Helicobacter pylori upregulates matrilysin (MMP-7) in epithelial cells in vivo and in vitro in a Cag dependent manner

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Background and aims: Matrix metalloproteinase-7 (MMP-7) is important in normal and pathological remodelling of epithelial-matrix interactions, and is upregulated in gastric cancer. *Helicobacter pylori* infection is the first stage in gastric carcinogenesis, and therefore our aim was to determine if *H pylori* upregulated gastric MMP-7 expression and if this was affected by strain virulence.

Methods: We took gastric biopsy specimens at endoscopy from *H pylori* infected (n = 17) and uninfected (n = 18) patients and assessed MMP-7 expression by ELISA, real time polymerase chain reaction (PCR), and immunohistochemistry (concentrating on epithelial cells in the proliferative zone). We PCR typed *H pylori* for *cagE* and *vacA*. We performed *H pylori*/cell line coculture studies with wild-type pathogenic and non-pathogenic *H pylori* strains and with *CagE*[−] and *VacA*[−] isogenic mutants.

Results: Gastric biopsy specimens from *H pylori*⁺ patients expressed higher levels of MMP-7 at the protein and mRNA levels in the antrum and corpus (for example, by ELISA: *H pylori*⁺ 0.182 OD units v *H pylori*[−] 0.059; p = 0.009 antrum). Epithelial cells from *H pylori*⁺ patients stained more intensely for MMP-7 than those from uninfected patients, including in the proliferative zone containing pluripotent cells (p < 0.03 antrum, p < 0.04 body). Upregulation of MMP-7 in epithelial cells was confirmed at the protein and mRNA levels by *H pylori*/cell line coculture. These experiments also showed that MMP-7 upregulation was dependent on an intact *H pylori* *cag* pathogenicity island but not on the vacuolating cytotoxin.

Conclusion: We speculate that increased expression of MMP-7 in *H pylori* gastritis may contribute to gastric carcinogenesis.

The main cause of peptic ulceration and gastric MALT lymphoma is *Helicobacter pylori*,^{1,2} and *H pylori* is the strongest risk factor for the development of distal gastric adenocarcinoma.³ The outcome of *H pylori* infection is dependent on host,⁴ environmental,⁵ and bacterial factors.^{6,7} Strains possessing the *cag* pathogenicity island, encoding a type IV bacterial protein secretion system,^{8–11} are more strongly associated with increased levels of inflammation and disease,⁶ as are those producing an active form of VacA, a pore forming toxin that induces cytoplasmic vacuolation in vitro.^{12–15}

Matrix metalloproteinases (MMPs) are a family of diverse zinc dependent proteolytic enzymes that are important in maintenance and remodelling of interactions between epithelial cells and basement membrane.¹⁶ They have many substrates, including collagen and elastin, and play an important role in promoting invasion and metastasis of cancer cells. MMPs also cleave cell surface bound substrates ("shedase" activity) such as membrane bound cytokines, cytokine receptors, and adhesion molecules, releasing soluble or inactive forms. MMP-7 (matrilysin) is the smallest member of the MMP family and part of the stromelysin subclass. It is upregulated in epithelial cells in gastric cancer.^{17–21} MMP-7 degrades various matrix substrates, including proteoglycans, gelatin, and elastin, and cleaves from the cell surface non-matrix substrates, including E-cadherin, pro-tumour necrosis factor α (TNF- α), and Fas ligand.^{22–26} A growing body of evidence suggests that MMP-7 plays an early role in tumorigenesis in colorectal cancer. The MMP-7 null Min mouse exhibits much reduced colonic tumour formation,²⁷ and MMP-7 transcripts are found in the

tumour epithelium of over 90% of colonic adenomas in both human and mice models.^{27,28}

Here we have examined if MMP-7 is upregulated in *H pylori* gastritis, as this is the first stage in the progression to gastric carcinoma. We show that *H pylori* upregulates MMP-7 expression at the mRNA level, and that MMP-7 is upregulated in inflammatory and epithelial cells, and crucially in the latter in the proliferative zone containing pluripotent cells. We show that this upregulation is caused by pathogenic strains of *H pylori*, and is dependent on the *cag* pathogenicity island, but not on the toxin, VacA.

METHODS

In vivo studies

Patients and biopsy samples

Patients were recruited from routine day case endoscopy lists performed at University Hospital, Nottingham. Patients were not included if they had taken a proton pump inhibitor, antibiotics, or bismuth containing compounds in the previous four weeks. The study had full ethical approval from the University Hospital Nottingham Ethics Committee. Details of patient demographics are shown in table 1. Gastric biopsy specimens were taken from the antrum and corpus, and

Abbreviations: MMPs, matrix metalloproteinases; MMP-7, matrix metalloproteinase-7 (matrilysin); FCS, fetal calf serum; PCR, polymerase chain reaction; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; Ct, threshold cycle; SDS-PAGE, sodium dodecyl sulphate-polyacrylamide gel electrophoresis; ELISA, enzyme linked immunosorbent assay; TNF- α , tumour necrosis factor α

Table 1 Patient demographics

	<i>H. pylori</i> +	<i>H. pylori</i> −
n	17	18
Sex (M/F)	9/8	8/10
Age (y) (median)	65	52.5
Diagnosis/reason for OGD	9 duodenal ulcer disease 4 non-ulcer dyspepsia 4 iron deficiency anaemia, normal OGD	6 GORD 5 non-ulcer dyspepsia 2 duodenal ulcer disease 2 iron deficiency anaemia, normal OGD 2 coeliac follow up 1 cancer of oesophagus

OGD, oesophagogastrroduodenoscopy; GORD, gastro-oesophageal reflux disease.

immediately snap frozen in liquid nitrogen for later RNA extraction and enzyme linked immunosorbent assay (ELISA) analysis. Adjacent biopsies were placed in formalin for routine histological analysis and for MMP-7 immunohistochemistry. Further adjacent biopsies from the antrum and body were used for the rapid urease test (Clotest; Ballard Medical Products, Draper, Utah, USA), and placed in Iso-sensitest media (Oxoid, Basingstoke, UK) supplemented with 5% fetal calf serum (FCS) for later *H. pylori* culture.

MMP-7 ELISA

The Quantikine human MMP-7 (total) ELISA kit (R&D Systems, Abingdon, UK) was used to assess total MMP-7 in gastric antral biopsies from the first 10 *H. pylori* positive patients and 11 *H. pylori* negative patients. Biopsies, which had been snap frozen in liquid nitrogen, were homogenised using an Ultra-Turrax T50 homogeniser (Becton Dickenson, Oxford, UK) for 30 seconds on ice in 1 ml of 20 mM HEPES with added protease inhibitor cocktail (P8340, Sigma Aldrich, Dorset, UK). A standard curve was prepared using recombinant human MMP-7 according to the manufacturer's instructions. A spiked assay performed prior to running samples suggested there was no significant interference at the concentrations present in the biopsies. All ELISA scores were corrected according to the A_{280} of the initial biopsy homogenate.

RNA extraction

Total RNA was extracted from antral and corporal gastric biopsies (for 26 patients) using the Qiagen RNeasy kit (Crawley, UK) with additional DNase digestion. Biopsies were initially homogenised as for the ELISA. RNA yields and purity were assessed using a GeneQuant pro RNA/DNA calculator (Biochrom; Amersham Pharmacia-Biotech, Chalfont St Giles, Bucks, UK).

Real time semiquantitative PCR and analysis

RNA was reverse transcribed using the Qiagen Omniscript Reverse Transcriptase kit with additional RNase inhibitor (10 units/reaction) and 1 μ M pdN6 salt random hexamer primer (Pharmacia, Amersham, UK). Reverse transcription was carried out at 37°C for one hour followed by five minutes at 93°C to inactivate the reverse transcriptase. A negative control (without Omniscript reverse transcriptase and random hexamer primer) was used for each sample. Real time polymerase chain reaction (PCR) was carried out using the QuantiTect SYBR Green PCR kit (Qiagen) using a GeneAmp 5700 Sequence Detection System (Applied Biosystems, California, USA) with 0.5 units of uracil-N-glycosylase per reaction and oligonucleotide primers specific for MMP-7 (5' AGCCAACTCAAGGAGATGC3' and 5' ACTCCACATCTGGGCTTCTG3') and glyceraldehyde-3-phosphate dehydrogenase (GAPDH)

(5' GGTGAAGGTCGGAGTCAACGGA3' and 5' GAGGGATCTCGCTCCTGGAAGA3'). PCR conditions were as follows: 50°C for two minutes, 95°C for 15 minutes followed by 40 cycles of 94°C (15 seconds), 56°C (30 seconds), and 72°C (one minute). Relative expression of MMP-7 cDNA amplification, ΔCt (ν GAPDH) was calculated using the formula $2^{Ct_{(GAPDH)} - Ct_{(MMP-7)}}$ where Ct (threshold cycle) represents the fractional cycle number at which the fluorescence passes the fixed threshold.^{29–30} The correct PCR product size was confirmed by electrophoresis on a 2% agarose gel.

Immunohistochemistry

Gastric biopsies were fixed in formol saline for 24 hours and subsequently processed and embedded in paraffin wax. Each biopsy was sectioned at 4 μ M, with sufficient sections to permit one negative control, and stained with a specific monoclonal antibody to MMP-7 at a dilution of 1:800 (Oncogene Research Products, Cambridge, UK; cat No OM71). The sections were picked up on Dako ChemMate microscope slides (gap 75 μ M) to allow immunoperoxidase staining on a Dako TechMate 500 Plus automated stainer (Dako, Ely, Cambs, UK). Staining was previously optimised (including pretreatment) for each antibody and a labelled streptavidin biotin technique employed to detect localisation of the antigens using diaminobenzine as the chromogen. An identical procedure (including pretreatment) was used for the negative control but the primary antibody was replaced with diluent only.

Briefly, the procedure required microwave antigen retrieval with 10 mM citrate buffer (pH 6.0). All staining was performed at room temperature with an incubation of one hour for the primary antibody.

Assessment of staining

Two observers (AZ, an experienced histopathologist, and JB) assessed MMP-7 staining intensity. Initial observations suggested staining intensity differed between areas of biopsies, dependent on depth from the surface epithelium. We were particularly interested in staining in the proliferative zone, so we graded staining intensity here and in superficial and deep zones. Zones were defined by splitting the area between superficial cells and stromal cells into thirds. Staining intensity was graded 0 (no staining) to 4 (intense staining). Both observers were blinded to the *H. pylori* status of the individuals and they scored slides separately: 95% concordance was reached on initial scoring. Discordant results were resolved by joint review, again with both scorers blind to the *H. pylori* status. Up to 200 inflammatory cells (where present) were also counted per field view (crossing all three zones), and the percentage expressing MMP-7 calculated.

H. pylori culture and PCR typing for *cagE* and *vacA*

Gastric biopsies were plated out within one hour on 5% horse blood agar plates and left for five days in a 5% CO₂ incubator at 37°C. Colonies of *H. pylori* were identified by morphology, Gram stain, and urease testing, and clonally expanded before freezing at −80°C. Genomic DNA was extracted as previously described³¹ and strains were PCR typed for the presence of *cagE*, a reliable marker for the presence of the *cag* pathogenicity island (5' AAGGGTAAAGAAATGGGACTGAAT 3' and 5' GGAAGCGTGATAAAAGAGCAATGT 3', conditions 95°C for two minutes, 35 cycles of 95°C for one minute, 56°C for two minutes, 72°C for four minutes, and 72°C for five minutes) and *vacA* (signal and mid region, as described previously^{32–33}). All PCR reactions were carried out on a Hybaid thermal cycler.

Definition of *H pylori* status

For the purposes of this study, patients were considered to be infected with *H pylori* if culture was positive, or in the case of negative culture, if histology showed characteristic organisms and the Clotest rapid urease test was positive.

In vitro studies

H pylori strains

The following strains were used for coculture experiments: 60190 (ATCC 49503, *cagPaI*⁺, *vacA* s1m1¹³), Tx30a (ATCC 51392, *cagPaI*[−], *vacA* s2/m2¹³), 60190CagE[−] (*cagE*[−] insertion isogenic mutant of 60190, *vacA* s1/m1), 60190VacA[−] (*cagPaI*⁺, disrupted *vacA*[−] insertion mutant of 60190³⁴). The mutant strain 60190CagE[−] was derived from the *cagE* (*picB*) mutant 84-183:pMT3:*km*.³⁵ A 3.4 kb fragment containing the disrupted *cagE* gene was PCR amplified from 84-183:pMT3:*km* and cloned into pGEM T-Easy (obtained from Promega Corp., Southampton, UK) to create pRT1. The chromosomal *cagE* gene of strain 60190 was then replaced with the disrupted *cagE* gene by natural transformation with pRT1, followed by allelic exchange and kanamycin marker rescue. PCR analysis and Southern blotting confirmed replacement of *cagE* with the disrupted allele. We confirmed that the mutant strain was phenotypically null for the *cag* encoded type IV secretion system by showing that, compared with wild-type, it had a markedly reduced ability to stimulate epithelial cell lines to express interleukin 8 and that it did not induce CagA phosphorylation in epithelial cells (data not shown). The mutant strain 60190VacA[−] has been described previously.³⁴

Bacterial coculture

H pylori strains 60190, Tx30a, and CagE[−] and VacA[−] isogenic mutants of 60190^{13 34} were grown on 5% horse blood agar plates (Oxoid) in a 5% CO₂ incubator at 37°C. HT29 cells (a human colonic adenocarcinoma cell line, obtained from the European Tissue Culture collection) were maintained in Dulbecco's modified Eagle's medium supplemented with 5% FCS. For coculture, 48 hour plates of *H pylori* were added to subconfluent HT29 (in the absence of FCS) in 75 cm² tissue culture flasks such that the final viable bacteria:epithelial cell ratio was approximately 100:1. Tissue culture flasks were placed in a 5% CO₂ incubator at 37°C for 24 hours. Supernatants were then aspirated and used for immunoblots and zymography, and cell pellets used for RNA extraction.

Immunoblot and zymographic analysis of supernatants

Equal volumes of untreated (media) and bacterial treated epithelial cell supernatants were analysed for the presence of MMP-7 by immunoblot and casein zymography. For immunoblots, samples were mixed with sodium dodecyl sulphate (SDS) running buffer, boiled, and centrifuged before application to 12.5% SDS-polyacrylamide gel electrophoresis (PAGE). For blotting, SDS-PAGE gels were blotted for one hour onto PVDF membranes at 150 mA, blocked in phosphate buffered saline-0.5% Tween with 5% skimmed milk powder (Oxoid) for one hour, and then incubated with primary antibody (monoclonal anti-MMP-7; Oncogene Research Products, Nottingham, UK) overnight, washed and incubated with peroxidase conjugated goat antimouse IgG antibodies (Sigma-Aldrich), washed, and then developed using ECL system (Amersham Pharmacia-Biotech). For casein zymography, samples were mixed with SDS sample buffer (Novex; Invitrogen, Paisley, UK), applied to a 4–16% blue casein zymogram gel (Invitrogen) and run using the manufacturer's recommended buffers. After running, the gels were placed in renaturing buffer and incubated overnight in developing buffer (both buffers from Invitrogen).

Areas of protease activity appeared as white bands on a blue background and were photographed using a digital camera.

RNA extraction and real time PCR analysis

RNA extraction, quantification, and real time PCR analysis was carried out in an identical manner to the in vivo studies.

Statistical analysis

All statistical analyses used the GraphPad Prism statistical package. Mann-Whitney U tests were used to compare median scores for histological grading. T tests were used to compare ΔCt values for mRNA and for comparing ELISA values.

RESULTS

We first aimed to assess whether MMP-7 expression in the gastric mucosa was upregulated by *H pylori* infection. To do this we performed a specific ELISA for total MMP-7 on gastric biopsy specimen homogenates from *H pylori* infected patients and uninfected control patients. MMP-7 was expressed in infected and uninfected gastric mucosa, with a threefold increase observed in *H pylori* infected patients (mean ELISA score (SEM): *H pylori*⁺ (n = 10) 0.182 (0.045) v *H pylori*[−] (n = 11) 0.059 (0.016); p = 0.009, unpaired t test). To confirm these results and to assess whether *H pylori* infection upregulated MMP-7 expression at the transcriptional level, we extracted total RNA from biopsy specimens, reverse transcribed, and quantified levels using real time PCR. Biopsies from *H pylori* infected patients expressed higher levels of MMP-7 mRNA in both the antrum (ΔCt (SEM): *H pylori*⁺ 0.038 (0.01) (n = 12) v *H pylori*[−] 0.008 (0.003) (n = 13); p = 0.007, t test) and corpus (*H pylori*⁺ 0.044 (0.021) (n = 12) v *H pylori*[−] 0.005 (0.002) (n = 13); p = 0.07). We had more samples for RNA analysis than for ELISAs because RNA extraction was performed first, and where this was unsuccessful the biopsy intended originally for ELISA was used.

Our principal interest in MMP-7 upregulation was in its implications for the pathogenesis of gastric adenocarcinoma. Thus we aimed firstly to assess whether upregulation occurred in epithelial cells and secondly whether it occurred in the proliferative zone, which contains gastric stem cells. To do this, we performed immunohistochemistry on biopsy specimens from the gastric antrum and corpus for MMP-7 using a specific anti-MMP-7 monoclonal antibody and assessed epithelial staining intensity in epithelial cells in the proliferative zone. Staining intensity scores were significantly higher in epithelial cells in the proliferative zone in gastric biopsy specimens from *H pylori* infected patients than in those from uninfected patients (median scores (inter-quartile range): antrum *H pylori*⁺ 3 (3–4), *H pylori*[−] 3 (2–3); corpus *H pylori*⁺ 3 (2–3.5), *H pylori*[−] 2 (2–2.5)), both in the antrum (p = 0.03 Mann-Whitney U test) and the corpus (p = 0.04) (fig 1A, B). This is illustrated clearly in fig 2, with intense proliferative zone staining in the *H pylori* infected patient (fig 2A) but not in the uninfected patient (fig 2B). There was a trend for increased intensity staining in superficial and deep zones for *H pylori* infected patients but these did not reach statistical significance (data not shown). Inflammatory cell MMP-7 expression is also of potential importance as MMP-7 released from inflammatory cells may exert paracrine effects on neighbouring epithelial cells. Thus, next we assessed the proportion of inflammatory cells staining for MMP-7 in *H pylori*⁺ and *H pylori*[−] biopsy specimens. In *H pylori*⁺ biopsy specimens, most inflammatory cells stained positively for MMP-7 whereas in *H pylori*[−] biopsy specimens most did not stain (mean (SEM) per cent inflammatory cells staining positively for MMP-7: antrum,

Figure 1 Dot plot showing epithelial cell staining grade (0–4) for the proliferative zone in the antrum (A) and corpus (B) for *Helicobacter pylori*+ and *H pylori*- patients. Grades were higher for *H pylori* infected patients in both the antrum ($p=0.03$ Mann-Whitney U test) and corpus ($p=0.04$).

H pylori+ 87.4 (2.8) v *H pylori*- 29.9 (4.1), $p<0.01$ *t* test; corpus, *H pylori*+ 80.4 (2.7) v *H pylori*- 38.6 (4.4), $p<0.01$).

Because of the variation in level of MMP-7 expression between *H pylori*+ biopsy specimens, especially with regard to epithelial cell expression, we next asked whether strains of differing virulence were associated with different levels of MMP-7 expression. To do this, we assessed *cagE* status and *vacA* type of *H pylori* isolates cultured from gastric antral biopsy specimens and correlated these with MMP-7 expression. Unfortunately, only three strains were *cagE* negative, but nevertheless, by MMP-7 ELISA, *cagE* positive strains appeared to induce higher levels of MMP-7 expression than *cagE* negative strains (mean (SEM): *cagE*+ 0.218 (0.06), $n=7$; *cagE*- 0.099 (0.019), $n=3$; $p=0.25$, unpaired *t* test). No obvious differences were demonstrated between *cagE*+ and *cagE*- strains by real time PCR or immunohistochemistry. *vacA* genotyping of strains revealed 2 s1/m1, 6 s1/m2, 1 s2/m2, and 1 s2/m1 (for ELISA and real time PCR). Not surprisingly, given the small numbers, no significant differences in MMP-7 expression could be demonstrated.

To define precisely the role of bacterial virulence factors in induction of MMP-7 expression and to confirm the effects of *H pylori* on MMP-7 expression by epithelial cells, we next performed a series of coculture experiments using a panel of *H pylori* isogenic mutant strains and the epithelial cell line HT29. We selected the HT29 cell line because it is known to express MMP-7 in response to appropriate stimuli.³⁶ Firstly, we analysed the effect of a pathogenic and a non-pathogenic *H pylori* strain on MMP-7 expression. Immunoblot analysis of HT29 supernatants after *H pylori* coculture showed an immunoreactive 29 kDa band (the predicted size for pro-MMP-7) after coculture with the *cag* positive vacuolating strain 60190 but no band following coculture with the *cag* negative non-vacuolating strain Tx30a, or for control cells without bacterial coculture. Next we defined the contribution of the vacuolating cytotoxin VacA and the *cag* PAI encoded

Figure 2 Antral biopsy stained for matrix metalloproteinase-7 (MMP-7) in a *Helicobacter pylori* infected patient (A) and uninfected patient (B). Note the intense staining for MMP-7 both within epithelial cells (particularly within the proliferative zone, arrows) and inflammatory infiltrate in (A).

type IV secretion system by comparing the effect on MMP-7 expression by HT29 cells of wild-type 60190 with the effects of its VacA- isogenic mutant (does not express full length or truncated VacA) and its CagE- isogenic mutant (does not express a functional *cag* encoded type IV secretion system). We showed that the VacA- mutant had identical effects to the parent strain, indicating that VacA was not necessary for the effect. In contrast, coculture with the CagE- mutant induced no MMP-7 expression, indicating that the effect was dependent on the *cag* PAI encoded type IV secretion system (fig 3A). To confirm these results, and to show that the 29 kDa proMMP-7 band had MMP-7 activity, we performed casein zymography with the same samples. Zymograms demonstrated caseinolytic activity at the same protein size, and increased activity was noted for strain 60190 and its VacA- isogenic mutant compared with the two strains lacking an intact *cag* pathogenicity island (Tx30a and 60190CagE-) (fig 3B). Finally, to further confirm our results and to assess whether MMP-7 was upregulated at the level of transcription (as in our *in vivo* studies) we performed real time PCR on RNA preparations from cocultured HT29 cells. As expected, highest levels of MMP-7 mRNA expression were observed after coculture with the strains possessing an intact *cag* PAI, 60190, and 60190VacA- (fig 4).

Figure 3 (A) Representative matrix metalloproteinase-7 (MMP-7) immunoblot of HT29 cell supernatants after coculture with *Helicobacter pylori* strains 60190, Tx30a, and the CagE⁻ and VacA⁻ isogenic mutants of 60190. A band of approximately 29 kDa is visualised for coculture with 60190 and 60190VacA⁻. This corresponds to the predicted size for pro-MMP-7. No bands are seen with untreated cells, non-pathogenic strain Tx30a, and the CagE⁻ isogenic mutant of 60190. Equal volumes of supernatant were loaded onto sodium dodecyl sulphate-polyacrylamide gel electrophoresis (n = 4). (B) Representative casein zymogram demonstrating increased intensity bands with 60190 and 60190VacA⁻. This 29 kDa band corresponds to the caseinolytic activity of pro-MMP-7.

DISCUSSION

We have demonstrated that *H. pylori* infection causes upregulation of MMP-7 in epithelial cells, in vivo and in vitro, and that this is dependent on an intact *cag* pathogenicity island. MMP-7 is an important metalloproteinase enzyme that is upregulated in gastric cancer. It promotes tissue invasion and metastasis in various cancers through degradation of extracellular matrix. Interestingly, it has also recently been shown to have potential pro-oncogenic effects through its “shedase” activity which may predispose to malignant transformation. Recently described substrates of MMP-7 shedase activity include E-cadherin, Fas ligand, and pro-TNF- α . E-cadherin is an important cell adhesion molecule which forms a key part of the adherens junctions between epithelial cells.³⁷ Changes in E-cadherin at the germline and somatic levels are associated with both intestinal and diffuse gastric cancer.^{38–40} Fas ligand has an important role in apoptosis, and one of the mechanisms by which *H. pylori* is thought to predispose to gastric carcinogenesis is through disruption of the balance between cell proliferation and apoptosis.^{41–43} TNF- α is a proinflammatory cytokine that is induced in vivo by *H. pylori*.⁴⁴ Induction of a chronic inflammatory state predisposes to gastric atrophy and precancerous changes in the gastric epithelium.⁴¹ Activation or alteration of any of these important oncogenic or inflammatory molecules by *H. pylori* potentially could be important in gastric carcinogenesis.

Our work using isogenic mutants clearly demonstrates a role for an intact *cag* pathogenicity island in the upregulation of MMP-7. The mechanism of upregulation of MMP-7 gene expression is likely to be complex as the promoter region is susceptible to a number of controls;⁴⁵ MMP-7 transcription has been shown to be dependent on various signalling pathways, including β -catenin signalling^{36–46} and activation of the PEA3 member of the Ets transcription factors.⁴⁷ Translocation and phosphorylation of CagA stimulates MAP kinases and the *cag* encoded type IV secretion system itself stimulates nuclear factor κ B activation and interleukin 8 transcription.^{48–49} Further work is needed to define which pathways are responsible for *H. pylori* *cag* mediated MMP-7 induction. Most of our patient strains were *cagE*⁺ by PCR analysis, yet there was considerable heterogeneity in MMP-7

Figure 4 Matrix metalloproteinase-7 (MMP-7) mRNA values (mean (SEM) threshold cycle (Δ Ct), corrected for glyceraldehyde-3-phosphate dehydrogenase) obtained by real time polymerase chain reaction for HT29 cell lysates after coculture with four *Helicobacter pylori* strains. Untreated control was uninoculated media added to HT29 cells (n = 3–5 per experiment). Interstrain differences did not reach conventional statistical significance but a similar trend to the protein data was observed.

expression in biopsies, and so clearly factors other than *cag* status may be important in MMP-7 upregulation, and the in vivo situation may be different from that in vitro.

Several groups have examined MMP-7 expression in gastric cancer and reported conflictingly on expression of MMP-7 in normal (non-malignant) tissue.^{17–20} Using a well defined monoclonal antibody raised against recombinant human MMP-7, we demonstrated clearly that MMP-7 is expressed in inflamed and to a lesser extent in non-inflamed non-malignant gastric mucosa, and we confirmed these findings by mRNA analysis. Importantly, for a potential mechanistic role in carcinogenesis, we have also shown that major differences exist in the proliferative zone between *H. pylori* infected and uninfected patients. Effects on cells within this pluripotent area are likely to be necessary for carcinogenesis.

There is considerable evidence to support a role for MMP-7 in the very early stages of colorectal cancer.^{27–30} Induction of MMP-7 in *H. pylori* induced gastritis, the initial stage in the proposed pathway to gastric adenocarcinoma,⁴¹ may be of pathogenic importance. Future strategies for treatment, and prevention, of gastric cancer may include use of inhibitors of metalloproteinase enzymes. Understanding what stimulates these oncogenic proinflammatory proteins adds to our current knowledge in this field. *H. pylori* mediated stimulation of MMP-7 is a potentially important carcinogenic effect of the bacterium.

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