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ORIGINAL ARTICLE

Pan-genomic analyses identify key *Helicobacter pylori* pathogenic loci modified by carcinogenic host microenvironments

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► Additional material is published online only. To view please visit the journal online (<http://dx.doi.org/10.1136/gutjnl-2017-313863>)

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Received 27 January 2017

Revised 30 June 2017

Accepted 15 July 2017

Published Online First

18 September 2017

ABSTRACT

Objective *Helicobacter pylori* is the strongest risk factor for gastric cancer; however, the majority of infected individuals do not develop disease. Pathological outcomes are mediated by complex interactions among bacterial, host and environmental constituents, and two dietary factors linked with gastric cancer risk are iron deficiency and high salt. We hypothesised that prolonged adaptation of *H. pylori* to in vivo carcinogenic microenvironments results in genetic modification important for disease.

Design Whole genome sequencing of genetically related *H. pylori* strains that differ in virulence and targeted *H. pylori* sequencing following prolonged exposure of bacteria to in vitro carcinogenic conditions were performed.

Results A total of 180 unique single nucleotide polymorphisms (SNPs) were identified among the collective genomes when compared with a reference *H. pylori* genome. Importantly, common SNPs were identified in isolates harvested from iron-depleted and high salt carcinogenic microenvironments, including an SNP within *fur* (FurR88H). To investigate the direct role of low iron and/or high salt, *H. pylori* was continuously cultured *in vitro* under low iron or high salt conditions to assess *fur* genetic variation. Exposure to low iron or high salt selected for the FurR88H variant after only 5 days. To extend these results, *fur* was sequenced in 339 clinical *H. pylori* strains. Among the isolates examined, 17% (40/232) of strains isolated from patients with premalignant lesions harboured the FurR88H variant, compared with only 6% (6/107) of strains from patients with non-atrophic gastritis alone ($p=0.0034$).

Conclusion These results indicate that specific genetic variation arises within *H. pylori* strains during in vivo adaptation to conditions conducive for gastric carcinogenesis.

INTRODUCTION

Helicobacter pylori persistently colonises the gastric mucosa of more than 50% of the world's population. *H. pylori* strains harbour remarkable genetic diversity as a species, as evidenced by variation of gene order and genetic content, the mosaic structure of genes and sequence diversity within conserved

genes.^{1–3} *H. pylori* exhibits a panmictic population structure, reflecting a high level of genetic exchange among strains,^{4 5} and recombination between strains can occur in vivo during naturally occurring mixed infections.³ Analyses of complete genomic sequences from a number of isolates indicate that *H. pylori* has incorporated genetic material from other organisms,^{4 5} and that variation occurs among single colony isolates of distinct *H. pylori* from an individual host.^{6 7}

In addition to being one of the most common bacterial infections worldwide, *H. pylori* is the strongest known risk factor for the development of gastric adenocarcinoma, and pathological outcomes are mediated by complex interactions among bacterial virulence determinants, host constituents and environmental factors. One *H. pylori* virulence determinant that increases gastric cancer risk is the *cag* pathogenicity island. *H. pylori* strains that harbour the *cag* island induce more severe gastric injury and further augment the risk for gastric cancer compared with *cag*-negative strains. The *cag* island encodes a bacterial type IV secretion system, which translocates the oncoprotein CagA into host cells to induce cellular morphological changes, proliferation and migration.^{2 8}

Two environmental factors associated with increased gastric carcinogenesis are high dietary salt intake and iron deficiency.⁹ Epidemiological studies have demonstrated a link between salt intake and increased gastric cancer risk,^{10 11} and high salt diets accelerate the development of gastric cancer in animal models of infection.^{12–14} Similarly, epidemiological studies have supported the concept that iron deficiency contributes to the risk of gastric cancer,^{15 16} and a recent study from our group demonstrated that iron depletion significantly increased the development of gastric adenocarcinoma in *H. pylori*-infected gerbils.¹⁷ Therefore, both high salt and low iron augment the severity of *H. pylori*-induced gastric inflammation and the development of premalignant and malignant lesions in rodent models of gastric cancer.

Several studies have investigated specific mechanisms through which iron deficiency or high salt may modify *H. pylori* and enhance the risk for gastric cancer. Iron deficiency and high salt-dependent



To cite: Noto JM, Chopra A, Loh JT, et al. *Gut* 2018;**67**:1793–1804.

Significance of this study

What is already known on this subject?

- ▶ *Helicobacter pylori* strains exhibit remarkable genetic diversity as a species and have a panmictic population structure, reflecting a high level of genetic exchange among strains.
- ▶ *H. pylori* is the strongest known risk factor for the development of gastric adenocarcinoma; however, the majority of *H. pylori*-infected individuals do not develop disease.
- ▶ Two environmental factors associated with increased gastric cancer risk are high dietary salt intake and iron deficiency. Both high salt and low iron significantly augment the severity of *H. pylori*-induced gastric inflammation and the development of premalignant and malignant lesions in rodent models of gastric cancer.

What are the new findings?

- ▶ Whole genome sequencing of *H. pylori* strains B128 and 7.13 and in vivo-adapted 7.13 output isolates harvested from animals maintained on iron-replete, iron-depleted, regular salt or high salt diets identified a small number of common polymorphisms that occurred within the context of iron deficiency and high salt intake.
- ▶ Specific cancer-related genetic loci were identified when *in vivo*-adapted carcinogenic *H. pylori* strain 7.13 was compared with its progenitor human *H. pylori* isolate B128, which does not cause cancer.
- ▶ Environmental-specific genetic loci were identified among *H. pylori* strains isolated from carcinogenic, iron-deficient or high salt, microenvironments.
- ▶ A single nucleotide polymorphism in *fur* was selected for by exposure to low iron or high salt conditions and was more frequently identified in clinical *H. pylori* strains from patients with premalignant lesions.

How might it impact clinical practice in the foreseeable future?

- ▶ Key *H. pylori* genetic loci that are susceptible to genetic alteration under *in vivo* environmental stress may serve as genetic biomarkers for *H. pylori* virulence potential and gastric cancer risk.

alterations of *H. pylori* per se include alterations in bacterial cell morphology, gene regulation and protein expression.^{17–26} Specifically, CagA expression and translocation into gastric epithelial cells are increased in response to both high salt and low iron conditions, and, under iron restriction, function of the *cag* type IV secretion system is enhanced.^{17 22 24} All of these modifications likely contribute to the increased risk of *H. pylori*-induced gastric cancer associated with these dietary alterations.^{14 17 22 24 26}

In this study, we tested the hypothesis that prolonged adaptation of *H. pylori* to an *in vivo* carcinogenic gastric microenvironment induced by iron deficiency or high salt would select for genetic variants important for pathogenesis. We previously identified a strain of *H. pylori*, 7.13, that reproducibly induces gastric cancer in rodent models of gastritis. This strain was derived via *in vivo* adaptation of a human clinical *H. pylori* strain, B128, which induces inflammation, but not cancer, in rodent gastric mucosa. Thus, *H. pylori* strains B128 and 7.13 are closely related genetically, but differ in oncogenic potential.²⁷ Whole genome sequence analyses were performed on *H. pylori* strains B128 and 7.13, and *in vivo*-adapted 7.13 output isolates exposed to iron-replete or iron-depleted conditions and

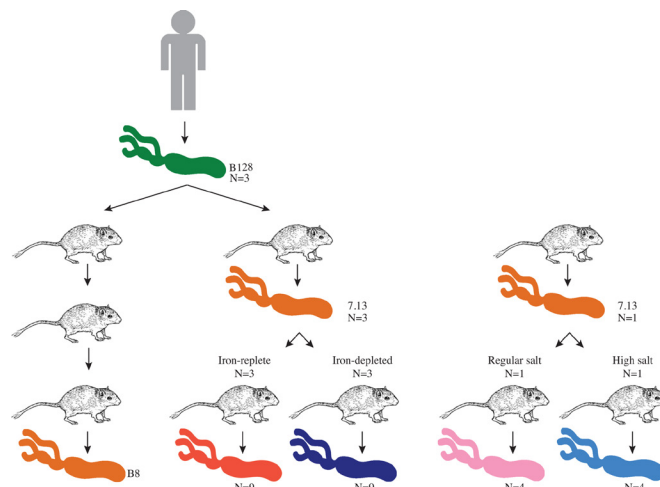


Figure 1 Experimental design. *Helicobacter pylori* strain B128 was originally isolated from a human patient.⁵⁴ Strain B128 (green) was used for orogastric challenge of Mongolian gerbils and was passed three times through gerbils in a previous study.²⁸ The *in vivo*-adapted output strain, designated *H. pylori* strain B8 (orange), was isolated from those gerbils, sequenced and used as the reference strain in this study.¹⁹ In an independent experiment, strain B128 (green) was also used for orogastric challenge of a single Mongolian gerbil, and the *in vivo*-adapted output strain isolated from this gerbil was designated *H. pylori* strain 7.13 (orange).²⁷ Carcinogenic *H. pylori* strain 7.13 was then used to infect another cohort of Mongolian gerbils maintained on either iron-replete or iron-depleted diets.¹⁷ Single colonies (n=3) from three independent gerbils maintained on iron-replete diet (n=9) and three independent gerbils maintained on iron-depleted diet (n=9) were subjected to whole genome sequence analysis. *In vivo*-adapted strain from iron-replete (red) and iron-depleted (blue) conditions was also compared with previously described *H. pylori* single colonies (n=4) harvested from one gerbil maintained on a regular salt (pink) or high salt (light blue) diet.²¹

indicate that targeted genetic variation in *H. pylori* arises during *in vivo* adaptation to conditions conducive for the development of gastric cancer.

RESULTS

H. pylori genetic alterations during *in vivo* adaptation

We initially conducted whole genome sequence analyses of human progenitor *H. pylori* strain B128 and its *in vivo* gerbil-adapted carcinogenic derivative strain 7.13. Sequences were assembled using the genome sequence of *H. pylori* strain B8, a closely related strain for which its complete genome sequence is available, as the reference strain.²⁸ In addition to these strains, we also performed whole genome sequence analysis using *in vivo* gerbil-adapted *H. pylori* isolates exposed to iron-replete or iron-depleted conditions. Three single colony isolates from *H. pylori* strains B128 and 7.13 and three single colonies from 7.13-infected gerbils maintained on either iron-replete (n=3) or iron-depleted (n=3) diets were used for whole genome sequence analysis (figure 1). *In vivo*-adapted strains from iron-replete and iron-depleted conditions were also compared with *in vivo*-adapted strains isolated from regular salt or high salt conditions¹⁴ (figure 1).

Whole genome sequence analysis

The total length of the *H. pylori* reference strain B8 genome (1673 997 bp) was completely covered, and the

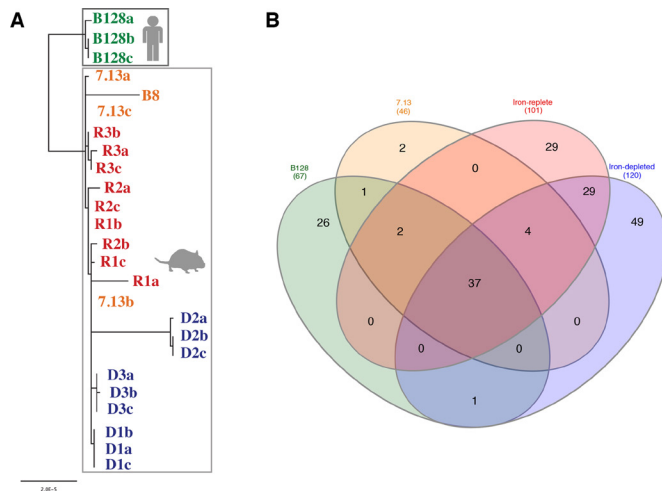


Figure 2 (A) Phylogenetic analyses of whole genome sequences from *Helicobacter pylori* strains B128 (green) and 7.13 (orange), and in vivo-adapted iron-replete (red) and iron-depleted (blue) strains. R1-3 and D1-3 designate independent gerbils maintained on either iron-replete ($n=3$) or iron-depleted ($n=3$), respectively, while a-c designate different single colonies isolated from each gerbil. *H. pylori* strains isolated from humans or gerbils are grouped within the grey boxes, respectively. The scale bar represents amino acid changes per site. (B) Venn diagram²⁰ showing the number of common and unique single nucleotide polymorphisms (SNPs) among human-adapted *H. pylori* strains B128 (green) and 7.13 (orange), and in vivo-adapted *H. pylori* strains isolated from gerbils maintained on iron-replete (red) and iron-depleted (blue) diets, all relative to the reference *H. pylori* strain B8. The number in the parentheses indicates the total number of unique SNPs identified in each strain and present exclusively in that strain, but not any other strain.

guanine-cytosine content was 38.8% for all sequenced strains. Overall sequence read count, average sequence read length, coverage and unmapped reads for *H. pylori* sequences are shown in online supplementary table S1. On average, the total read count was 645 132 bp, the mean read length was 263 bp, the fold coverage was 102 and the percentage of unmapped reads was 6.6% for all *H. pylori* strains analysed in this study.

Phylogenetic analysis confirmed that human *H. pylori* B128 isolates are more closely related to each other than to *H. pylori* strains adapted to gerbil stomachs (figure 2A). Consistent with in vivo adaptation within the same host, the reference *H. pylori* strain B8, which is also gerbil adapted, is more closely related to the gerbil-adapted strain 7.13 than to its parental human-adapted strain B128 (figure 2A). Furthermore, *H. pylori* strains isolated from gerbils under iron-replete conditions are more closely related to each other than to strains isolated from gerbils maintained on iron-depleted diets (figure 2A). These findings demonstrate that in vivo adaptations to different hosts (human vs gerbil) and to different environmental conditions (iron-replete vs iron-depleted) induce *H. pylori* genetic changes.

The number of unique single nucleotide polymorphisms (SNPs) among all sequenced *H. pylori* strains, relative to *H. pylori* reference strain B8, is shown in figure 2B.²⁹ The human-adapted strain B128 had 26 unique SNPs (ie, SNPs present exclusively in strain B128, but not in any other strain) (figure 2B, online supplementary table S2). The gerbil-adapted strain 7.13 only had two unique SNPs (figure 2B, online supplementary table S2), highlighting the similarity among strains adapted to the gerbil host. However, subsequent *H. pylori* adaptation to

iron-replete (29 SNPs) or iron-depleted (49 SNPs) conditions resulted in the greatest number of unique SNPs (figure 2B, online supplementary table S2), reinforcing the importance of genetic adaptation to different environmental conditions.

When all of the sequences were analysed, a total of 180 genetic loci with single and multinucleotide polymorphisms were identified, including 33 within intergenic regions and 147 within coding regions (online supplementary table S3). When each single colony was analysed individually for total polymorphisms, there was variation among the single colonies (online supplementary tables S4 and S5). The *H. pylori* human isolate B128 had, on average, 98 polymorphisms, 12 insertions and 10 deletions. Of the polymorphisms within coding regions of strain B128, 67% resulted in a non-synonymous change (online supplementary table S4). Among the three single colonies, gerbil-adapted *H. pylori* strain 7.13 contained, on average, 47 polymorphisms, nine insertions and three deletions. Of the SNPs within coding regions of strain 7.13, 65% resulted in a non-synonymous change (online supplementary table S4). Similarly, among the nine single colonies harvested from three gerbils maintained on iron-depleted diets, there were, on average, 52 polymorphisms, 12 insertions and five deletions, while in vivo-adapted strains isolated from gerbils maintained on iron-replete diets had, on average, 43 polymorphisms, 11 insertions and three deletions. Of the SNPs within coding regions of the iron-depleted and iron-replete strains, 54% and 52% resulted in a non-synonymous change, respectively (online supplementary table S5). Based on the number of variants identified, most of the genetic variation arose through in vivo adaptation to a new gerbil host. However, all *H. pylori* isolates were found to be unique, including isolates from a single host.

Many of the genetic alterations resulting in deletions or insertions occurred within genetic loci important for *H. pylori* pathogenesis, including polymorphisms within loci regulating chemotaxis (*cheA*), adhesion (*hopZ*, *oipA*, *sabA*), survival (*kataA*), iron acquisition or active transport (*tonB*) and *cag* type IV secretion system function (*cagY*) (table 1).

Among the 180 polymorphisms identified, 72 were located within genes with predicted function and resulted in non-synonymous amino acid changes (table 2). Similar to the insertions and deletions, many of these variants were within genes encoding proteins that function in pathogenesis, including motility (*flil*, *flif*), adhesion (*babA*, *babB*), iron acquisition or active transport (*tonB*) and *cag* IV secretion system function (*cagY*). When we compared unique SNPs within coding regions between in vivo-adapted strains isolated from gerbils maintained on iron-depleted versus iron-replete diets, we identified 35 polymorphisms, distributed among 15 genes, including *babB*, *cagY*, *pepP*, *oppD*, *hcpD*, *hcpE*, *prfB*, and various outer membrane and hypothetical proteins. Additional SNPs were present in both groups, but were more prevalent in iron-depleted versus iron-replete strains; these included SNPs within *babA*, *babB* and *fur*.

The SNP (FurR88H) located within *fur*, a gene encoding the ferric uptake regulator, was identified previously in in vivo-adapted *H. pylori* strains isolated from a gerbil maintained on a high salt diet.³⁰ Therefore, we compared the number of SNPs from in vivo-adapted strains isolated from gerbils maintained on iron-depleted diets with those previously isolated from a gerbil maintained on a high salt diet. Specifically, we sought to identify SNPs present in these isolates that were either not present or present at a lower frequency in strains isolated from control gerbils maintained on iron-replete or regular salt diets. We identified five SNPs distributed among four genes, including HPB8_593, HPB8_716 (*cagY*), HPB8_1139 and HPB8_1145

Table 1 Continued

Insertions	B128 single colonies			7.13 single colonies			7.13 iron-depleted single colonies			7.13 iron-replete single colonies														
	a	b	c	a	b	c	D1	D2 a	D2 b	D2 c	D3 a	D3 b	D3 c	R1 a	R1 b	R1 c	R2 a	R2 b	R2 c	R3 a	R3 b	R3 c		
HPB8 locus																								
149625 Intergenic																			52					
210808 Intergenic														50										
236057																								
293971 Intergenic		58	34																					
397298 <i>fucT1</i>	55	35	36																					
471641 Intergenic	100	95	97																					
607701 Intergenic																								
628559 Intergenic		28	28																					
631022 Intergenic																								
631033 Intergenic		85	85																					
666812 <i>nuoT74</i>		90	80																					
759720 Intergenic																								
819619 <i>olpA</i>																								
833169 <i>fucT7</i>		67	70																					
883216 <i>hyuA1</i>		63	67																					
883595 <i>hyuA1</i>		93	99																					
1064308 <i>katA</i>		100	97																					
1082193																								
1197792 Intergenic																								
1197193 Intergenic		45	40																					
1217501 Intergenic		90	90																					
1332440 Intergenic		59	59																					
1332612																								
1414196																								
1458196																								
1566403 Intergenic		79	69																					
1566404 Intergenic		83.7	84.8																					
1621919																								
1657270 Intergenic		66	74																					
1657271 Intergenic		79	76																					

D1-3 and R1-3 designate independent gerbils maintained on either iron-non-depleted (n=3) or iron-replete (n=3) diets, respectively, while a-c designate different single colonies isolated from each gerbil. Colour-coded regions within each single colony represent deletions or insertions that were present in each isolate, and the number in each box represents the percentage of reads that contained each single nucleotide polymorphism. When a percentage range is shown, this represents multinucleotide polymorphisms present.

* Deletion or insertion results in a frameshift mutation.

Table 2 Unique genetic loci with polymorphisms resulting in non-synonymous amino acid changes in *Helicobacter pylori* strains B128 and 7.13, and in vivo-adapted strains isolated from gerbils maintained on iron-depleted or iron-replete diets

Variant	B128 single colonies			7.13 iron-depleted single colonies										7.13 iron-replete single colonies											
	a	b	c	a	b	c	D1a	D1b	D1c	D2a	D2b	D2c	D3a	D3b	D3c	R1a	R1b	R1c	R2a	R2b	R2c	R3a	R3b	R3c	
HP88 locus																									
118890 <i>flhI</i>							K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R	K>R
132888 <i>tonB1</i>		K>E																							
211182 <i>babB</i>			T>I	T>I			T>I	G>R																	
211347 <i>babB</i>			G>R	G>R																					
211415 <i>babB</i>							D>N	D>N																	
211583 <i>babB</i>																									
211592 <i>babB</i>		K>E	K>E	K>E			K>E	K>E																	
211690 <i>babB</i>		N>K	N>K	N>K			N>K	N>K																	
211694 <i>babB</i>							E>K	E>K																	
211838 <i>babB</i>		K>Q	K>Q	K>Q			K>Q	K>Q																	
211844 <i>babB</i>		G>S	G>S	G>S																					
212150 <i>babB</i>		G>S	G>S	G>S			G>S	G>S																	
212315 <i>babB</i>		E>K	E>K	E>K			E>K	E>K																	
263909 <i>rpsL</i>							R>K	R>K																	
263985 <i>rpsL</i>							T>M	T>M																	
264366 <i>rpsG</i>		D>N	D>N	D>N			D>N	D>N																	
264374 <i>rpsG</i>																									
273162 Hypothetical																									
273165 Hypothetical																									
342359 <i>pal</i>		T>A	T>A	T>A																					
559618 Hypothetical		E>K	E>K	E>K																					
563546 Hypothetical																									
591318 Putative OMP																									
591626 Putative OMP																									
591635 Putative OMP																									
591638 Putative OMP																									
616637 DNA methyltransferase		D>N	D>N	D>N																					
629024 <i>babA</i>		S>L	S>L	S>L																					
629189 <i>babA</i>																									
629257 <i>babA</i>		G>R	G>R	G>R																					
629425 <i>babA</i>		D>N	D>N	D>N																					
629434 <i>babA</i>		K>E	K>E	K>E																					
629532 <i>babA</i>		N>K	N>K	N>K																					
629536 <i>babA</i>		E>K	E>K	E>K																					
629680 <i>babA</i>		K>Q	K>Q	K>Q																					
629680 <i>babA</i>		K>Q	K>Q	K>Q																					
629680 <i>babA</i>		G>S	G>S	G>S																					
629992 <i>babA</i>		G>S	G>S	G>S																					
630157 <i>babA</i>		G>S	G>S	G>S																					
692170 <i>cagY</i>																									
692262 <i>cagY</i>																									
692887 <i>cagY</i>																									
693460 <i>cagY</i>																									
693465 <i>cagY</i>																									

Continued

Table 2 Continued

Variant	B.128 single colonies			7.13 single colonies			7.13 iron-depleted single colonies			7.13 iron-replete single colonies																													
	Location	Gene	HPB8 locus	a	b	c	a	b	c	D1 a	D1 b	D1 c	D2 a	D2 b	D2 c	D3 a	D3 b	D3 c	R1 a	R1 b	R1 c	R2 a	R2 b	R2 c	R3 a	R3 b	R3 c												
693471		<i>cagY</i>	716										V>I	V>I	V>I																								
693483		<i>cagY</i>	716										L>K	L>K	L>K																								
693497		<i>cagY</i>	716										S>Q	S>Q	S>Q																								
693505		<i>cagY</i>	716										R>R	R>R	R>R																								
693508		<i>cagY</i>	716										T>W	T>W	T>W																								
693513		<i>cagY</i>	716										A>K	A>K	A>K																								
727820		Hypothetical	750	L>W	L>W	L>W																																	
798239		Glycosyltransferase	817	A>T	A>T	A>T																																	
799896		Glycosyltransferase	818																																				
846179		<i>mec</i>	865																																				
913806		<i>meaE</i>	927	P>S	P>S	P>S																																	
1084103		Putative OMP	1104																																				
1084106		Putative OMP	1104																																				
1084553		Putative OMP	1104																																				
1084556		Putative OMP	1104																																				
1084587		Putative OMP	1104																																				
1122559		<i>tur</i>	1145																																				
1130504		<i>pepP</i>	1155																																				
1195655		<i>flif</i>	1220																																				
1221163		Polysaccharide deacetylase	1252																																				
1283634		Conserved hypothetical OMP	1309																																				
1289275		<i>appD</i>	1313																																				
1302387		<i>hcpE</i>	1328																																				
1369139		<i>prfB</i>	1395																																				
1377477		<i>hcpD</i>	1405																																				
1405574		Hypothetical	1436																																				
1533082		Predicted coding region	1561																																				
1533085		Predicted coding region	1561																																				
1533088		Predicted coding region	1561																																				

Colour-coded regions represent non-synonymous amino acid changes isolated from each gerbil. Colour-coded regions represent non-synonymous amino acid changes isolated from specific genetic polymorphisms. Specific amino acid changes are designated within each box.

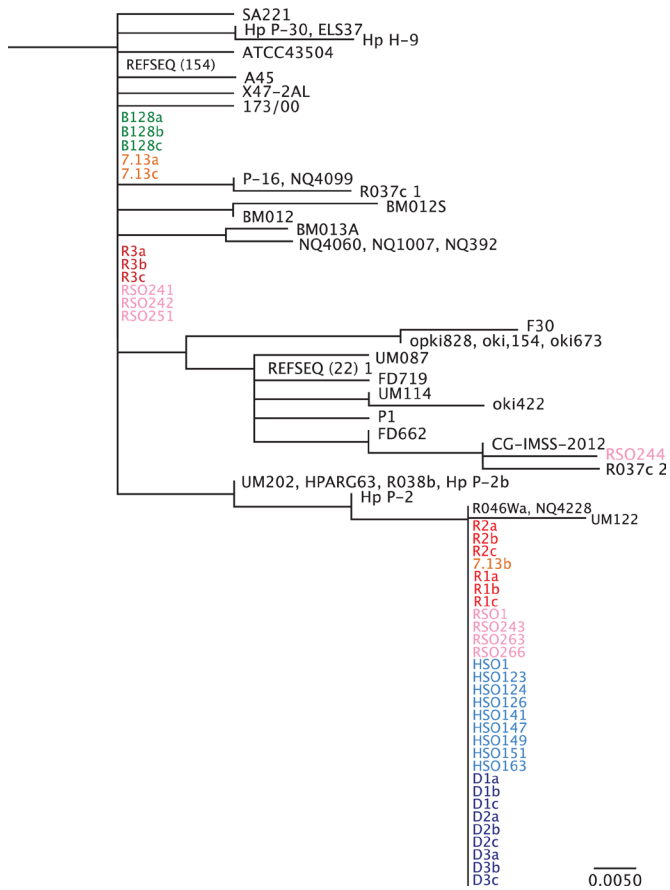


Figure 3 Phylogenetic analysis of Fur amino acid sequence. Phylogenetic analysis was performed for full-length Fur from all available *Helicobacter pylori* sequence data within the National Center for Biotechnology Information NCBI database. *H. pylori* single colonies from strains B128 (green) and 7.13 (orange), and in vivo-adapted strains isolated from gerbils maintained on iron-replete (red) and iron-depleted (blue) diets as well as in vivo-adapted strains isolated from gerbils maintained on regular salt (pink) and high salt (light blue) diets were included in these analyses. R1-3 and D1-3 designate independent gerbils maintained on either iron-replete (n=3) or iron-depleted (n=3), respectively, while a–c designate different single colonies isolated from each gerbil. HSO and RSO designate independent high salt output and regular salt output *H. pylori* strains, respectively. REFSEQ (#) represents the number of unique *H. pylori* sequences from different *H. pylori* strains that cluster under the same phylogeny. Although all Fur sequences from the NCBI database were used, this phylogenetic analysis shows only the branch to which the newly sequenced strains cluster. The scale bar represents amino acid changes per site.

(*fur*) (online supplementary table S6) in iron-depleted and high salt *H. pylori* in vivo-adapted output strains, suggesting that certain loci are subject to variation following in vivo adaptation to different host microenvironments.

Analysis of sequence variation in fur

To investigate mechanisms underpinning these changes in greater depth, phylogenetic analysis of Fur in *H. pylori* strains B128 and 7.13, and in vivo-adapted strains isolated from gerbils maintained on iron-replete, iron-depleted, high salt or regular salt diets was performed (figure 3). In vivo-adapted strains isolated from gerbils maintained on iron-depleted or high salt diets exhibited a high degree of identity within Fur, and segregated

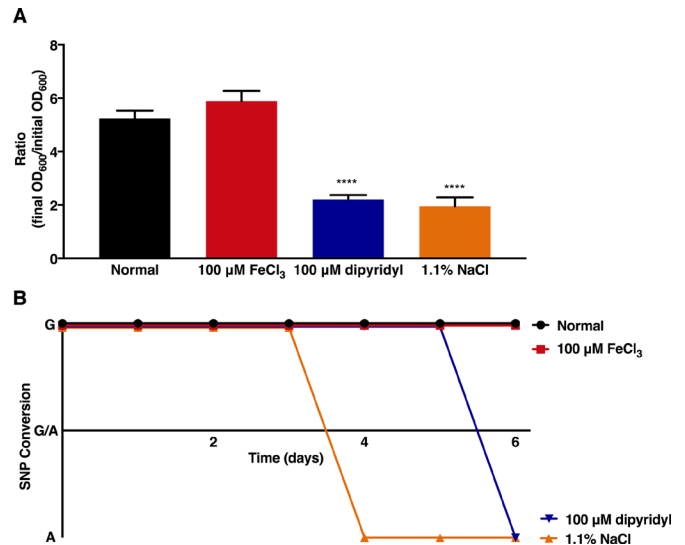


Figure 4 Analysis of genetic variation within *fur* following continuous culture in vitro under high salt or low iron conditions. (A) *Helicobacter pylori* strain 7.13 was grown in normal Brucella broth, modified Brucella broth with iron supplementation (100 μM FeCl₃), iron chelation (100 μM dipyritydil) or high salt (1.1% NaCl) for 20 hours and continuously over a 6-day time course. The growth rate or ratio of the final OD₆₀₀ to the initial starting OD₆₀₀ is represented as mean values with SE from experiments performed on at least six independent occasions. A one-way analysis of variance with multiple comparisons was used to determine statistical significance. ****p<0.0001. (B) *H. pylori* strain 7.13 was continuously cultured in vitro under these conditions for 6 days to assess the presence (CAC) or absence (CGC) of the SNP in *fur* (FurR88H). SNP, single nucleotide polymorphism.

based on the FurR88H variant, suggesting that this region may be a susceptible genetic locus subject to variation under these conditions. The presence of the *fur* SNP in some regular salt²¹ and iron-replete strains in addition to one 7.13 single colony suggests that this variant is present at a low frequency within *H. pylori* populations and is favoured under certain conditions such as high salt and low iron.

To extend these findings, we next investigated the direct effects of high salt or low iron per se on genetic variation within *fur*. *H. pylori* strain 7.13 was continuously cultured in vitro for 6 days under high salt (1.1% NaCl), in the presence of an iron chelator (100 μM dipyritydil) to simulate iron depletion, or supplementation with iron (100 μM FeCl₃). As expected, *H. pylori* growth under high salt or low iron was significantly attenuated (figure 4A). Sequence analysis revealed that adaptation to high salt and/or iron depletion in vitro resulted in selection of the *fur* SNP (FurR88H) after only 4 to 5 days, respectively, and this variant was maintained throughout the duration of growth in vitro (figure 4B). Exposure of *H. pylori* to normal growth conditions or normal growth conditions supplemented with iron did not induce sequence variation within *fur*. These data indicate that in vitro adaptation to high salt or low iron induces genetic variation in *fur* in vitro, suggesting that adaptation within the context of environmental stress may be regulated by these dietary changes in vivo.

To expand on these in vitro studies and specifically address the relationship between presence of the FurR88H variant and iron deficiency in vivo, we performed sequence analysis on 224 in vivo-adapted *H. pylori* strains isolated from gerbils maintained on iron-replete or iron-depleted diets. The FurR88H variant was

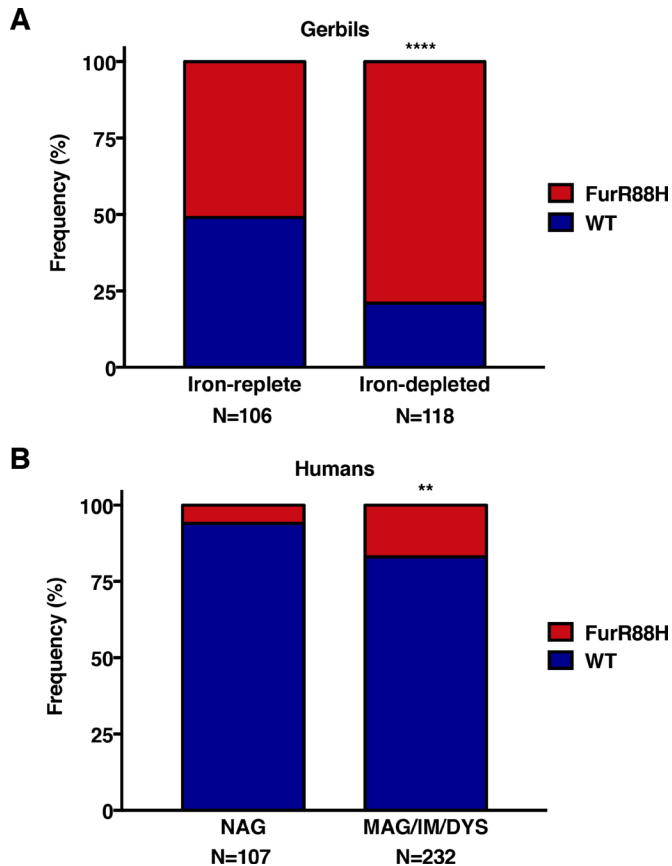


Figure 5 Analysis of genetic variation within *fur* in vivo. The frequency of the FurR88H variant was examined among (A) 224 in vivo-adapted *Helicobacter pylori* strains isolated from gerbils maintained on iron-replete or iron-depleted diets and (B) 339 clinical *H. pylori* strains isolated from three independent and well-defined patient cohorts within Colombia and the USA.^{31–33} Fischer's exact test was used to determine statistical significance. ** $p < 0.005$ and **** $p < 0.0001$. DYS, dysplasia; IM, intestinal metaplasia; MAG, multifocal atrophic gastritis; NAG, non-atrophic gastritis alone.

present at a significantly higher frequency among gerbils maintained on iron-depleted diets (93/118, 79%) compared with those maintained on iron-replete diets (54/106, 51%; $p < 0.0001$, figure 5A). These data indicate that in vivo adaptation to environmental iron deficiency leads to genetic adaptation within *fur*.

Finally, we examined genetic variation in *fur* among 339 clinical *H. pylori* strains isolated from three independent and well-defined patient cohorts within Colombia and the USA (online supplementary table S7).^{31–33} Sequence analysis of *fur* revealed that 14% (46/339) of these clinical *H. pylori* strains harboured the same FurR88H variant identified in in vivo gerbil-adapted strains isolated from conditions of high salt or iron deficiency (online supplementary table S7). Among the clinical *H. pylori* isolates examined, 17% (40/232) of strains from patients with premalignant lesions (multifocal atrophic gastritis, intestinal metaplasia, dysplasia) harboured the FurR88H variant, compared with 6% (6/107) of strains from patients with non-atrophic gastritis alone ($p = 0.0034$, figure 5B). These results demonstrate that this specific *fur* SNP is likely important for in vivo adaptation to a new host and within subpopulations of humans at increased risk for gastric cancer.

DISCUSSION

Bacterial population structures differ based on the taxa under investigation. Some species, such as *Mycobacterium tuberculosis*³⁴ and *Yersinia pestis*,³⁵ are of such recent origin that little sequence diversity has accumulated. In such largely clonal species, only a few coding sequences are variably present among different isolates.^{36–38} However, bacteria with high sequence diversity and frequent homologous recombination, such as *H. pylori*, harbour different population dynamics.³⁹

H. pylori has co-evolved with humans since their origin, and such lifelong evolution is associated with selection of host-specific variants within particular genes necessary for survival and adaptation to the human host.⁸ Survival and persistence within the human host depends on the ability of *H. pylori* to rapidly respond to changing environmental conditions and circumvent host defense mechanisms initiated during colonisation.⁸ Rearrangement of genomic DNA allows a variety of pathogens to alter expression of surface antigens and evade host immunity, and *H. pylori* has one of the highest rates of genetic recombination of any known bacterial species,⁴⁰ suggesting that this process confers a selective advantage in colonisation and survival. Indeed, *H. pylori* mutants defective in homologous recombination are spontaneously cleared,⁴¹ reinforcing the tenet that genetic recombination and variation are critical for *H. pylori* survival within the human host.

In addition to high rates of recombination, *H. pylori* displays exceptional genetic variability and intraspecies diversity.^{4 40} *H. pylori* has a highly plastic genome, reflecting elevated rates of recombination and development of point mutations, which promotes bacterial divergence and intraspecies diversity within a population.^{42 43} *H. pylori* exists within its gastric niche as a bacterial population in a continuous state of genetic variation, which allows rapid adaptation to changing environmental conditions in its current host as well as an ability to successfully colonise a new host.^{2 44 45} In this study, we hypothesised that prolonged adaptation of *H. pylori* to an in vivo carcinogenic gastric environment induced by iron deficiency would facilitate genetic changes involved in survival, persistence and increased virulence. Indeed, we demonstrated that *H. pylori* strains isolated from gerbils maintained on iron-replete diets are more closely related to each other than to strains isolated from gerbils maintained on iron-depleted diets, suggesting that specific variants are advantageous for survival and persistence in altered microenvironments. In addition, the current analysis confirmed that *H. pylori* B128 isolates recovered from a human stomach are more closely related to each other than to *H. pylori* strains adapted to gerbil stomachs, and that there are specific genetic variations that arise following adaptation to a new host. The diversity among 7.13 single colony isolates suggests that passage of B128 through a new gerbil host resulted in a more diverse population of isolates poised for further adaptation in vivo. As a result of frequent recombination and genetic variation, almost all *H. pylori* isolates from unrelated hosts and differing environments possess unique sequences.^{4 39}

Further and consistent with other reports,^{6 7} we have demonstrated that variability exists among single colony isolates from each individual *H. pylori* strain. As a result of this diversity, *H. pylori* has been previously termed a quasispecies, a population of genetic variants comprising a single strain that allows for rapid selection and adaptation to the changing gastric microenvironments of the host.^{45–47} Recent changes in DNA sequencing technology have afforded the opportunity to assess the genetic diversity of *H. pylori* populations in much greater depth. We

have now demonstrated that polymorphisms exist within single colonies, suggesting that even greater levels of within-host population diversity exist than previously demonstrated. Furthermore, we identified numerous genetic variants that arise under the selective pressure of iron deficiency, and some of these variants were also identified in *H. pylori* isolates exposed to high salt.

Among the various SNPs that resulted in non-synonymous variants, the majority arose within genetic loci prone to variation during adaptation to a new host or environmental condition. Many of these included outer membrane proteins that are particularly susceptible to selective pressure for survival and persistence. Adhesins that underwent genetic modification included *babA* and *babB*, which have been shown to undergo specific recombination in other models of *H. pylori* infection.^{48–50} Another genetic locus, *cagY*, which encodes an essential component of the *cag* type IV secretion system, has been shown to be particularly susceptible to variation *in vivo*.^{51 52} Another targeted locus was *fur*, which encodes a transcriptional regulator that controls expression of a large repertoire of genes and is an essential factor for survival and persistence of *H. pylori* in the stomach. *Fur* controls bacterial iron homeostasis, and also plays a central role in bacterial metabolism, energy production and immune regulation.⁵³ The specific SNP in *fur* (FurR88H) identified following adaptation to low iron conditions was also identified in another study of *in vivo* adaptation to high salt.³⁰ In this study, the *fur* SNP was directly linked to increased expression of genes controlling iron acquisition and homeostasis as well as increased resistance to high salt conditions and oxidative stress.³⁰ Due to the role of *Fur* in regulating iron homeostasis, it is likely that this SNP also promotes increased survival and persistence of *H. pylori* under low iron conditions. Collectively, our data suggest that the accumulation of polymorphisms allows *H. pylori* to rapidly adapt to changing microenvironments to promote survival and persistence within the host.

METHODS

Mongolian gerbils

Male Mongolian gerbils (Charles River Laboratories) were housed in the Vanderbilt University Animal Care Facilities and maintained on iron-depleted (TestDiet 5TWD), iron-replete (TestDiet 5STQ),¹⁷ regular salt or high salt (Purina 5001).¹⁴ Gerbils were orogastrically challenged with carcinogenic *H. pylori* strain 7.13. *H. pylori* strain 7.13 was originally isolated as a single colony following *in vivo* adaptation of the human *H. pylori* strain B128 to the Mongolian gerbil model and was then subcultured following minimal passage for single colony purification (figure 1).²⁷ Single colony purified strain 7.13 was isolated from a frozen stock, expanded on trypticase soy agar plates with 5% sheep blood (BD Biosciences) and then grown in Brucella broth (BD Biosciences) supplemented with 10% FBS (Atlanta Biologicals) for 16 hours at 37°C with 5% CO₂ prior to gerbil challenge.¹⁷ Gerbils were then euthanised 12–16 weeks postchallenge. The Vanderbilt University Institutional Animal Care and Use Committee (IACUC) approved all experiments and procedures.

H. pylori culture

H. pylori strain B128 was originally isolated from a single gastric biopsy of a human patient with gastric ulceration.⁵⁴ B128 was subsequently used for orogastric challenge of a gerbil, and the *in vivo*-adapted output strain isolated from this gerbil was designated *H. pylori* strain 7.13.²⁷ *H. pylori* strain 7.13 reproducibly induces gastric cancer in rodent models,^{14 17 27} while B128 only induces

gastritis, but not cancer in these models.²⁷ Three single colonies of B128 and 7.13 were isolated and expanded. In a more recent study, carcinogenic strain 7.13 was then used to infect another cohort of gerbils maintained on either iron-replete or iron-depleted diets.¹⁷ *In vivo*-adapted single colonies were recovered from gerbils maintained on iron-replete (n=3) and iron-depleted (n=3) diets, and single colonies were isolated and expanded.

In this study, we analysed *in vivo*-adapted output strains that were cultured from these gerbils. Specifically, we analysed three single colonies cultured from three gerbils maintained on an iron-replete (n=9) or iron-depleted (n=9) diets, and these were compared with single colonies cultured from one gerbil maintained on regular salt (n=4) or high salt (n=4). All *H. pylori* isolates were minimally passaged on trypticase soy agar plates with 5% sheep blood (BD Biosciences) and in Brucella broth (BD Biosciences) supplemented with 10% FBS (Atlanta Biologicals) for 16 hours at 37°C with 5% CO₂.

H. pylori *in vitro* adaptation to high salt or low iron conditions

H. pylori strain 7.13 was grown in modified Brucella broth containing 1% Bacto tryptone (BD Biosciences), 1% Bacto Proteose Peptone No. 3 (BD Biosciences), 0.2% yeast extract (Difco), 0.1% dextrose (Fisher Scientific) with high sodium chloride (1.1% NaCl, Sigma), dipyrindyl (100 μM 2,2-bipyridyl, Sigma) or addition of iron (100 μM FeCl₃, Sigma) approximately 20 hours at 37°C with 5% CO₂ and continuously over a 6-day time course. Approximately 5 × 10⁸ colony forming units (CFUs) were harvested at each time point during mid-log phase for DNA extraction and used to inoculate a fresh broth culture for continuous culture *in vitro*.

H. pylori whole genome sequence analysis

H. pylori cultures were harvested, and bacterial DNA was extracted using the Wizard Genomic Purification Kit (Promega). *H. pylori* DNA was sheared using Covaris, yielding an average fragment length of 550 bp. Libraries were prepared using Truseq Nano LT Kit (Illumina) with unique indexes. Postquantitation was performed using the Kapa Library Quantitation Kit (Kapa Biosystems). Libraries were sequenced on the MiSeq Sequencer using the 600V3 Kit (Illumina). For analysis, raw sequence reads were quality trimmed using CLCbio Genomics Workbench V. 8.0 (Qiagen). Alignment files were exported from the CLCbio Workbench in BAM file formats and were then imported into Visual Genomics Analysis Studio, software developed at the Institute for Immunology and Infectious Diseases at Murdoch University, and Geneious V. 6.1.8 (Biomatters) for further analysis. Analyses were performed using a 25% cut-off, which required at least 25% of the reads from at least one single colony to contain the polymorphism, to allow detection of intrapopulation variance. All sequence reads were aligned with the genome sequence of *H. pylori* strain B8 (GenBank accession number NC_014256.1), a closely related strain whose complete genome sequence is available.²⁸ B8 was chosen as the reference strain because *H. pylori* strains 7.13 and B8 each originated from the same parental *H. pylori* strain B128 and each was generated by experimentally infecting gerbils with strain B128. Although B128 (GenBank accession number ABSY0000000) and 7.13 (GenBank accession number NZ_LAQK0000000) have been previously sequenced, these strains were also sequenced in this study to directly compare these sequences within the newly derived strains using the same sequencing technology. All sequences have been deposited to GenBank (BioProject PRJNA362878). Sequence data for

H. pylori strains isolated from gerbils on a high salt diet or a regular diet²¹ were analysed using the same criteria. Specifically, we sought to identify SNPs present in isolates from gerbils on iron-depleted or high salt diets, but not present or present at a lower abundance in isolates from gerbils maintained on iron-replete or regular salt diets.

DNA extraction, PCR and sequence analysis

Approximately 5×10^8 CFUs were pelleted by centrifugation and stored at -20°C . DNA was extracted from *H. pylori* using the PureLink Pro 96 Genomic DNA Purification Kit (Invitrogen). DNA was then used as template to amplify a 500bp product using *fur*-specific primers: 5'TCCGCCAAAAAGACAAAAAC3' and 5'GGGCAAGACTTTCACCTTGA3'. PCR products were prepared for sequence analysis using ExoSAP-IT Express PCR Product Cleanup Kit (Affymetrix), quantified using spectrophotometric nucleic acid quantification (BioTek) and sequenced (GeneWiz). Geneious V. 6.1.8 (Biomatters) was used for subsequent analysis.

H. pylori clinical isolates

Clinical *H. pylori* strains were isolated from three independent and well-defined patient cohorts within Colombia and the USA.^{31–33} Online supplementary table S7 includes information on the clinical *H. pylori* strains, including strain identification number, patient country of origin, age, sex and histological diagnosis.

Statistical analysis

Mean values with SE are shown from experiments performed on at least six independent occasions. One-way analysis of variance with multiple comparisons and Fisher's exact tests were used to determine statistical significance. $p < 0.05$ was considered statistically significant.

Study approval

All animal and human studies were conducted in accordance with the Declaration of Helsinki principles and have been approved by Vanderbilt University IACUC and Institutional Review Board, respectively.

Acknowledgements We would like to acknowledge the following funding sources: R01CA190612 (KTW), R01DK053620 (KTW), P01CA028842 (KTW), R01AI039657 (TLC), R01AI118932 (TLC), Department of Veterans Affairs 2101B×0 00627 (TLC), R01CA077955 (RMP), R01DK058587 (RMP), P30DK058404 (RMP), P01CA116087 (RMP, TLC, KTW).

Contributors JMN contributed to the study design, performed experiments, gathered and analysed data, and drafted the manuscript. AC generated and analysed whole genome sequences. JTL generated and provided sequence data from *Helicobacter pylori* strains harvested from gerbils maintained on regular or high salt diets. JRG assisted with all animal experiments and isolation of in vivo-adapted *H. pylori* strains. MBP provided all patient information from the two Colombian patient cohorts and clinical *H. pylori* isolates from these subjects. MW and SL generated and analysed whole genome sequences. ACB and KTW provided feedback on the manuscript. TLC contributed to the study design and provided sequence data from *H. pylori* strains harvested from gerbils maintained on regular or high salt diets. SM contributed to the study design and the whole genome sequence analysis. DAI contributed to the study design, analysed sequence data, and helped with drafting and editing the manuscript. RMP contributed to the study design and helped with drafting and editing the manuscript.

Competing interests None declared.

Patient consent Obtained

Ethics approval Institutional Review Board, Vanderbilt University Medical Center.

Provenance and peer review Not commissioned; externally peer reviewed.

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