

Guidelines

Section 4 Management of gastritis

CQ17. Should all *H. pylori*-positive individuals receive eradication therapy?

Statement 17

H. pylori infected individuals should be offered eradication therapy, unless there are competing considerations.

Grade of recommendation strong

Evidence level: high

Consensus level: 100%

Comment

H. pylori is a major human pathogen that causes chronic and progressive gastric mucosal damage and is aetiologically related to peptic ulcer, gastric cancer and gastric atrophy. It is also closely associated with gastric MALT lymphoma, dyspepsia, hyperplastic gastric polyps and idiopathic thrombocytopenic purpura.^{5 12 46 47 61 98-104} *H. pylori*-positive individuals are also the major reservoir for transmission of the infection.

The decision to eradicate a chronic infection in a society should be based on quantitative data regarding the outcome of untreated infections. *H. pylori* causes a chronic infection, similar, for example, to asymptomatic syphilis or tuberculosis, and the final outcome for any individual cannot be predicted.¹⁰⁵ *H. pylori* infection differs from many other chronic infectious diseases because it is always transmissible, thus putting others at risk. Because the gastric damage is progressive, the lack of an obvious clinical manifestation at diagnosis has no predictive value for life-time risk to an individual patient, their family or to the community. Benefits of *H. pylori* eradication for an individual depend in part on the degree and extent of damage that has already occurred and the reversibility of that damage. Potential benefits of eradication include stopping the progression of mucosal damage, stabilisation or reduction in risk of developing gastric cancer, resolution of mucosal inflammation, stabilisation or improvement of gastric mucosal function, return of the normal mechanisms governing acid secretion, cure of *H. pylori*-related PUD, reduction in risk of gastrointestinal complications of NSAID therapy and prevention of future development of *H. pylori*-related peptic ulcer.^{2 5 11 28 46 47 106-115}

For society, the benefits include reduction of the reservoir of infected individuals capable of transmitting the infection to others, and avoidance of the costs associated with diagnosis, management and outcomes of *H. pylori*-related diseases that are prevented. Thus, *H. pylori*-infected patients should be offered eradication therapy unless there are competing considerations such as comorbidities, re-infection rates in their communities, competing health priorities of society and financial cost. It has to be remembered, however, that there are concerns about the negative impact of eradication therapies on human health, such as increase in allergy or obesity and perturbation of microbiota.^{116 117}

CQ18. What is the optimal timing for *H. pylori* eradication in asymptomatic subjects?

Statement 18

The maximum benefit of *H. pylori* eradication is obtained if it is done while the mucosal damage is still non-atrophic.

Grade of recommendation: strong

Evidence level: high

Consensus level: 100%

Comment

H. pylori eradication always confers a benefit by halting progression of gastric mucosal damage, reducing the reservoir of

infected individuals and reducing or preventing *H. pylori*-associated diseases. The maximum benefit of eradication for an individual is obtained if eradication is done while the *H. pylori*-induced mucosal damage has not progressed beyond the non-atrophic stage. This population is found in countries where gastric cancer is still prevalent and is concentrated in the younger generation. *H. pylori* eradication of adolescents and young adults has an additional advantage of reducing or preventing transmission of the infection to their children.

As noted above (Section 3), the risk for development of gastric cancer correlates with the extent and severity of atrophic gastritis. It is impossible to define the risk for an individual based on age. Cancer risk in any population relates to the rate of progression of gastric mucosal damage, which is high in populations at high risk of cancer and low in *H. pylori*-infected populations with a low cancer risk. Thus, while it is possible to identify an average age at which the transition from non-atrophic to atrophic phenotype occurs for any population, one should expect that any age group will contain individuals with a wide range of damage, ranging from uninfected (normal) to advanced atrophy. This emphasises the need for risk stratification based on objective parameters including a validated histological staging system rather than on age, to identify whether one eradication treatment is needed or whether the patient might require surveillance.

The incidence of gastric cancer increases with age, which is a surrogate marker for the time required for progression of atrophic gastritis. When atrophic gastritis becomes extensive and severe, the risk increases exponentially. Cancer is the culmination of a multistep process of genetic instability, with cancer cells possessing mutations in coding regions, somatic gene rearrangements and epigenetic changes such as methylation. Current data are consistent with the notion that *H. pylori* eradication halts the progression of damage and reduces or eliminates the *H. pylori*-associated events that increase genetic instability in the gastric mucosa. These include infection-associated DNA double-strand breaks,¹¹⁸ impaired DNA mismatch repair,¹¹⁹ aberrant activation-induced cytidine deaminase expression, which induces nucleotide alterations involved in DNA mutations,¹²⁰ aberrant methylation in a number of gene promoters in the gastric mucosa, including cell growth-related genes, DNA-repair genes, tumour-suppressor genes, the cell adherence gene E-cadherin and CpG islands of microRNA genes¹²¹⁻¹²³ and aberrant microRNA expression.¹²⁴ *H. pylori* infection also causes an inflammatory response with mucosal infiltration of acute and chronic inflammatory cells. Cancer risk is increased in relation to the ability of the infecting strain to cause inflammation (eg, those possessing the Cag pathogenicity island). However, all strains cause inflammation, and gastric cancer is associated with infections lacking putative virulence factors. Thus all *H. pylori* infections should be considered pathogenic and should be eradicated.

Because of the damage and premalignant changes, *H. pylori* eradication cannot 'reset the clock' to zero (ie, no risk) but can stop the progression of risk and stabilise or decrease the subsequent risk.

CQ19. Do we need to adopt eradication regimens according to the geographical area?

Statement 19

Eradication regimens should be based on the best locally effective regimen, ideally using individual susceptibility testing or community antibiotic susceptibility, or antibiotic consumption data and clinical outcome data. The agents available differ in

different regions and this, in part, dictates what regimens are possible.

Grade of recommendation: strong

Evidence level: high

Consensus level: 100%

Comment

The success of a proven successful *H. pylori* eradication regimen depends on the pattern of resistance in the population and on the common host genotypes of drug metabolising enzymes in the population. The prevalence of *H. pylori* resistance to commonly used antimicrobial agents greatly varies geographically and is linked to consumption of antibiotics in the region,¹²⁵ so the preferred eradication regimen often differs between regions. Ideally, treatment regimens should be chosen based on susceptibility testing. Within any region, only regimens that reliably produce eradication rates of $\geq 90\%$ in that population should be used for empirical treatment.^{5 126–129}

CQ20. Does eradication of *H. pylori* prevent gastric cancer?

Statement 20

Eradication of *H. pylori* reduces the risk of gastric cancer. The degree of risk reduction depends on the presence, severity and extent of atrophic damage at the time of eradication.

Grade of recommendation: strong

Evidence level: high

Consensus level: 100%

Comment

H. pylori infection is the most important cause of gastric cancer as it is estimated that 89% of non-cardia gastric cancer, representing 78% of all cases of gastric cancer, can be attributed to chronic *H. pylori* infection.¹³⁰ Prevention of *H. pylori* infections removes the primary cause of gastric cancer and will thus reduce the incidence of gastric cancer in that population. The effectiveness of *H. pylori* eradication for prevention of gastric cancer depends on the severity and extent of atrophic damage at the time of eradication and ranges from essentially complete prevention for those with non-atrophic gastritis to stabilisation or reduction of risk in those with established atrophic changes.^{94 95} As noted in Section 3, risk can be stratified using a variety of approaches, such as one of the validated histological stratification systems (eg, OLGA or OLGIM),^{16–18} and *H. pylori* eradication can stabilise risk and halt the progression of risk.^{28 94} Prevention of acquisition of *H. pylori* infections and eradication of the infection before the development of atrophic changes are forms of primary prevention. Secondary prevention involves identification and surveillance of those at risk in order to remove intraepithelial lesions and early gastric cancer(s) before they become invasive.^{5 71 72 77 131} There may be also a role for cancer immunotherapy to treat premalignant lesions and halt their progression to more advanced lesions.¹³²

CQ21. Should the outcome of eradication therapy always be assessed (ie, test for cure)?

Statement 21

The outcome of eradication therapy should always be assessed, preferably non-invasively.

Grade of recommendation: strong

Evidence level: high

Consensus level: 100%

Comment

Failure of eradication is common and allows the mucosal damage to progress, and so eradication should always be confirmed,

preferably using a non-invasive test such as a urea breath test or a validated monoclonal-based stool antigen test.⁵ For patients requiring endoscopic follow-up, such as after endoscopic removal of a gastric adenoma, histological assessment can be used. Confirmation of cure also provides an early warning system for the increasing antibiotic resistance in a population that will manifest as increasing rates of treatment failure.^{125 128 129}

CQ22. Which patients need long-term follow-up after eradication?

Statement 22

H. pylori eradication may not completely eliminate the risk of gastric cancer. Patients who remain at risk, as defined by the extent and severity of atrophy, should be offered endoscopic and histological surveillance.

Grade of recommendation: strong

Evidence level: high

Consensus level: 97.3%

Comment

Long-term follow-up such as regular endoscopic surveillance should be based on estimating the risk of developing gastric cancer after *H. pylori* eradication (ie, risk stratification).^{95 133} Cancer risk correlates with the extent and severity of atrophic gastritis and risk stratification should be confirmed using a validated histological risk scoring systems such as OLGA or OLGIM.^{16–18} In areas with proven expertise in endoscopic scoring, a system such as that of Kimura and Takemoto can be used initially, although histological confirmation is still recommended.^{134 135} Patients whose *H. pylori* infection was diagnosed non-invasively (eg, urea breath test or stool antigen) should be considered for histological assessment. These patients should include those within the age range in which atrophic changes are common in that population and those with a history of gastric ulcer as well as those with a pretreatment serum pepsinogen I of ≤ 70 ng/mL and a pepsinogen I:II ratio ≤ 3 .^{136–138} All those at especially high risk, including those at risk for intraepithelial neoplasia (dysplasia) or early gastric cancer, are candidates for regular endoscopic surveillance.

DISCUSSION

The global consensus meeting on *H. pylori* gastritis has set a new landmark for gastritis, which has continued to be an ill-conceived clinical entity placed between a histological picture and upper abdominal symptoms.

In spite of the fact that gastritis had been long recognised as an important clinical entity, generations of gastroenterologists have neglected the importance of treatment of this nosological entity. Rudolf Schindler described chronic gastritis as a serious disease and a precursor of gastric cancer and considered their relationship as being of outstanding importance in the fight against gastric cancer.¹³⁹

The discovery of *H. pylori* has revolutionised the pre-existing concepts of gastritis by assigning a specific aetiology to this entity underlying PUD and gastric cancer. The majority of these serious conditions are manifestations developed on the background of chronic gastritis caused by a unique infectious agent, *H. pylori*. For PUD, guidelines unanimously recommend eradication as the primary treatment for those with positive *H. pylori* tests. However, there has been no consensus on how and when to manage individuals with *H. pylori* gastritis itself, which is crucial to the efficiency of gastric cancer prevention because most patients with chronic gastritis may remain asymptomatic until the appearance of severe complications. Furthermore, both gastritis and duodenitis were recognised as important causes of upper gastrointestinal bleeding,¹⁴⁰ encouraging our attention to

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these conditions now that anti-thrombotic therapies are increasingly being used.

To further compromise the concept of gastritis as a significant clinical entity, the term 'gastritis' has historically, but wrongly, been used as a substitute for a clinical diagnosis of FD. Historical studies, however, failed to demonstrate a significant association between histological findings of gastritis and the dyspeptic symptom complex.^{141 142} Hence, a potential pathogenetic role for *H. pylori* in causing dyspeptic symptoms was initially considered doubtful and its eradication in FD controversial.^{143 144} Meta-analysis of a large number of controlled trials with longer follow-up confirmed that eradication of *H. pylori* in patients with FD conveys a small but statistically significant benefit.¹² Consequently, dyspepsia attributable to *H. pylori* gastritis involves an underlying organic cause and should be excluded from the FD category. Additionally, 'dyspeptic' patients should not automatically be labelled as having 'gastritis' without any histological confirmation.

Diagnostic assessment of gastritis has been advanced by the recent introduction of high-resolution endoscopy with image-enhanced modalities, and magnification is now used routinely in major hospitals in Japan. This endoscopic technology allows the identification of mucosal changes (for targeted biopsies) more precisely, leading to more accurate evaluation of cancer risks such as preneoplastic changes. Wider use of this new endoscopic system outside Japan may be limited at present.

The Kyoto consensus meeting focused attention on gastritis in all its clinical expression and dealt with four main topics: classification of gastritis in relation to ongoing ICD revision, FD and *H. pylori* infection, diagnosis of gastritis and the management of gastritis. The methodology of the meeting adopted all modern means for reaching consensus and included an internet-based Delphi method with full access to published data in a completely 'neutral' environment.

In summary, The Kyoto meeting proposed an aetiology-based classification for gastritis and concluded that *H. pylori* gastritis is an infectious disease. As such, *H. pylori* gastritis requires treatment whether or not it is associated with symptoms because it represents a condition that may evolve towards serious complications, including peptic ulcer and gastric neoplasia.

Consensus was reached on the existence of a separate category of patients with dyspeptic symptoms that are due to *H. pylori* gastritis. In these patients, eradication therapy is the recommended first-line treatment. Because of the diagnostic problems related to 'gastritis', these patients should be labelled as having *H. pylori*-associated dyspepsia and are identified by sustained dyspeptic symptom relief after eradication.

For the diagnosis of gastritis, it was agreed that risk stratification systems such as OLGA and OLGIM are useful as are the serological markers. In view of recent technological advancements, image-enhanced endoscopy should be encouraged for identifying mucosal changes which carry a high risk of developing into gastric neoplasia. Finally, it was recommended that early eradication therapy, ideally before preneoplastic changes occur, should be undertaken. However, the feasibility of implementing this strategy should be regionally tailored. As eradication therapy does not guarantee elimination of the risk of gastric cancer, follow-up should be considered for patients who have preneoplastic conditions.

Although there are still many remaining areas to be discussed, we believe the outcome of the Kyoto consensus meeting presented in this report will improve patient care and will provide a cornerstone for further refinement and research in the area of gastritis.

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Analysis of *Helicobacter pylori* genotypes in clinical gastric wash samples

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Abstract *Helicobacter pylori* is a key factor in the development of gastric cancer; indeed, clearance of *H. pylori* helps prevent gastric cancer. However, the relationship between gastric cancer and the abundance and diversity of *H. pylori* genotypes in the stomach remains unknown. Here, we present, for the first time, a quantitative analysis of *H. pylori* genotypes in gastric washes. A method was first developed to assess diversity and abundance by pyrosequencing and analysis of single nucleotide polymorphisms in 23S ribosomal RNA (rRNA), a gene associated with clarithromycin resistance. This method was then validated using arbitrarily mixed plasmids carrying 23S rRNA with single nucleotide polymorphisms. Multiple strains were detected in many of 34 clinical samples, with frequency 24.3 ± 24.2 and 26.3 ± 33.8 % for the A2143G and A2144G strains, respectively. Importantly, results obtained from gastric washes were similar to those

obtained from biopsy samples. The method provides opportunities to investigate drug resistance in *H. pylori* and assess potential biomarkers of gastric cancer risk, and should thus be validated in large-scale clinical trials.

Keywords *Helicobacter pylori* · Gastric wash · 23S rRNA · Pyrosequencing

Introduction

Gastric cancer is the third leading cause of cancer death in the world, with prognosis determined by tumor stage at diagnosis and treatment [1, 2]. Diagnostic tools such as gastrointestinal endoscopy followed by pathological analysis and/or fluoroscopy have proven useful; however, the mortality rate has remained high throughout the world [3]. Gastric cancer is believed to result in part from the accumulation of genetic alterations that stimulate oncogene overexpression and/or silence tumor suppressors [4–6]. Epigenetic silencing of tumor-related genes due to aberrant DNA methylation has also been recently reported [7–14]. Notably, aberrant DNA methylation occurs more frequently than mutations in pathologically differentiated adenocarcinoma [15]. *Helicobacter pylori*, which elicits chronic inflammation, is a key factor underlying such aberrant DNA methylation in the stomach mucosa [5].

H. pylori, identified in 1982 by Barry Marshall and Robin Warren [16], is a helix-shaped Gram-negative bacterium associated with gastric diseases such as gastritis [17, 18], gastric and duodenum ulcer [19, 20], gastric cancer [4, 6, 12, 13, 21, 22], mucosa-associated lymphoid tissue lymphoma [23], as well as ulcers due to non-steroidal anti-inflammatory drugs [24–26]. *H. pylori* is typically cleared by standard first-line therapies, including proton-pump inhibitors, potassium-competitive acid blockers, amoxicillin, and clarithromycin

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[27, 28]. However, these therapies are becoming less effective because of clarithromycin resistance [29], which, in turn, is reportedly due to A2143G, A2143C, and A2144G point mutations in 23S ribosomal RNA (rRNA) [29–32]. Unfortunately, clarithromycin-resistant strains cannot be identified based on currently available qualitative methods such as *H. pylori* IgG test [33, 34], stool antigen test [35, 36], urea breath test (UBT) [37, 38], and rapid urease test [37, 39].

In this manuscript, we describe a new approach to quantify multiple strains of *H. pylori* in gastric washes. In this approach, developed by co-author Watanabe and colleagues (patent WO2007/132844) [30, 40–43], stomach washes are performed with saline during endoscopy, a topical procedure in which only a small portion of abnormal tissue is excised. As cells are abundantly exfoliated from the gastric mucosa during washing, undamaged human and *H. pylori* DNA can be recovered from the wash and assayed by sensitive and quantitative techniques. Of these, Sanger sequencing is the most reliable for detection of microbial species, although the abundance of multiple genotypes is difficult to quantify by this method. In addition, the method is unsuitable for the clinic because of complex sample processing, long turn-around time, low throughput, and high cost. On the other hand, pyrosequencing methods, in which bases are called by sequential addition of dNTPs, enable genotyping, as well as quantitative analysis of single nucleotide polymorphisms, insertions, and deletions. Thus, we analyzed gastric washes by pyrosequencing to determine the abundance and diversity of *H. pylori* genotypes in each patient [30].

Material and methods

Patient characteristics

Both gastric wash and biopsy samples were collected from 17 patients (34 samples) who underwent endoscopy at Hokkaido University Hospital, Hokkaido, Japan, from April 2014 to December 2015. The study was conducted in accordance with all rules and regulations of the Hokkaido University Institutional Review Board (#014-0459), and informed consent was obtained from each patient. Patients were tested by UBT urea breath test (Otsuka Pharmaceutical Co., Ltd., Tokyo, Japan), Helicocheck rapid urease test (Otsuka Pharmaceutical Co., Ltd., Tokyo, Japan), and *H. pylori* IgG E-plate (Eiken Chemical Co., Ltd., Tokyo, Japan). A patient who tested positive on at least one test was deemed infected (Table 1).

Sample collection of gastric washes

Approximately 10 min prior to endoscopy, patients were asked to swallow 100 mL water containing 80 mg dimethylpolysiloxane (Gascon, Kissei Pharmaceutical Co., Ltd., Matsumoto, Japan), 1 g sodium bicarbonate, and 20,000 units pronase (Pronase MS, Kaken Pharmaceutical Co., Ltd., Tokyo, Japan). Gastric washes were collected in specimen containers (No. 111219, Fortegrow Medical, Tochigi, Japan), which were directly fitted to the endoscope modulator. Gastric washes were manually aspirated under vacuum

Table 1 Patient characteristics

No.	Age	Sex	RUT	UBT	HP-IgG	Histological assessment ^a	Clinical HP examination
1	52	M	–	1.3	<3	Normal	–
2	67	F	–	1.8	<3	Normal	–
3	71	F	–	0	<3	Normal	–
4	65	F	+	54.6	1.1	Marked	+
5	63	M	+	24.7	29	Marked	+
6	57	F	+	13.6	27	Marked	+
7	61	M	–	0.1	<3	Normal	–
8	68	F	+	10.6	27	Marked	+
9	84	M	+	4.6	43	Marked	+
10	73	F	+	25.3	70	Marked	+
11	40	F	–	0	<3	Normal	–
12	83	F	+	4.7	25	Marked	+
13	62	M	+	5.1	14	Marked	+
14	69	M	+	2.8	18	Marked	+
15	77	M	+	4.3	21	Marked	+
16	63	M	+	21	26	Marked	+
17	50	M	+	3.8	56	Marked	+

^aHistological assessment was graded by updated Sydney system

through the suction channel of the endoscope, centrifuged immediately, and resulting pellets were frozen at -80°C . Tissue samples with diameter approximately 5 mm were then collected using Radial Jaw (Boston Scientific Corp., Natick, MA), with guidance from a GIF-Q260 endoscope fitted to an EVIS LUCERA system (Olympus, Inc., Tokyo, Japan). Disposable sample collection tubes, connector tubes, and other endoscopic devices were used. The endoscope was washed after each procedure according to guidelines, using 0.55 % DISOPA (Johnson and Johnson, Langhorne, PA) and an automatic washing machine.

DNA extraction

DNA was extracted from gastric wash and biopsy samples by phenol chloroform. Briefly, tissues or frozen pellets from gastric washes were resuspended in 10 % SDS and proteinase K, mixed vigorously, and incubated at 37°C for 6 h. Samples were then mixed vigorously for approximately 30 s with one volume of 25:24:1 phenol:chloroform:isoamyl alcohol and

centrifuged at room temperature for 5 min at $16,000\times g$. The aqueous layer was then transferred to a fresh tube and extracted in the same manner another two times. Final extracts were then mixed with 100 % ethanol, centrifuged at 4°C for 5 min at $16,000\times g$, and stored at -20°C overnight to precipitate DNA. Precipitates were collected by centrifugation, washed with 70 % ethanol, and centrifuged at 4°C for 2 min at $16,000\times g$. As much of the supernatant was removed as possible, and pellets were resuspended in $500\ \mu\text{L}$ Tris-EDTA buffer. Final DNA concentration and quality were measured on a ND-1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE).

Construction of plasmids encoding variants of *H. pylori* 23S rRNA

Wild-type, A2143G, A2143C, and A2144G point mutants of *H. pylori* 23S rRNA (NCBI database accession no. U27270) were separately inserted into pTAKN-2 plasmids.

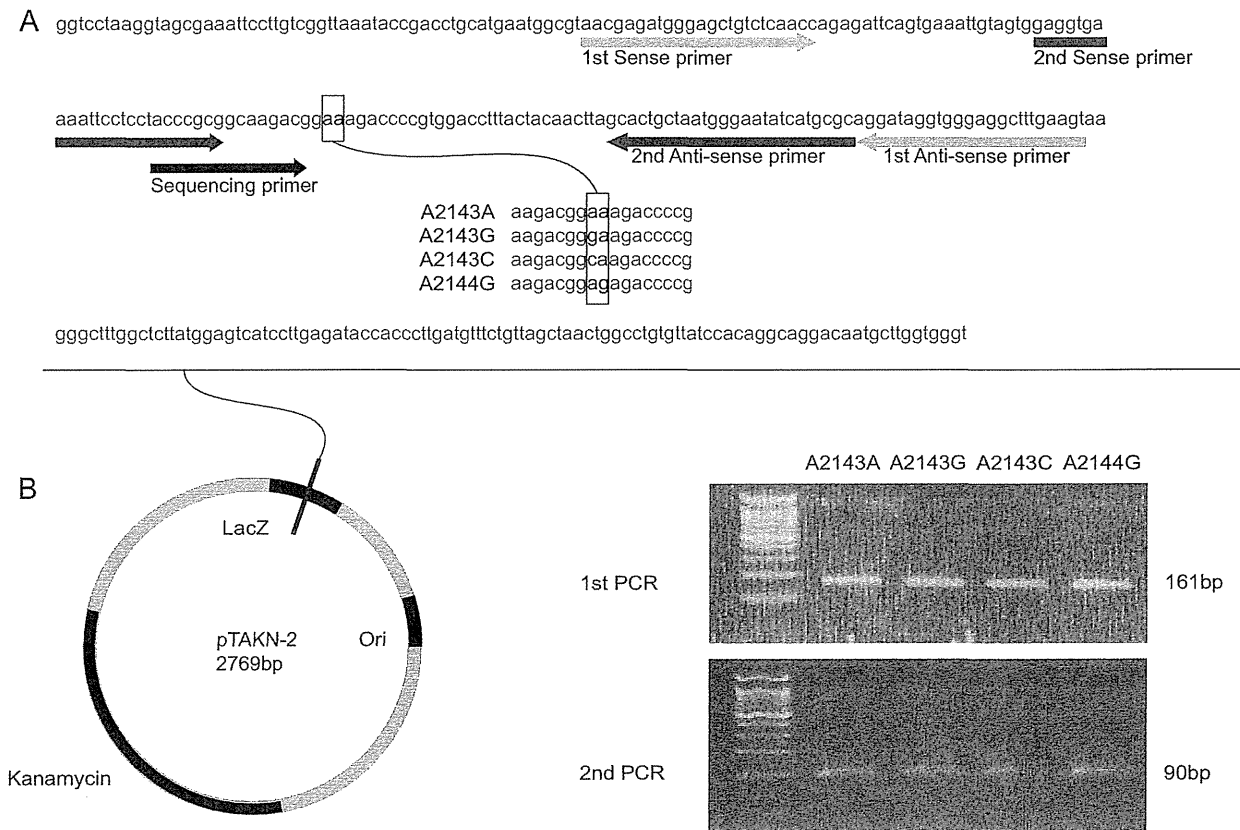


Fig. 1 23S rRNA sequence, primers, and plasmids. **a** Primers for nested PCR and pyrosequencing. *Helicobacter pylori* 23S rRNA was first amplified with the 1st sense/antisense primer set, and then by the 2nd sense/biotin antisense primer set. Biotin-tagged products from nested PCR were then analyzed by pyrosequencing to quantify A2143C, A2143G, and A2144G point mutants. **b** Fragments of wild-type or

mutated 23S rRNA were separately inserted into pTAKN-2, left. Right, gel electrophoresis of products from the first PCR reaction, with expected size 161 bp, and of products from the second PCR reaction, which amplified a 90-bp region encompassing A2143 (wild type), A2143C, A2143G, and A2144G

Quantitative pyrosequencing analysis of multiple *HPs*

Pyrosequencing enables quantitative analysis of the abundance of polymorphisms at a given site. To validate this

approach, plasmids containing wild-type and mutated 23S rRNA in arbitrary ratios of 0, 30, 50, 70, and 100 % were analyzed. 23S rRNA was then amplified and biotinylated by nested PCR from gastric wash and biopsy samples. In

Table 2 Ratio of *H. pylori* genotypes in plasmids, gastric wash, and biopsy samples

No.	Template DNA	161 bp					
		2143			2144		
		A	C	G	A	G	
A							
1	Plasmid DNA A 100 % G 0 %	100	0	0	99	1	
2	Plasmid DNA A 70 % G 30 %	69	0	31	72	28	
3	Plasmid DNA A 50 % G 50 %	51	0	49	54	46	
4	Plasmid DNA A 30 % G 70 %	25	0	75	35	65	
5	Plasmid DNA A 0 % G 100 %	1	0	99	7	93	
B							
No.	Biopsy/gastric washes	Clinical HP exam	161 bp			2144	
			2143			A	G
			A	C	G	A	G
1	Biopsy	–	48	0	52	68	32
	Gastric washes			N/A		88	12
2	Biopsy	–	56	0	44	81	19
	Gastric washes			N/A		N/A	
3	Biopsy	–	56	0	44	62	38
	Gastric washes			N/A		N/A	
4	Biopsy	+	30	0	70	10	90
	Gastric washes		54	0	46	14	86
5	Biopsy	+	100	0	0	99	1
	Gastric washes		100	0	0	99	1
6	Biopsy	+	41	0	59	14	86
	Gastric washes		22	0	78	5	95
7	Biopsy	–	65	1	34	82	18
	Gastric washes			N/A		N/A	
8	Biopsy	+	100	0	0	98	2
	Gastric washes		100	0	0	99	1
9	Biopsy	+	100	0	0	99	1
	Gastric washes		100	0	0	99	1
10	Biopsy	+	100	0	0	99	1
	Gastric washes		100	0	0	99	1
11	Biopsy	–	75	1	25	85	15
	Gastric washes			N/A		N/A	
12	Biopsy	+	100	0	0	97	3
	Gastric washes		100	0	0	98	2
13	Biopsy	+	82	0	17	92	8
	Gastric washes		100	0	0	98	2
14	Biopsy	+	71	0	28	84	16
	Gastric washes		58	11	31	79	21
15	Biopsy	+	63	0	36	86	14
	Gastric washes		57	5	38	79	21
16	Biopsy	+	76	0	24	51	49
	Gastric washes		79	0	21	48	52
17	Biopsy	+	29	0	71	3	97
	Gastric washes		25	0	75	1	99

the first reaction, a 255-bp fragment was amplified with sense primer “acgagatgggagctgtctcaacc” and antisense primer “agcattgtcctgcctgtggataac.” Amplification products were then used as template in the second reaction to amplify a 90-bp fragment with sense primer “gagtgaaaattcctcctaccg” and antisense primer “gcgcatgatattcccattagcagtc.” Reactions consisted of touchdown PCR with denaturation at 95 °C for 30 s, annealing at appropriate temperatures for 30 s, and extension at 72 °C for 30 s. Finally, amplification products were analyzed by pyrosequencing on a Pyromark Q24 (QIAGEN, Valencia, CA) using primer “acccgggcaagacg.” Sequence to analyze A2143V “GVAAGACCCC GTGGACCTTT ACTACAA” and A2144R “RAGACCCCGT GGACCTTT AC TACAAC.”

Abundance of *H. pylori* 23S rRNA in clinical samples

We analyzed 34 clinical samples (17 gastric washes and 17 biopsies) by SYBR Green real-time PCR, with *H. pylori* 23S

rRNA as target and human *GAPDH* as reference. *H. pylori* 23S rRNA was amplified with sense primer “acgagatgggagctgtctcaacc” and antisense primer “agcattgtcctgcctgtggataac,” while human *GAPDH* was amplified with sense primer “cgagatccctccaaatcaa” and antisense primer “ctgcaatgagcctacagca.” Reactions were performed on an ABI 7500 Real-Time PCR System (Applied Biosystems, Foster, CA) according to the manufacturer’s instructions. Data were analyzed in SDS2.1 by comparative cycle threshold (Δ Ct).

Statistical analysis

Mean and 95 % confidential interval were calculated for clinicopathologic features. Correlation between results from gastric wash and biopsy samples was analyzed by Mann–Whitney test for continuous variables, with $p < 0.05$ considered significant. All statistical analyses were performed in PRISM for Windows, Version 4 (GraphPad Prism 6.0.7, Inc., San Diego, CA).

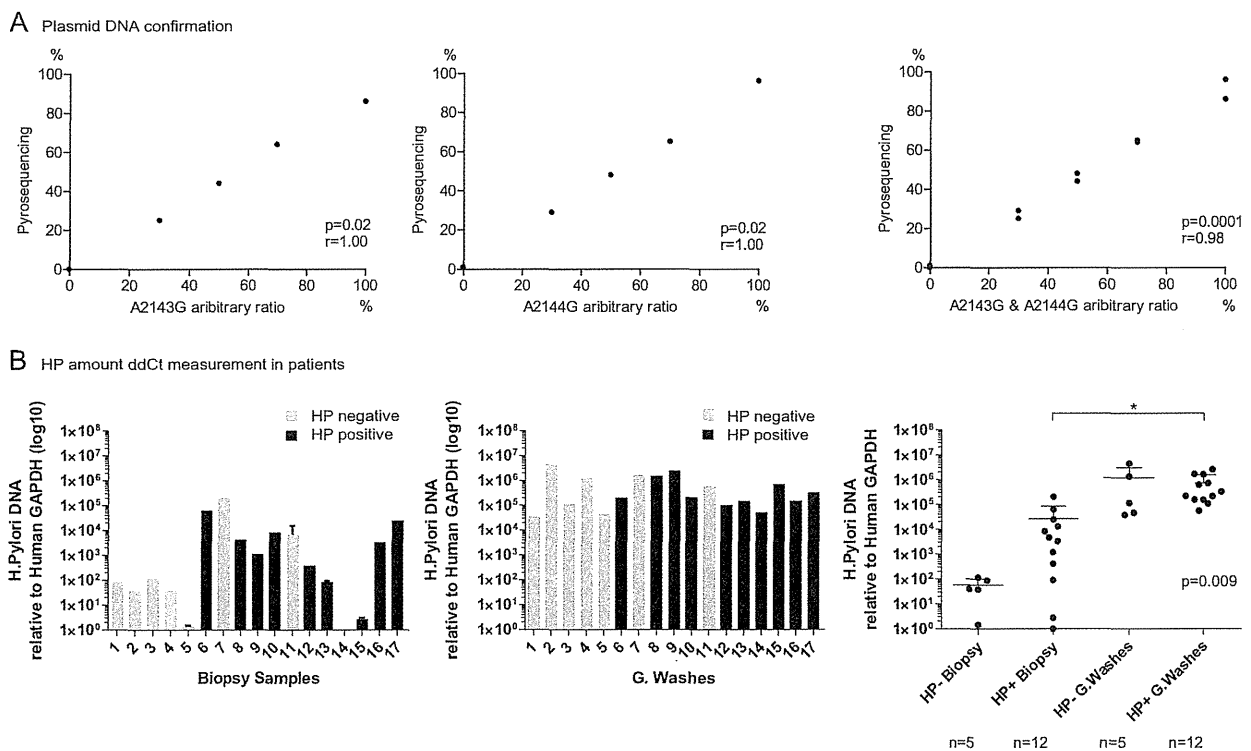


Fig. 2 Validation of pyrosequencing, and abundance of *Helicobacter pylori* in clinical samples. **a** Plasmids containing wild-type, A2143G, and A2144G 23S rRNA were mixed in arbitrary ratios of 0, 30, 50, 70, and 100 % and analyzed by pyrosequencing. Significant correlation was observed between expected and experimentally determined ratios, with $r = 1.00$ for A2143G ($p = 0.02$), 1.00 for A2144G ($p = 0.02$), and 0.98 for both ($p = 0.0001$). **b** *H. pylori* 23S rRNA was quantified using real-time PCR, with human *GAPDH* as reference. Results are copy numbers

obtained by Δ Ct. Copy numbers were lower in biopsy samples (56.94 ± 45.1) that tested negative on qualitative tests than in samples that tested positive ($27,013 \pm 58,715$), although the difference was not statistically significant ($p = 0.33$). However, copy numbers were comparable in all gastric wash samples. Further, copy numbers were significantly higher in gastric wash samples that tested positive on qualitative tests ($707,706 \pm 821,525$) than in biopsy samples that tested positive ($27,013 \pm 58,715$; $p < 0.009$)

Results

Pyrosequencing is suitable to genotype *H. pylori*

Pyrosequencing was validated as a tool to genotype *H. pylori* using pTAKN-2 plasmids containing wild-type 23S rRNA mixed in arbitrary ratios of 0, 30, 50, 70, and 100 % with A2143G, A2143C, and A2144G point mutations (Figs. 1a, b, and 5 and Table 2a), which are associated with resistance to clarithromycin. Ratios were strongly correlated between pyrosequencing and expected values, with $r=1.00$ for A2143G ($p=0.02$), 1.00 for A2144G ($p=0.02$), and 0.98 for both ($p=0.0001$), indicating that pyrosequencing is a robust method to genotype *H. pylori* (Fig. 2a).

Amplification of *H. pylori* 23S rRNA from clinical samples

The abundance of *H. pylori* genotypes were assessed in gastric wash and biopsy samples (Table 1) obtained from 17 patients without critical primary illnesses, and without ulcers or tumors, as determined by endoscopy. The patient population consisted of nine males and eight females with mean age 65

± 11.4 years, of whom five tested negative for *H. pylori* on urea breath test, rapid urease test, and *H. pylori* IgG test. The remaining 12 patients tested positive for *H. pylori* on at least one test. DNA was successfully extracted from all 34 samples, and *H. pylori* 23S rRNA was amplified by nested PCR from all samples, including those determined by qualitative tests to be uninfected (Fig. 2b).

H. pylori abundance in clinical samples

To investigate the discrepancy between nested PCR and qualitative tests, we used real-time PCR to estimate the abundance of *H. pylori* in all clinical samples, as measured by 23S rRNA relative to human *GAPDH*. On average, the abundance of 23S rRNA was lower in biopsy samples that tested negative on qualitative tests (56.94 ± 45.1) than in gastric washes samples that tested negative ($27,013 \pm 58,715$). However, the difference was not statistically significant ($p=0.33$, Fig. 2b). On the other hand, 23S rRNA was significantly more abundant ($p<0.009$) in gastric wash samples that qualitatively tested positive ($707,706 \pm 821,525$) than in biopsy samples that tested positive ($27,013 \pm 58,715$) (Fig. 2b).

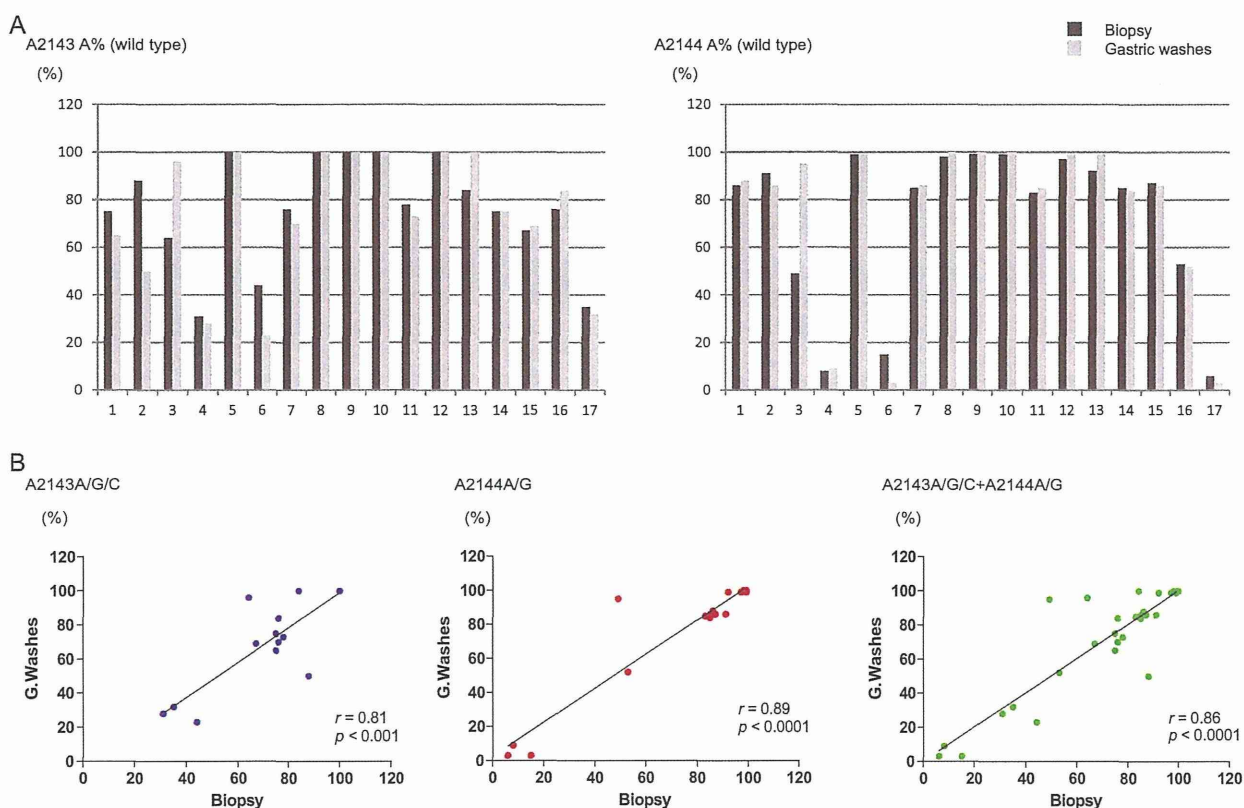


Fig. 3 Analysis of *Helicobacter pylori* genotypes in clinical samples. The ratio of wild type to A2143G and A2144G strains of *H. pylori* was significantly correlated between biopsy and gastric wash samples, as

shown in **a** bar graphs and **b** scatter plots. The correlation coefficient r was 0.81 for A2143 ($p=0.001$), 0.89 for A2144 ($p=0.0001$), and 0.86 for both ($p=0.0001$)

Abundance of *H. pylori* genotypes in clinical samples

We examined the prevalence of A2143G, A2143C, and A2144G point mutants in gastric wash and biopsy samples. A2143C was not detected (Table 2b). However, the prevalence of A2143G and A2144G was significantly correlated between gastric wash and biopsy samples, with $r=0.81$ for A2143G ($p=0.001$), 0.89 for A2144G ($p=0.0001$), and 0.86 for both ($p=0.001$) (Fig. 3b). Wild-type alleles (A2143 and A2144) were similar in frequency in both samples. However, these alleles were, in most cases, slightly more abundant in biopsy samples than in gastric washes, except for samples 3 and 13, in which these alleles are notably more abundant in the gastric wash. It is possible that the difference in these cases is due to the nature of the data collected, which is localized (or “point”) for biopsies, but more extensive (or “plane”) for gastric washes. Thus, analyses using gastric washes are probably more informative, because “plane” information may better reflect the state of the whole stomach (Fig. 3a, b).

Discussion

According to the World Health Organization, cancer is a major cause of mortality worldwide, with 8.2 million deaths reported in 2012. Of these, 1.59 million were attributed to lung cancer,

745,000 were due to liver cancer, 723,000 were due to gastric cancer, and 694,000 were due to colorectal cancer. Breast and esophageal cancer accounted for 521,000 and 400,000 deaths, respectively. Although morbidity from gastric cancer has gradually decreased in recent years, it remains a serious issue [44], especially in Japan, where gastric cancer is just behind lung cancer in terms mortality and where incidence is the second highest in the world after South Korea.

The development and progression of gastric cancer have been examined in many studies, and several risk factors have been identified. Of these, persistent infection with *H. pylori* is considered a key risk factor, along with lifestyle habits, smoking, and diet. *H. pylori* was first classified as a carcinogen in 1994 by the International Agency for Research on Cancer, a specialized arm of the World Health Organization. Indeed, two independent clinical studies by the Agency and by the Japan Gast Study Group indicated that *H. pylori* is involved in more than 80 % of gastric cancer cases and in 90 % of cases of cardia cancer, which is common in Japan. This finding suggested that clearance of *H. pylori* may reduce the incidence of gastric cancer [22].

H. pylori is believed to have originated in the human stomach in Africa approximately 60,000 years ago and spread to the Americas through Central Asia, Europe, and East Asia. This long period of interaction with humans and consequent co-evolution was accompanied by several mutations and has

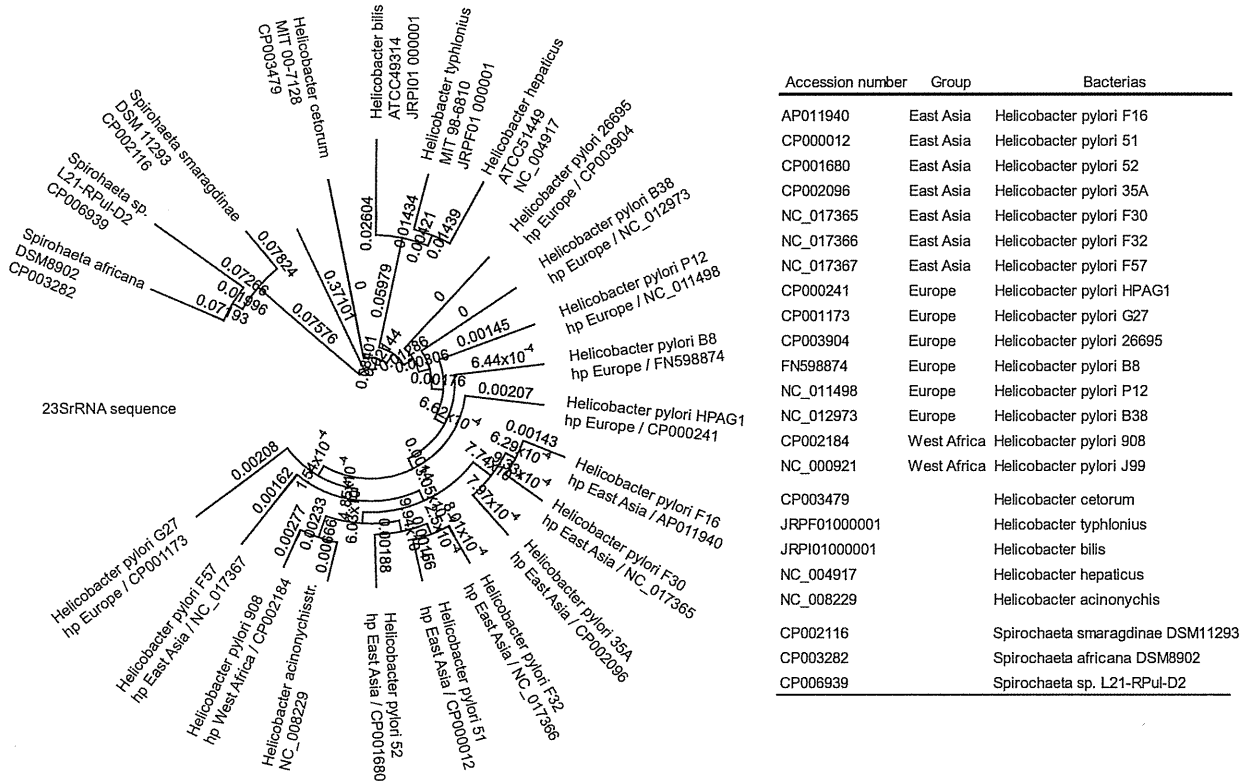


Fig. 4 23S rRNA in *Helicobacter* sp. A fragment of 23S rRNA nearly specific to *H. pylori* was identified by bioinformatic analysis

resulted in several distinct lineages, including hpAfrica, hpSahul, hpAsia, hspEastAsia, hpEurope, hspMaori, and hpAmerica. The East Asian lineage harbors a *cag* pathogenicity island, a genetic element associated with atrophic gastritis or gastric cancer and is believed to have been exogenously acquired by horizontal gene transfer [45].

Clarithromycin-resistant *H. pylori* has recently emerged as a consequence of therapy, which typically consists of clarithromycin, amoxicillin, and proton-pump inhibitors. This resistance has been attributed to A2143C/G and A2144G polymorphisms in 23S rRNA, a component of the 50S subunit of the ribosome. However, we hypothesized that these variants do not accumulate by sudden mutation events, but by gradually displacing wild-type *H. pylori* from the stomach. We tested this hypothesis by evaluating 23S rRNA in clinical samples. This study represents the first comprehensive and quantitative analysis of *H. pylori* genotypes in a single stomach [46–48].

We first identified a specific target sequence in 23S rRNA by bioinformatic analysis in Geneious Pro 5.5.6 (Biomatters Ltd., Auckland, New Zealand) and developed a diagnostic procedure based on pyrosequencing, which enables

quantification of multiple genotypes in a given sample using primers and probes that target the same site (Fig. 4). We first validated this approach using arbitrary mixtures of plasmids containing fragments of wild-type or polymorphic 23S rRNA (Figs. 2a and 5 and Table 2). Although an endoscopic biopsy is more commonly used for analysis, we next also used gastric wash samples after lavage of the whole stomach, because we believe it is important to obtain more general data on the abundance and diversity of *H. pylori* in the entire stomach (Figs. 2b and 3a, b). This approach is similar to pyrosequencing analysis of DNA methylation in the cancer-specific genes MINT25, RORA, GDNF, ADAM23, PRDM5, and MLF1 using biopsy and gastric wash samples from patients with primary gastric cancer [41, 42]. These protocols were described in *Gastroenterology* in 2009 and in *Tumor Biology* in 2011.

Overall, there was significant correlation between results obtained from gastric wash and biopsy samples, although moderate differences were observed in two cases. Indeed, these differences may be due to the “point” and “plane” nature of data collected from biopsy and gastric wash, respectively (Fig. 3a, b).

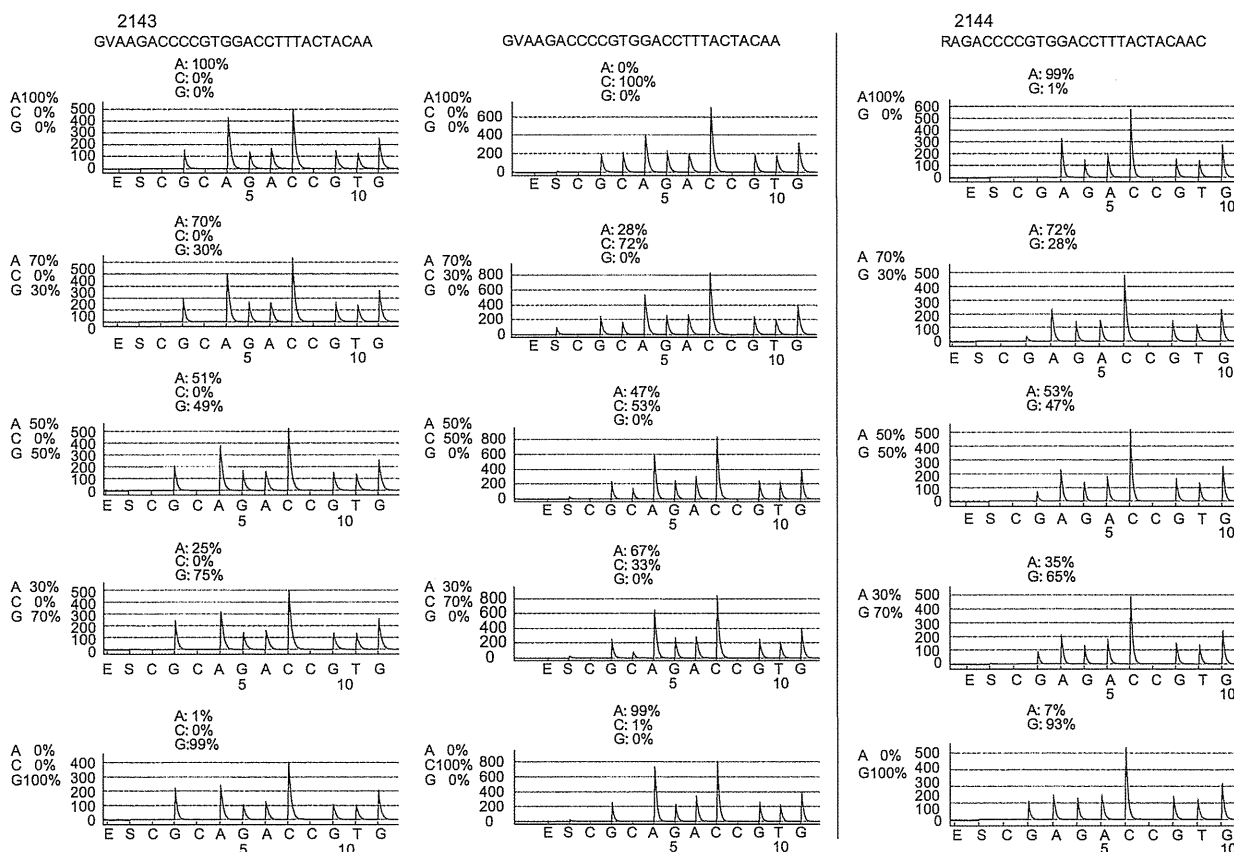


Fig. 5 Pyrograms of polymorphisms in *Helicobacter pylori* 23S rRNA. Pyrosequencing was validated using wild-type 23S rRNA mixed at arbitrary ratios of 0, 30, 50, 70, and 100 % with **a** A2143G, **b** A2143C, and **c** A2144G

In any case, *H. pylori* was detected in all samples, including those that tested negative on multiple, currently available qualitative tests (Fig. 3a). We suggest that PCR is more sensitive than antibody, antigen and radioactive material-based tests. Indeed, we were able to amplify *H. pylori* 23S rRNA from all samples by nested PCR. We note that dense bands at 161 bp were not observed in the first round of PCR for gastric wash samples 1–3, 7, and 11. These samples are annotated “N/A” in Table 2b. However, 90-bp bands were observed for these samples in the second PCR reaction (Table 2b), suggesting that DNA in these samples may be damaged, fragmented, etc [49]. (Fig. 2b). Notably, we found that multiple *H. pylori* genotypes are simultaneously present at various ratios in a single stomach.

However, we note that many elderly patients receive anti-coagulant drugs for cerebral infarction, atrial thrombus, and cardiac arrhythmia. Consequently, attending physicians sometimes hesitate to prescribe endoscopic biopsy for these patients because of the risk of GI bleeding. Thus, gastric washes may be more suitable instead. In addition, more general data on the entire stomach may be collected from such washes. Indeed, we have already reported in *Gastroenterology* in 2009 and *Tumor Biology* in 2011 that DNA methylation analysis of gastric washes is useful to assess markers of cancer risk. However, this is the first analysis of gastric washes for *H. pylori*. Nevertheless, a large-scale prospective clinical trial with a more heterogeneous patient population is needed in order to compare biopsies and gastric washes more fully.

In summary, our procedure enables detection of *H. pylori* at higher sensitivity than qualitative tests, as well as quantification of multiple genotypes. Hence, this method might be useful to diagnose *H. pylori* infection, devise personalized treatment strategies, and measure or monitor the impact of treatments on drug-resistant strains. However, the approach was tested on a limited number of samples from patients with a narrow range of clinical characteristics and should be further evaluated in a large-scale prospective study with a more heterogeneous patient population.

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Authors' contributions S.M., Y.W., and H.Y. conceived the study, designed and executed experiments, analyzed data, prepared figures and tables, and wrote the manuscript. S.O. analyzed data, and K.M. helped write the manuscript. R.O. and S.M. executed experiments and analyzed data. S.O. and K.M. obtained clinical samples. M.K. designed experiments, analyzed data, and helped write the manuscript. F.I. provided intellectual support. T.K., M.K., and N.S. supervised all aspects of the study.

Compliance with ethical standards The study was conducted in accordance with all rules and regulations of the Hokkaido University Institutional Review Board (#014-0459), and informed consent was obtained from each patient.

Conflicts of interest None

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どこまで行う *Helicobacter pylori* 除菌療法

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KeyWords ◎*Helicobacter pylori* ◎胃癌予防 ◎除菌治療

Headline

- 1 胃がんは *Helicobacter pylori* 感染に伴って起こる感染症である。 *H. pylori* 除菌による胃がん予防効果についての臨床研究が報告されている。
- 2 わが国のコホート試験では、対象者の胃がん発症率が高い場合に、 *H. pylori* 除菌の胃がん抑制効果が明らかになっている。また、わが国のランダム化試験では *H. pylori* 除菌により早期胃がん内視鏡治療後の異時性がんは有意に抑制された。
- 3 初発がんに対するランダム化試験では、胃がん発症率が低いので、多数例の登録と長期間の観察が必要となるが、メタ解析では有意が出ている。ただ、 *H. pylori* 除菌の成功後も胃がんリスクは長期に継続することも分かっており、除菌後の経過観察も重要である。

胃の分化型および未分化型腺がんは *H. pylori* 感染に伴う慢性炎症を背景にして発症するので、胃がんは *H. pylori* 感染症の一つである。胃がんの発生病因は *H. pylori* 感染以外にもあるが、 *H. pylori* 感染に他の因子が加わることで発がんしやすくなる。すなわち、 *H. pylori* 未感染者に高濃度塩分の摂取等の環境因子や加齢因子が存在しても発がんは起こりにくい。一方、 *H. pylori* 感染者の全員に胃がんが起こるわけではなく、発がんには *H. pylori* 感染に伴う炎症状態が重要な役割を負っている¹⁾。 *H. pylori* 未感染者胃がんは胃がん全体の1%に満たない^{2,3)} (図1)。

H. pylori の除菌治療が胃がんの一次予防法として期待されている⁴⁾。これまで、スナネズミを用いた動物実験では除菌治療が有意に胃がん発生を抑制し、さらには早い時期に除菌したほうがその効果は強いという成績がある^{5,6)}。

初発胃がんに対する *H. pylori* 除菌効果

わが国から *H. pylori* 除菌群と対照群における胃がん発症率を比較したコホート試験がいくつ報告されている^{7~11)}。胃がん発症率が低い企

業健診者を対象にした試験では有意な結果を認めなかったが、胃・十二指腸潰瘍患者を対象に除菌成功群と非除菌群を3~5年の経過観察を行った四つの試験では、per protocol 解析では除菌群での胃がん発生が有意に少ない結果であった。また、台湾の national data base (NDB) を用いた大規模なコホート試験では、除菌まで平均1年を要した晩期除菌群よりも、すぐに除菌した早期除菌群での胃がん発生率は有意に低値であった¹²⁾。除菌が1年遅くなることで、その後の胃がん発生率に差が生じるとの成績であった。

初発胃がんに対する *H. pylori* 除菌の予防効果を検討したランダム化比較試験は、論文化されていないわが国の研究も含めて重複試験を除くと5試験ある^{13~18)}。平均7.3年の経過観察では有意差がなかったが、15年の経過観察報告で、 *H. pylori* 除菌群における胃がん発生は有意に抑制されたとの報告以外は、個々の試験では有意差を認めていない。初発がんを対象にした場合には、登録症例数に限りがあるために有意差が出るには15年以上の経過観察が必要である。最近のメタ解析ではリスク比が0.66(95%信頼区

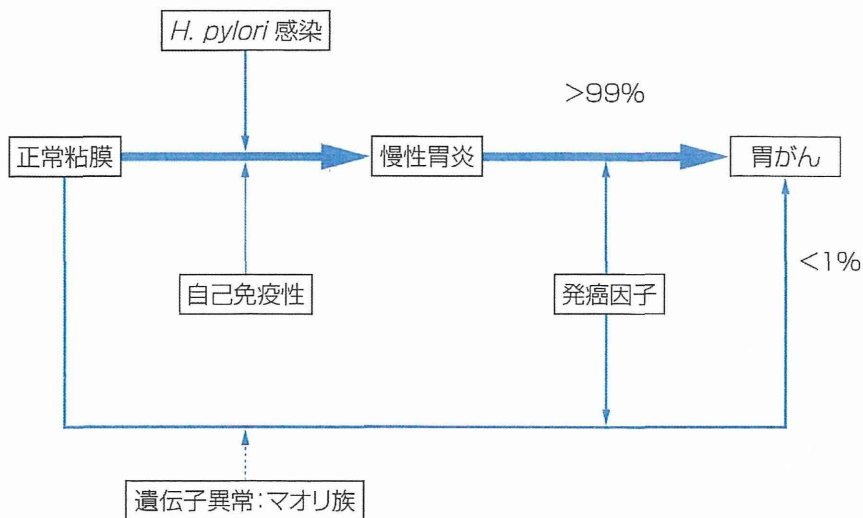


図1 胃癌発生と *H. pylori* 感染

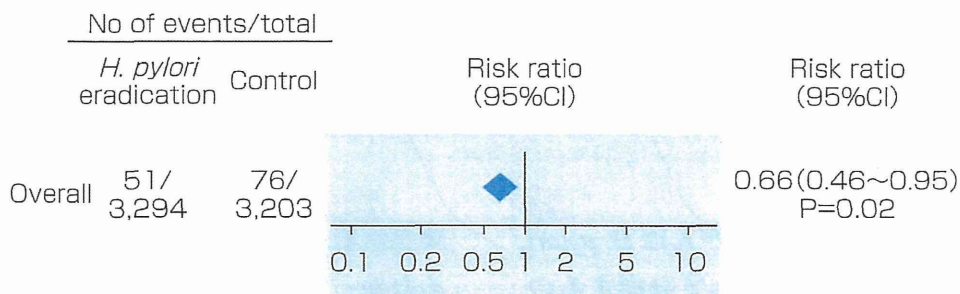


図2 初発胃癌に対する *H. pylori* 除菌のメタ解析

間 0.46-0.95) と *H. pylori* 除菌の胃癌予防効果が確認された¹⁹⁾ (図 2)。

内視鏡治療後の異時がんに対する *H. pylori* 除菌効果

早期胃癌の内視鏡的治療後に、胃癌再発病変として遺残再発や異時性多発がんを認めることは少ない。内視鏡的切除後の遺残再発については、経過観察中に切除痕に接してがんを再び認めたものと定義でき、不十分な内視鏡的治療が原因とされる。一方、内視鏡的切除後の経過観察中に、切除した部位とは別の部位に異時がん(二次がん)を認めることがある。異時がんの発生は内視鏡治療後長年に渡って年率 1~5% と一定の割合で続く。

これまで早期胃癌内視鏡治療後の異時がんに対する *H. pylori* 除菌効果を検討した論文は、ランダム化比較試験、非ランダム化比較試験、

後ろ向き試験が報告されている。Uemura らの非ランダム化比較試験では、早期胃癌の内視鏡的治療後に、*H. pylori* 除菌群と非除菌群に分け除菌群で有意に異時がんの発生が抑制された²⁰⁾。Japan Gast Study Group (JGSG) はランダム化試験として行い、異時がんの発生は有意差に除菌群で低く、不完全切除による遺残再発には有意差を認めなかった²¹⁾。除菌後最長 10 年(平均 5 年)までの長期観察で、*H. pylori* 除菌による胃癌抑制作用は長期間に渡って継続されている。韓国でのランダム化試験の成績では有意差を認めなかったが、わが国の試験とは登録時期が内視鏡治療直後である点に違いがある²²⁾。わが国の成績でも内視鏡治療直後に登録された群と内視鏡治療後の経過観察中に登録された群とでサブ解析すると、*H. pylori* 除菌に有意差を認めるのは経過観察群のみであった。内視鏡治療直後の群では、除菌時に存在していた見逃し

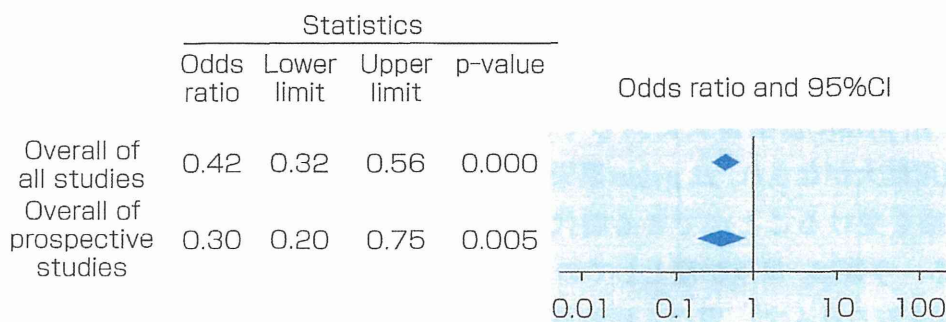


図3 異時胃癌に対する *H. pylori* 除菌のメタ解析

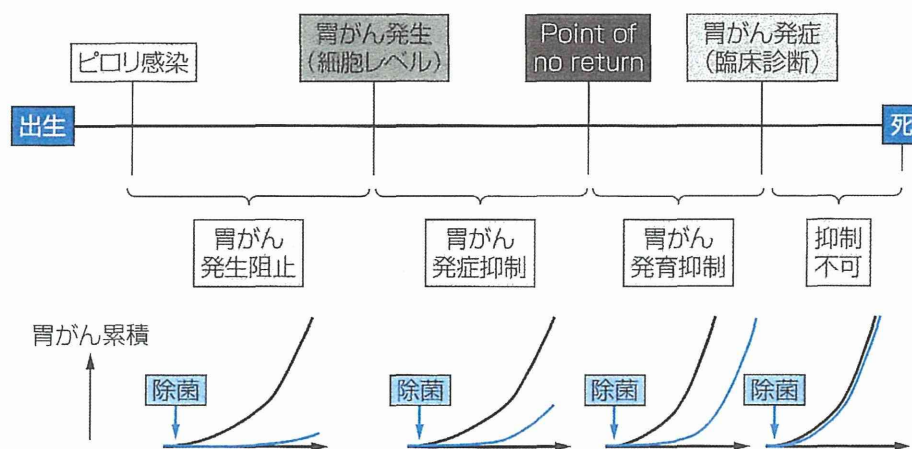


図4 *H. pylori* 除菌時期と胃癌の発育進展に与える影響

がんが早期の経過観察中に発見される割合が多くなるために、除菌効果がマスクされる。最近、前向き試験や後ろ向き試験のメタ解析が報告され、*H. pylori* 除菌治療が有意に異時がんの発生を抑制することが確認された(オッズ: 0.42, 95% CI: 0.32-0.56)²³⁾(図3)。

H. pylori 除菌による胃癌予防の限界

早期胃癌の成長速度は対数正規分布を示すことが報告されており、胃癌の発育速度は doubling time で評価できる²⁴⁾。胃癌細胞が発生してから、臨床的に胃癌と診断される5 mmの胃癌になる期間はおおよそ5~20年とされる。*H. pylori* 感染(A)から胃癌細胞の発生(B0)までは胃粘膜の炎症状態によるが通常は40~60年位はかかると考えられる。*H. pylori* 除菌が胃癌の発育進展に与える影響は除菌の時期によって異なり、A~B0では細胞レベルでの胃癌発生の阻止、B0~B1では胃癌発症の

抑制、B1~B2では胃癌の発育進展の抑制、B2~Cは抑制不可である(図4)。臨床試験ではB1の手前で除菌すると、胃癌発生は抑制できるが、B1を過ぎた時点で除菌を行っても最終的には胃癌が発症する。

除菌後症例を長期観察を行うと、除菌後10年以上経過しても胃癌の発生が認められることが明らかになった²⁵⁾。すなわち、*H. pylori* 除菌によって胃癌予防が可能であっても、除菌時期によっては、除菌後も胃癌リスクは長期に渡って継続する。したがって、*H. pylori* 除菌後も長期にわたって内視鏡検査を中心とした画像検査を続けることが非常に重要である。

おわりに

胃癌、肝がん、子宮頸がんは感染症が原因で、感染のコントロールによって予防が可能ながんである。わが国の胃癌死亡を減らすには、*H. pylori* 除菌による一次予防、胃癌サー

ベイルランスによる二次予防を組み合わせた胃がん予防策を軌道に乗せることが必要である²⁶⁾。2013年2月に *H. pylori* 感染胃炎に対して *H. pylori* 除菌の適用拡大がなされ、*H. pylori* 感染者全員が除菌治療を受けることができる時代になったといえる。今後は、保険診療としての *H. pylori* 除菌治療を取り込んで、胃がん検診を取り込んだ胃がん予防対策が重要である。除菌による胃がん予防効果は70歳以降でもある程度期待できるので、重篤な合併症がなく本人が除菌治療を受ける意志があれば高齢者は除菌を施行しない理由にはならない。

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