordjevic et al., 2004). For growth studies, sterile tubes containing 6 ml of Friis broth were simultaneously inoculated with 300 µl of *M. hyopneumoniae* strain 232 culture and incubated for 8, 16, 24, 28, 32, 40, 48, 56 and 72 h as described previously (Djordjevic et al., 1994). *Escherichia coli* M15 [pREP4] cells (Qiagen, Alameda, California) were grown at 37°C in Luria-Bertani medium (Sambrook et al., 1989). When appropriate, antibiotics were used at the following concentrations: ampicillin 100 µg/ml and kanamycin 25 µg/ml. Protein expression was induced by the addition of 100 µM isopropyl-β-D-thiogalactopyranosidase (IPTG).

*Proteomic analyses: 2-D gel electrophoresis and postseparation analyses.*
Two-dimensional gel electrophoresis (2-DGE) was carried out as described previously (Cordwell et al., 1997). Conditions used for the solubilisation of *M. hyopneumoniae* proteins, isoelectric focusing and SDS-PAGE have been described previously in detail (Djordjevic et al., 2004). Briefly, *M. hyopneumoniae* bacterial cells were resuspended in 1 ml of sample buffer for each 0.1 g of bacterial pellet. Cells were disrupted with a Microson Ultrasonic sonicator (Misonix, Farmingdale, New York) for 6 x 30 sec at a power setting of 14 W and centrifuged (120 min, 50 000 x g) in a Beckman TL100 ultracentrifuge (Beckman Coulter, Fullerton, California). A total of 250 µg of *M. hyopneumoniae* protein extract was diluted with sample buffer to a volume of 100 µl for application to the anodic end of each IPG strip in an applicator cup. Isoelectric focusing was performed on a Multiphor II electrophoresis unit (Amersham Biosciences, Piscataway, New Jersey) for 85 kVh at 20°C. IPG strips were detergent exchanged, reduced, and alkylated in buffer containing 6 M urea, 2% SDS, 20% glycerol, 5 mM tributyl phosphine, 2.5% (v/v) acrylamide monomer, a trace amount of bromophenol blue dye, and 375 mM Tris-HCl (pH 8.8) for 20 min prior to loading the IPG strip onto the top of a 8-18% 20 cm by 20 cm polyacrylamide gel. Second-dimension electrophoresis was carried out at 5°C using 3 mA/gel for 2 h followed by 20 mA/gel until the bromophenol blue dye had run to the end of the gel. Gels were fixed in 40% methanol and 10% acetic acid for 1 h, stained overnight in Sypro Ruby (Molecular Probes, Eugene, Oregon) and images acquired using a Molecular Imager Fx apparatus (Bio-Rad Laboratories, Hercules, California). Gels were then double stained in Coomassie blue G-250. Protein spots were excised from gels using a sterile scalpel blade and placed into 96-well V bottom trays (Greiner Bio-One, Longwood, Florida). The methods used for post-separation analyses are as described previously (Djordjevic et al., 2004). A list of monoisotopic peaks corresponding to the mass of generated tryptic peptides was used to search a modified translated version of the
M. hyopneumoniae genome (Minion et al., 2004). N-terminal Edman sequencing was performed as previously described (Nouwens et al., 2000).

Molecular analyses, cloning and expression.

Plasmid DNA was prepared using a plasmid MidiPreparation kit (Qiagen, Alameda, California) as per manufacturer’s instructions. DNA sequence analysis was performed using the Sanger method. PCR was carried out using a DTCS Quickstart Master Mix (Beckman Coulter, Fullerton, California), according to the manufacturer’s instructions and analysed using a CEQ8000 Genetic Analyser (Beckman Coulter, Fullerton, California). Both pQE-9 specific primers and internal primers were used to initiate sequencing of DNA and were purchased from Sigma-Aldrich (Sydney, Australia). Hexahistidyl P159 fusion proteins were constructed using pPCR-Script (Stratagene, La Jolla, California) and pQE-9 (Qiagen, Alameda, California) cloning vectors. Primer sequences used to amplify each of the four fragments are given in Table 1. The underlined sequences correspond to the following restriction sites: SalI in the forward primers and PstI in the reverse primers. Recombinant proteins F1\textsubscript{P159}-F4\textsubscript{P159} span nucleotides 91-791 (amino acids 31-264), 792-1557 (amino acids 265-519), 1675-2727 (amino acids 558-909) and 2875-4215 (amino acids 958-1405) respectively within the \textit{p159} gene sequence (accession number AF279292). PCR was carried out using Expand DNA Polymerase Enzyme (Roche, Basel, Switzerland) on a PC-960 thermocycler (Corbett Research, Mortlake, Australia). The template for the amplification of the entire \textit{p159} gene was M. hyopneumoniae 232. The resulting 4233 bp amplicon was cloned into the pCR2.1 TA plasmid (Invitrogen, Carlsbad, California). The nine tryptophan-encoding TGA codons present in this ORF were converted to TGG by site-directed mutagenesis using the QuikChange Site Directed Mutagensis Kit (Stratagene, La Jolla, CA) according to the manufacturers suggested protocol. The resulting clone was designated
PCR fragments were digested with *Sal*I and *Pst*I and cloned into *Sal*I and *Pst*I-digested pPCR-Script plasmid (Stratagene, La Jolla, California). Constructs with the proper fragment orientation were identified by restriction digestion and DNA sequence analysis and were designated p159PCR1-4. Plasmid DNA from p159PCR1-4 were digested with *Sal*I and *Pst*I and cloned into the pQE9 plasmid (Qiagen, Alameda, California) using T4 DNA ligase (Roche, Basel, Switzerland) and transformed into *E. coli* M15 [pREP4] cells (Qiagen, Alameda, California) by electroporation using a Gene Pulsar (Bio-Rad Laboratories, Hercules, California) and the pre-set *E. coli* protocol at 2.5 kV. Correct constructs were identified as above and designated p159QE1-4. Protein expression was induced by the addition of 100 μM IPTG and proteins were purified using Ni-NTA agarose as per the manufacturer’s instructions (Qiagen, Alameda, California). The presence of possible transmembrane domains was investigated using the TMPred program available via the Swiss European Molecular Biology Network (EMBnet) website (www.ch.embnet.org/software/TMPRED_form.html).

*Latex bead preparation and PK15 cell culture.*

As per previously published methods (Dombek et al., 1999; Molinari et al., 1997), latex beads (3 μm; Sigma-Aldrich, St. Louis, Missouri) were coated with purified recombinant P159 fragments F1<sub>P159</sub>-F4<sub>P159</sub>. Briefly, 10<sup>8</sup> bead particles in 50 μl PBS were incubated with 5 μg of purified proteins in PBS overnight at 4°C. After washing steps, free binding sites on the bead surface were blocked by incubation with 200 μl of 10 mg/ml BSA in PBS for 1 h at room temperature. The efficiency of particle loading was verified by fluorescence-activated cell sorter analysis with anti-F1<sub>P159</sub>-F4<sub>P159</sub> rabbit serum (results not shown). Beads were washed and the volume adjusted to 2.5 ml with Dulbecco modified Eagle medium
PK15 cells were seeded on 12-mm-diameter glass coverslips (Nunc, Wiesbaden, Germany) placed on the bottom of 24-well tissue culture plates (Nunc, Wiesbaden, Germany) at $1.5 \times 10^5$ cells per well and allowed to grow to semi-confluent monolayers at $37^\circ C$ in a 5% CO$_2$ atmosphere. After addition of 250 µl of the bead suspension, the cells were incubated for 2, 4, 7 and 22 h at $37^\circ C$ in a 5% CO$_2$ atmosphere. Cells were washed three times with PBS to remove unbound beads. Cells were either processed for scanning electron microscopy (Molinari et al., 1997) or for double immunofluorescence as described below. Further studies were conducted pre-incubating the latex beads with a saturating concentration of heparin (500 µg/ml), purified F$_{1P159}$, F$_{2P159}$, F$_{3P159}$, and F$_{4P159}$ proteins (1 µg each), or anti-F$_{1P159}$-F$_{4P159}$ sera (25 µg) separately for 1h at $37^\circ C$ in a 5% CO$_2$ atmosphere before addition to the PK15 cells.
Antisera to each fragment of P159 were generated by subcutaneous immunization of New Zealand White rabbits with hexahistidyl-tagged products purified by nickel-affinity chromatography. Pre-immune sera were collected prior to immunization for the preparation of control serum. Rabbits were then each immunized on two occasions 21 days apart using Freund’s incomplete adjuvant (Sigma-Aldrich, St. Louis, Missouri), and immune responses monitored by immunoblotting. Rabbits were euthanased, and serum collected as described previously (Wilton et al., 1998). Horse radish peroxidase-conjugated sheep anti-rabbit immunoglobulin antibodies were purchased commercially (Chemicon, Temecula, California).

*M. hyopneumoniae* whole cell protein preparations and purified hexahistidyl F1\textsubscript{P159}-F4\textsubscript{P159} proteins along with *M. hyopneumoniae* growth assay samples were subjected to electrophoresis on 12% SDS-PAGE gels as described previously (Laemmli, 1970). After electrophoresis, proteins were electrophoretically transferred onto polyvinylidene difluoride membrane using a Hoefer Scientific TE Series Transphor Electrophoresis Unit (Hoefer, San Francisco, California) as described previously (Burnette, 1981). Immunoblotting experiments were performed with rabbit polyclonal antibodies raised against F1\textsubscript{P159}-F4\textsubscript{P159}, either separately or pooled. Peroxidase conjugated sheep anti-rabbit was used as the secondary antibody and detected using diaminobenzidine (DAB; Sigma-Aldrich, St. Louis, Missouri).

PK15 cells (after incubation with the coated latex beads) were washed with PBS and then fixed by the addition of 0.5 ml/well of pre-cooled fixation buffer (1% paraformaldehyde in PBS), the tray was placed on ice for 1 h and then stored at 4°C overnight. The PK15 cells were blocked by the addition of 200 µl/well of PBS with 10% FCS and incubated for 30 min at room temperature. The blocking solution was then removed and the cells incubated separately with 200 µl/well of the anti-F1\textsubscript{P159}-F4\textsubscript{P159} rabbit polyclonal antibodies (40-50 µg/ml) for 45 min at room temperature. Cells were incubated with goat
anti-rabbit Alexa 488 (green) (Molecular Probes, Eugene, Oregon) for 1h at room temperature and subsequently washed with PBS. Cells were permeabilized with Triton X-100 (200 µl/well of a 0.1% triton X-100 in PBS solution) for 5 min at room temperature, washed in PBS, followed by incubation with 200 µl/well of the anti-F1-F4 rabbit polyclonal antibodies (40-50 µg/ml) for 45 min at room temperature. After washing, cells were treated with goat anti-rabbit Alexa 568 (red) (Molecular Probes, Eugene, Oregon) for 1 h and washed three times in PBS. Some cells were further incubated with 200 µl of a 0.1 mg/ml Hoechst stain (Molecular Probes, Eugene, Oregon) solution in PBS for 5 min before being washed three times in PBS. Cells were then mounted onto a glass slide. After this labeling procedure, extracellular beads appear yellow/green whereas intracellular beads are stained orange/red. Images were recorded using a Zeiss inverted microscope 100 M with an attached Zeiss Axiocam HRc digital camera.

Immunogold labelling of whole *M. hyopneumoniae* cells was performed as follows: Parlodion/carbon coated 300 mesh nickel grids (Pro Sci Tech, Queensland, Australia) were floated on drops of *M. hyopneumoniae* (strain 232) suspension in a moist petridish for 2 min. The grids were then incubated for 1 min with phosphate buffer (pH 6.8) containing 1% BSA, 0.5% Tween 20 and 0.02% sodium azide. The grids were then floated on drops of undiluted anti- F2 and anti-F4 sera, pre-immune for control and post-immune for tests, and incubated at 37°C for 90 min. The grids were washed with phosphate buffer (pH 6.8) 3 x 5 min and then floated on drops of protein A gold (15 nm, BBInternational, Cardiff, UK) diluted 1:50 for 45 min. The grids were washed with phosphate buffer and distilled water and stained with 2% aqueous uranyl acetate (Merck, Whitehouse Station, New Jersey). The grids were blotted dry and examined under a Philips 208 transmission electron microscope.
Trypsin treatment of *M. hyopneumoniae*

*M. hyopneumoniae* cells (0.5 g) were treated with trypsin as described previously (Wilton et al., 1998). Briefly, trypsin was added to cell suspensions of *M. hyopneumoniae* at trypsin concentrations of 0, 0.1, 0.5, 1, 3, 5, 10, 50 and 150 µg/mL and incubated at 37°C for 15 min. Cell suspensions were then lysed in sample buffer (60 mM Tris, pH 6.8; 1% [w/v] SDS; 1% [v/v] β-mercaptoethanol; 10% [v/v] Glycerol and 0.01% [w/v] bromophenol Blue) and heated to 95°C for 10 min. Lysates were analysed by SDS-PAGE and immunoblotting with a pool of F1P159-F4P159 antiserum.

**Heparin binding assays.**

Paraformaldehyde (1% paraformaldehyde in PBS) fixed *M. hyopneumoniae* strain 232 cells at an optical density of 0.04 (in 0.1 M NaHCO₃, pH 9.5) or aliquots (100 µl) of recombinant proteins F1P159-F4P159 (5 µg/ml in 0.1 M NaHCO₃, pH 9.5) were applied to 96-well polystyrene microtitre plates (Linbro/Titretek; ICN Biochemicals, Aurora, Ohio). The plates containing the *M. hyopneumoniae* cells were centrifuged at 2000 x g for 10 min, while the plates containing recombinant proteins were allowed to adsorb overnight at room temperature. The wells were then blocked with 100 µl aliquots of PBS containing 2% (w/v) skim milk for 1 h at room temperature. Biotinylated heparin (Sigma-Aldrich, St. Louis, Missouri) in PBS containing 1% skim milk was next applied to the wells in 100 µl aliquots and incubated for 1.5 h at room temperature. After 3 washes with 0.05% (v/v) Tween20 in PBS, bound biotinylated heparin was detected using 100 µl aliquots of peroxidase conjugated streptavidin (Roche, Basel, Switzerland) diluted 1:3000 with a 1 h incubation at room temperature. The wells were washed as above prior to the addition of substrate solution (100 µl) containing 0.55 mg/ml 2,2’-azino-bis(3-ethylebenzthiazoline-6-sulfonic acid) diammonium salt (ABTS; Sigma-Aldrich, St. Louis, Missouri) in 0.1 M citrate, 0.2 M
phosphate, pH 4.2, containing 0.03% (v/v) hydrogen peroxide. The absorbance of the product formed was measured at 414 nm using a Multiskan Ascent ELISA plate reader (Thermo Labsystems, Franklin, Massachusetts). In other experiments, a competitive binding assay was used in which unlabeled glycosaminoglycans; heparin, fucoidan, heparan sulfate, mucin, chondroitin sulphate A and chondroitin sulfate B (all from Sigma-Aldrich, St. Louis, Missouri) were pre-incubated with biotinylated heparin for 15 min before the addition of 100 µl aliquots of the mixture to coated and blocked wells. Control experiments showed that none of the P159 fragments could bind to streptavidin-peroxidase or the ABTS solution, establishing that the heparin binding is not an artifact of binding to a compound used in the detection system. Graph construction and non-linear regression with one-site binding and one-site competition analysis was performed using GraphPad Prism version 4 (GraphPad Software, San Diego, California).

A cell pellet of *E. coli* M15 [pREP4] cells (Qiagen, Alameda, California) containing the pQE9 F1$_{p159}$-F4$_{p159}$ plasmids from a 300 ml culture were re-suspended in a solution of 50 mM DTT, 2% triton X-100, 1 mg/ml lysozyme. The suspension was subjected to sonication and then centrifuged at 16, 000 × g for 15 min at 10°C and the supernatant was applied to a 7.5 ml heparin-agarose column (Sigma-Aldrich, St. Louis, Missouri) that had been pre-equilibrated with 0.01 M Tris-HCl (pH 7.6). The column was washed with 45 ml 0.01 M Tris-HCl (pH 7.6) and bound proteins eluted at a flow rate of 1 ml/min with a linear 0-0.5 M NaCl gradient in 0.01 M Tris-HCl (pH 7.6). The peak fractions (from the wash and elution’s) at 280 nm absorbance were subjected to electrophoresis on 12% SDS-PAGE gels as described previously (Laemmli, 1970). After electrophoresis, proteins were electrophoretically transferred onto polyvinylidene difluoride membrane using a Hoefer Scientific TE Series Transphor Electrophoresis Unit (Hoefer, San Francisco, California) as described previously (Burnette, 1981). Immunoblotting experiments were performed using
rabbit polyclonal antibodies raised separately to F1_{P159}\text{-}F4_{P159}. Peroxidase conjugated sheep anti-rabbit was used as the secondary antibody and detected using diaminobenzidine (DAB; Sigma-Aldrich, St. Louis, Missouri).

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group A streptococci: M1 protein-mediated invasion and cytoskeletal rearrangements. 


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Restriction sites for SalI in the forward (F) primers and PstI in the reverse (R) primers used for cloning the p159 fragments F1_{p159}-F4_{p159} into pQE-9 are underlined. SDM refers to site-directed mutagenesis.
Figure legends

**Fig. 1.** 2-D gel electrophoresis and peptide mass fingerprint analysis of P159.  (A) 2-D gel (8-18% polyacrylamide gradient) of *M. hyopneumoniae* strain 232 whole cell lysate; proteins were initially resolved using a pH 6-11 first dimension isoelectric focusing strip. P159 cleavage fragments P27, P52 and P110 identified by peptide mass mapping are indicated. Spot trains (often seen for proteins resolved by 2D electrophoresis) may be due to bona fide posttranslational modifications that evoke a pI shift (e.g. phosphorylation) or are artifactual arising by non-enzymatic deamidation of Asn to Asp. (B) Peptide mass mapping was performed using MALDI-TOF (MS) analysis on tryptic digests of P159 proteins boxed in panel A. The N-terminal sequence of P27 as determined by Edman degradation is underlined. The predicted transmembrane region is double underlined. (C) Diagrammatic representation of the P159 molecule depicting P27, P110 and P52. The four P159 recombinant fragments (F1<sub>P159</sub>-F4<sub>P159</sub>) constructed for this study are also shown. The cleavage site between P27 and P110 is predicted to occur between amino acids 219-303 whilst cleavage between P110 and P52 is predicted to occur between amino acids 841-978.

**Fig. 2.** Immunoblot analyses using F1<sub>P159</sub>, F2<sub>P159</sub>, F3<sub>P159</sub>, and F4<sub>P159</sub> antisera. Panels A-D show whole cell protein extracts of *M. hyopneumoniae* strain 232 (lane 1) and a sample of purified F1<sub>P159</sub>, F2<sub>P159</sub>, F3<sub>P159</sub>, and F4<sub>P159</sub> proteins (lane 2, panels A-D respectively) reacted with anti-F1<sub>P159</sub> (panel A), anti-F2<sub>P159</sub> (panel B), anti-F3<sub>P159</sub> (panel C), and anti-F4<sub>P159</sub> sera (panel D). Antisera were diluted 1/100. All preparations were boiled for 5 min in Laemmli buffer. Black arrowheads indicate the position of recombinant proteins F1<sub>P159</sub>-F4<sub>P159</sub>. White arrowheads indicate the position of dominant cleavage fragments recognised by antisera in
whole cell lysates of *M. hyopneumoniae*. The asterix (*) identifies a multimeric form of recombinant protein F4<sub>P159</sub>. An immunoblot containing comparable amounts of whole cell lysates of *M. hyopneumoniae* strain 232 harvested at different times during the growth cycle reacted with pool of anti F1<sub>P159</sub>-F4<sub>P159</sub> sera is shown in panel E. Lanes 1-9 correspond to *M. hyopneumoniae* cultures harvested at 8, 16, 24, 28, 32, 40, 48, 56 and 72 hours post inoculation respectively. An immunoblot containing comparable amounts of whole cell lysates of various *M. hyopneumoniae* strains reacted with a pool of anti F1<sub>P159</sub>-F4<sub>P159</sub> sera is shown in panel F. Lane 1-5 were loaded with lysates of strains 232, J, SUE, C1735/2, and Beaufort respectively.

**Fig. 3.** Localization of P159 cleavage products on the surface of *M. hyopneumoniae* strain 232. Panel A shows an immunoblot of whole cell preparations of freshly cultured *M. hyopneumoniae* strain 232 cells exposed to different concentrations of trypsin ranging from 0, 0.1, 0.5, 1, 3, 5, 10, 50 and 150 µg/ml for 15 minutes (lanes 1-9 respectively) reacted with a pool of rabbit anti-F1<sub>P159</sub>-F4<sub>P159</sub> sera. Panels B-E show electron micrographs of intact, freshly cultured *M. hyopneumoniae* strain 232 cells labeled with pre-immune, control sera collected prior to immunization with recombinant proteins F2<sub>P159</sub> and F4<sub>P159</sub> (panels B and D respectively) or hyper-immune rabbit anti-F2<sub>P159</sub> and anti-F4<sub>P159</sub> sera (panel C and E respectively). Colloidal gold-conjugated anti-rabbit Ig (15 nm particles) was used to detect P159 cleavage fragments recognized by these sera. Cells were stained with 2% aqueous uranyl acetate. Arrows indicate gold particles. Bars = 500 nm.

**Fig. 4.** Binding of biotinylated heparin to *M. hyopneumoniae* strain 232. Binding of biotinylated heparin to the surface of *M. hyopneumoniae* strain 232 is shown in panel A. Increasing concentrations of biotinylated heparin were added to 96-well microtitre plates.
coated with *M. hyopneumoniae* strain 232. Figures shown are means ± SEM of triplicate determinations, indicated by error bars. A ligand blot containing *M. hyopneumoniae* strain 232 whole cell lysate probed with biotinylated heparin is shown in panel B.

**Fig. 5.** Binding of recombinant P159 fragments (F1\textsubscript{P159}-F4\textsubscript{P159}) to biotinylated heparin.

Increasing concentrations of biotinylated heparin were added to 96-well microtitre plates coated with 5 µg/ml of each of the four P159 fragments. □ represents the total binding and ∆ represents non-specific binding measured by mixing the biotinylated heparin with a 50 fold excess (2.4 mg/ml) of non-biotin labeled heparin prior to incubation with the recombinant P159 fragments. The specific binding curve, represented by the symbol ○, was obtained by subtracting non-specific binding from the total binding values. Figures shown are means ± SEM of triplicate determinations, indicated by error bars. Controls with specific antisera show that each protein was successfully coated to the ELISA plate.

**Fig. 6.** Inhibition studies with various glycosaminoglycans. Different glycosaminoglycans were examined for their ability to inhibit the binding of recombinant P159 fragments to biotinylated heparin. Panel A shows how unlabeled heparin affects the ability of F1\textsubscript{P159} (□), F2\textsubscript{P159} (∆), F3\textsubscript{P159} (○) and F4\textsubscript{P159} (◊) to bind biotinylated heparin. Panels B and C show how unlabeled fucoidan ■, heparan sulfate ▲, chondroitin sulfate A ●, and chondroitin sulfate B ♦ affect the ability of F3\textsubscript{P159} and F4\textsubscript{P159} to bind biotinylated heparin respectively. Inset are inhibition curves showing an expansion of the optimal inhibition range of 0-600 µg/ml. In these experiments, varying concentrations (0-40 times the saturating concentration of 60 µg/ml) of glycosaminoglycan inhibitors were each pre-incubated with biotinylated heparin (60 µg/ml). Error bars represents mean values ± SEM from triplicate experiments.
**Fig. 7.** Scanning electron micrographs depicting the interaction of *M. hyopneumoniae* with PK15 cells. Panel A shows *M. hyopneumoniae* interacting with PK15 cells. Panel B shows the inhibition of *M. hyopneumoniae* adherence due to the presence of F4P159 protein. Adhering *M. hyopneumoniae* cells are indicated by an arrow. Panel C shows the inhibition of adherence due to the presence of heparin. Scale bars are given at the bottom of each image.

**Fig. 8.** Double immunofluorescence microscopy of PK15 cells exposed to latex beads coated with recombinant P159 proteins. Beads determined to reside intracellularly are identified with white arrows. Panel A shows PK15 cells incubated with F1P159-coated latex beads after 22 h incubation. These images are indistinguishable from control images of PK15 cells exposed to naïve latex beads and show that F1P159 does not play a direct role in adherence. Panel B shows F2P159-coated latex beads after 7 h of incubation adhering to the surface of (yellow/green) and penetrating into (orange/red) PK15 cells. Panel C shows a similar image as depicted in B except the nucleus of the PK15 cells were stained with Hoechst stain. Panel D depicts the same image as panel C but with a different exposure time showing the extracellular (yellow/green) beads and the intracellular (orange/red) beads. Panel E shows F3P159-coated beads interacting with a cluster of PK15 cells after 4 h of incubation. Panel F depicts F4P159-coated beads interacting with PK15 cells after 7 h incubation. Beads were identified on the surface (yellow/green beads) and within (orange/red beads) PK15 cells.

**Fig. 9.** Scanning electron micrographs depicting the interaction of latex beads separately coated with recombinant P159 fragments F2P159 and F4P159 with PK15 cells. Panels A and B depict F2P159- and F4P159-coated latex beads adhering to and residing within PK15 cells respectively. Panel C represents an enlargement of the area (marked by an arrow) in panel A showing an F2P159-coated bead adhering to and another within a PK15 cell 2 h after
incubation. Similarly, panel D represents the arrow marked area in panel B showing a F4$_{P159}$-coated bead adhering to and another within a PK15 cell 2 h after incubation. Panels E and F depict F4$_{P159}$-coated latex beads adhering to and residing inside PK15 cells 2 and 4 h after incubation respectively. The scale bars are given at the bottom of each image.

Fig. 10. Effect of separately pre-incubating F2$_{P159}$-F4$_{P159}$ proteins and heparin on the abilities of latex beads coated with P159 fragments to interact with PK15 cells. F2$_{P159}$-coated latex beads pre-incubated with F2$_{P159}$ bound poorly to PK15 cells (panel A). F4$_{P159}$-coated latex beads pre-incubated with F4 protein bound poorly to PK15 cells (panel B). An adherent bead is highlighted by an arrow. F4$_{P159}$-coated latex beads pre-incubated with heparin bound poorly to PK15 cells (panel C). Scale bars represent 10 µm. Panel D summarises data derived from three individual assays (20 cells counted per assay). Error bars represent the standard deviation. Latex beads were pre-incubated with a saturating concentration of heparin (500 µg/ml) or protein (1 µg) for 1h before addition to the PK15 cells. Numbers of adhering (extracellular) and invasive (intracellular) beads were quantified by double immunofluorescence analysis.
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Fig. 2

A | B | C | D
---|---|---|---
1 | 2 | 1 | 2 | kDa
118 | 85 | 48 | 32 | 26 | 19

E

1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | kDa
118 | 85 | 48 | 32 | 26 | 19

F

1 | 2 | 3 | 4 | 5 | kDa
170 | 100 | 72 | 55 | 40 | 33 | 24 | 17
Fig. 4

A

B

[Biotinylated Heparin] (µg/ml)

[OD]

kDa

170
100
72
55
40
33
24
17
Fig. 5

**F1**

**F2**

**F3**

**F4**

[Biotinylated Heparin] (µg/ml)

OD
Fig. 6

A

B

C

[Unlabeled Heparin] (µg/ml)

[Inhibitor] (µg/ml)

OD

OD

OD

0 500 1000 1500 2000 2500 3000

0 500 1000 1500 2000 2500 3000

0 500 1000 1500 2000 2500 3000
Fig. 8.