

การดื้อต่อยา amoxicillin ในเชื้อ *Helicobacter pylori* ซึ่งแยกได้จากผู้ป่วยไทย



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**AMOXICILLIN RESISTANCE IN *HELICOBACTER PYLORI* ISOLATED
FROM THAI PATIENTS**



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for the Degree of Master of Science in Medical Microbiology (Inter-Department)**

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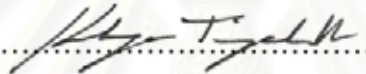
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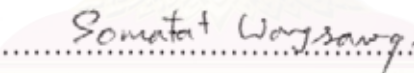
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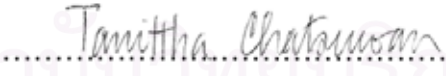
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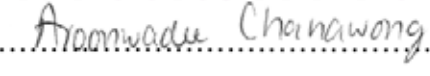
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ปริญญพร ประเสริฐสิน: การดื้อต่อยา amoxicillin ในเชื้อ *Helicobacter pylori* ซึ่งแยกได้จากผู้ป่วยไทย (AMOXICILLIN RESISTANCE IN *HELICOBACTER PYLORI* ISOLATED FROM THAI PATIENTS) อาจารย์ที่ปรึกษา : อ. ดร.ชนิษฐา ฉัตรสุวรรณ, 84 หน้า. ISBN 974-17-4802-7

Amoxicillin เป็นหนึ่งในยาปฏิชีวนะที่ใช้ในการรักษาโรคติดเชื้อ *Helicobacter pylori* ในปัจจุบันการดื้อต่อยา amoxicillin ของเชื้อ *H. pylori* มีแนวโน้มเพิ่มสูงขึ้นในหลายประเทศ การศึกษาครั้งนี้มีวัตถุประสงค์เพื่อหาความชุกของการดื้อต่อยา amoxicillin ของเชื้อ *H. pylori* ที่แยกได้จากผู้ป่วยไทย โดยตรวจหาค่า MIC โดยวิธี E-test และศึกษากลไกการดื้อต่อยา amoxicillin ของเชื้อ *H. pylori* โดยตรวจหาการกลายพันธุ์ของยีน *pbp1* โดยการเพิ่มปริมาณ DNA ด้วยเทคนิค PCR และหาลำดับเบสของยีน *pbp1* โดยวิธี DNA Sequencing เชื้อที่ใช้ในการศึกษาครั้งนี้แยกได้จากตัวอย่างชิ้นเนื้อของผู้ป่วยที่มารับการตรวจสอบกล้องส่องระบบทางเดินอาหาร ที่หน่วยระบบทางเดินอาหาร โรงพยาบาลจุฬาลงกรณ์ระหว่างเดือนสิงหาคม พ.ศ. 2546 ถึง เดือนมิถุนายน พ.ศ. 2547 จำนวน 357 คน สามารถเพาะแยกเชื้อ *H. pylori* ได้ 50 สายพันธุ์ (14%, 50/357) เมื่อทำการทดสอบหาค่า MIC ต่อยา amoxicillin ทุกสายพันธุ์พบว่า เชื้อจำนวน 49 สายพันธุ์ (98%) ให้ผลไวต่อยา amoxicillin และเชื้อจำนวน 1 สายพันธุ์ (2%) (MIC 0.75 µg/ml) ให้ผลดื้อต่อยา amoxicillin ซึ่งค่า MIC₅₀ มีค่า <0.016 µg/ml และค่า MIC₉₀ มีค่า 0.016 µg/ml เมื่อทำการวิเคราะห์ลำดับนิวคลีโอไทด์ในยีน *pbp1* ของเชื้อสายพันธุ์ที่ดื้อต่อยา 1 สายพันธุ์ (HP-1144) และสายพันธุ์ที่ไวต่อยาจำนวน 5 สายพันธุ์ โดยเปรียบเทียบกับ *H. pylori* 26695 พบว่าในสายพันธุ์ที่ไวต่อยาเกิดการเปลี่ยนแปลง amino acid ใน PBP1 42 ตำแหน่ง ได้แก่ 13, 16, 17, 35, 45, 79, 114, 120, 125, 148, 242, 243, 322, 324, 332, 352, 374, 392, 406, 408, 414, 432, 469, 479, 504, 508, 509, 515, 534, 535, 543, 547, 556, 589, 593, 595, 611, 648, 649, 653, 654, 656 และมี amino acid ขาดหายไปหนึ่งตำแหน่ง ส่วนสายพันธุ์ที่ดื้อต่อยาพบการเปลี่ยนแปลง amino acid 15 ตำแหน่ง ได้แก่ 17, 35, 79, 125, 148, 324, 479, 504, 508, 509, 515, 535, 543, 648 และ 649 โดยทั้ง 15 ตำแหน่ง ที่พบในสายพันธุ์ที่ดื้อต่อยานั้นเป็นตำแหน่งที่พบการเปลี่ยนแปลงในสายพันธุ์ที่ไวต่อยา นอกจากนี้ยังพบว่า การเปลี่ยนแปลงของ amino acid ใน PBP1 ในตำแหน่งที่ 406, 414, 515, 535, 543, 556, 593, 648, 649, และ 656 ที่มีผู้รายงานว่ามีความสัมพันธ์กับการดื้อต่อยา amoxicillin นั้น พบได้ในสายพันธุ์ที่ไวต่อยา เมื่อทำการทดสอบเอนไซม์ beta-lactamase โดยวิธี chromogenic cephalosporin ใน HP-1144 พบว่าเชื้อไม่สร้างเอนไซม์ beta-lactamase ดังนั้นกลไกการดื้อต่อยา amoxicillin ใน HP-1144 อาจจะไม่มีความสัมพันธ์กับการเกิดการกลายพันธุ์ ในยีน *pbp1* และการสร้างเอนไซม์ beta-lactamase แต่อาจใช้กลไกอื่นๆ ได้แก่ การลดการผ่านเข้าสู่เซลล์ของยา, การเปลี่ยนแปลง outer membrane protein และ efflux pump เป็นต้น

สาขาวิชาจุลชีววิทยาทางการแพทย์
ปีการศึกษา 2548

ลายมือชื่อนิสิต.....*ศุภณว ปะเสด็จสิน*.....
ลายมือชื่ออาจารย์ที่ปรึกษา.....*ดร.ชนิษฐา ฉัตรสุวรรณ*.....

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Amoxicillin is an important component of combination therapies for *Helicobacter pylori* eradication and there is an increasing rate of amoxicillin resistance in many countries. The purpose of this study is to investigate the prevalence of amoxicillin resistance in *H. pylori* isolated from Thai patients and to determine the molecular mechanism of amoxicillin resistance in *H. pylori* by detecting mutations in the *pbp1* gene. The minimal inhibitory concentration (MIC) of amoxicillin was examined by the E-test. Mutations in the *pbp1* gene were analyzed by PCR and DNA sequencing. Fifty *H. pylori* isolates were obtained from 357 patients (14%, 50/357) who underwent upper gastrointestinal endoscopy at King Chulalongkorn Memorial hospital between August 2003 to June 2004. Of the 50 isolates, 49 (98%) were susceptible to amoxicillin and only one isolate was resistant (2%) (MIC 0.75 µg/ml). MIC₅₀ and MIC₉₀ were <0.016 and 0.016 µg/ml, respectively. The DNA sequences of *pbp1* were determined by sequencing both amoxicillin – susceptible and amoxicillin – resistant *H. pylori* isolates. Of the 6 isolates, 5 were susceptible to amoxicillin (MICs range = < 0.016 – 0.25 µg/ml) and one isolate, HP-1144, was resistant to amoxicillin (MIC = 0.75µg/ml). When compared with amino acid sequence of PBP1 of *H. pylori* 26695 from GenBank, the result from this study showed forty-two different amino acid substitutions in both amoxicillin-sensitive and resistant isolates at positions 13, 16, 17, 35, 45, 79, 114, 120, 125, 148, 242, 243, 322, 324, 332, 352, 374, 392, 406, 408, 414, 432, 469, 479, 504, 508, 509, 515, 534, 535, 543, 547, 556, 589, 593, 595, 611, 648, 649, 653, 654, 656 and one amino acid deletion at position 400. Fifteen amino acid changes were shared among resistant and susceptible strains. All mutations in the resistant isolate, HP-1144, were found in susceptible isolates (positions 17, 35, 79,125,148, 324,479, 504, 508, 509, 515, 535, 543, 648 and 649). Interestingly, our results showed that mutations in PBP1 at position 406, 414, 515, 535, 543, 556, 593, 648, 649 and 656 which others investigators reported to be linked to amoxicillin resistance were present in our amoxicillin susceptible isolates. HP-1144 was tested for production of beta-lactamase using the chromogenic cephalosporin method and beta-lactamase activity was not detected. Therefore, mutation in PBP1 and production of beta-lactamase may not be associated with amoxicillin resistance in HP-1144. Other mechanisms must be involved in amoxicillin resistance such as decreased membrane permeability, alterations in OMPs and efflux pump.

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ABBREVIATIONS

A	adenosine
AC	amoxicillin
Ala (A)	alanine
Asn (N)	asparagine
Asp (D)	aspartic acid
Arg (R)	arginine
bp	base pair
C	cytidine
CO ₂	carbon dioxide
CH	clarithromycin
°C	degree Celsius
Cys (C)	cysteine
dATP	deoxyadenosine 5'-triphosphate
dCTP	deoxycytidine 5'-triphosphate
ddATP	dideoxyadenosine 5'-triphosphate
ddCTP	dideoxycytidine 5'-triphosphate
ddGTP	dideoxyguanosine 5'-triphosphate
ddTTP	dideoxythymidine 5'-triphosphate
DDW	double distilled water
ddNTPs	dideoxynucleotide-tri-phosphate
dGTP	deoxyguanosine 5'-triphosphate
DNA	deoxynucleic acid
dNTPs	deoxynucleotide-tri-phosphate
dTTP	deoxythymidine 5'-triphosphate
DW	distilled water
EDTA	ethylenediamine tetraacetic acid
<i>et al.</i>	<i>et alii</i>
E- test	epsilometer test

ABBREVIATION (CONTINUED)

g	gram
G	guanosine
Gly (G)	glycine
Glu (E)	glutamic acid
Gln (Q)	glutamine
HCl	hydrochloric acid
HPLC	high performance liquid chromatography
hr	hour
His (H)	histidine
i.e.	id test
Ile (I)	isoleucine
Lys (K)	lysine
Leu (L)	leucine
M	molar
mg	milligram
MgCl ₂	magnesium chloride
MIC	minimum inhibitory concentration
min	minute (s)
ml	milliliter
mM	millimolar
mmol	millimole
Met (M)	methioine
NaCl	sodium chloride
Na ₂ HPO ₄	sodium phosphate dibasic, anhydrous
NaOH	sodium hydroxide

ABBREVIATION (CONTINUED)

NCCLS	National Committee for Clinical Laboratory Standards
Phe (F)	phenylalanine
PCR	polymerase chain reaction
<i>Pfu</i>	<i>Pyrococcus furiosus</i>
pmol	picomol
Pro (P)	proline
sec	second
Ser (S)	serine
T	thymidine
TAE	tris-acetate-EDTA
Thr (T)	threonine
Tris	Tris-(hydroxymethyl)-aminoethane
Trp (W)	tryptophan
Tyr (Y)	tyrosine
U	unit
µg	microgram
µl	microliter
µM	micromolar
UV	ultraviolet
V	volt

CHAPTER I

INTRODUCTION

Helicobacter pylori is a Gram – negative curved rod or spiral microaerophilic bacterium that colonizes in the gastric mucosa of the distal portion of the human stomach (1, 2). *H. pylori* infection has a worldwide distribution. More than half of the world's population is infected. However, its prevalence varies widely according to different geographic areas, age, race and socioeconomic status. Colonization of the human stomach by *H. pylori* is usually associated with peptic ulcer disease, gastritis, gastric cancer and mucosa-associated lymphoid tissue lymphomas (2-5). Use of a single antibiotic or an antibiotic combined with bismuth is ineffective. Successful treatment of *H. pylori* infection most often use two or more antibiotics and the addition of either bismuth or a proton pump inhibitor (6-9). Triple therapy, in with a bismuth or proton pump inhibitor is combined with two antibiotics from clarithromycin, metronidazole, amoxicillin and tetracycline, is the most widely used regimen. Eradication rates of approximately 90% are obtained by using these regimens (9). However, antibiotic resistance has been reported and is one of the major causes of treatment failure. The prevalence of antibiotic resistance varies with geographical regions. Many studies have indicated that prevalence of metronidazole and clarithromycin resistance varies between 9%-80% and 1.7% - 46.4% respectively, with the highest prevalence occurring in people from developing countries (10-20). Amoxicillin resistance has been reported to be rare, however, recent data from Bangladesh, Thailand, Mexico and China have shown an increasing rate of amoxicillin resistance, ranging from 6.6% to 71.9% (10, 20-22).

Amoxicillin is a beta-lactam antibiotic that binds to penicillin-binding proteins (PBPs). Resistance to beta-lactam in Gram-negative bacteria is most often due to the production of beta-lactamase. Other resistance mechanisms include alterations in PBPs, decreased membrane permeability of antibiotic into the bacterial cell, or combination of these resistance strategies (23, 24). It has been demonstrated that resistance to amoxicillin in *H. pylori* was associated with mutations in the *pbp1* gene (25-27) and beta-lactamase activity was not detected in amoxicillin-resistant isolates

(25-31). Amoxicillin is often used in *H. pylori* treatment regimens and there is an increasing rate of amoxicillin resistance in many countries. Therefore, it is important to update amoxicillin susceptibility in *H. pylori* isolated from Thai patients. The purpose of this study is to investigate the prevalence of amoxicillin resistance in *H. pylori* isolated from Thai patients and to determine the molecular mechanism of amoxicillin resistance in *H. pylori* by detecting mutations in the *pbp1* gene.



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CHAPTER II

OBJECTIVES

- I. To investigate the prevalence of amoxicillin resistance in *H. pylori* isolated from Thai patients.
- II. To determine mutations in the *pbp1* gene in amoxicillin-resistant *H. pylori*.



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CHAPTER III

LITERATURE REVIEW

1. BACTERIOLOGY

Helicobacter pylori was first isolated from a stomach biopsy by Warren and Marshall in 1982 (1) and initially named *Campylobacter pyloridis* because of phenotypic characteristic similar to those of *Campylobacter*. However, it was found to be different from other *Campylobacter species* and has been reclassified to a new genus, *Helicobacter*, and given the species name *H. pylori*. *H. pylori* is a Gram-negative spiral or curved rod bacterium. It is typically 0.2 to 1.2 μm in diameter and 1.5 to 10 μm in length and have rounded ends (2). It is typically located in the mucosa of the distal portion of the human stomach. This bacterium is unusual in having sheathed flagella with terminal knobs. It has four or seven unipolar-sheathed flagella (2). *H. pylori* has a spiral shape in young cultures but can assume coccoid forms in older cultures. It has corkscrew motility. This bacterium is microaerophilic and slow growing in culture media. Growth of *H. pylori* requires complex medium with supplementation such as whole blood, heme or serum. Colonies are small and translucent and normally take 3-5 days at 37 °C under microaerophilic condition to appear (32, 33). *H. pylori* grows best in freshly prepared medium. An important characteristic is its ability to produce an abundance of urease. Urease production is a consistent finding in *H. pylori* that colonizes the human stomach. Furthermore, *H. pylori* produces other enzymes, including catalase, oxidase, lipase, mucinase, and hemolysin. A vacuolating cytotoxin (VacA) is responsible for epithelial cell damage (34).

2. EPIDEMIOLOGY

H. pylori is found primarily in human and may be the most common bacterial infection in human. Many people appear to be infected with *H. pylori* and have no clinical disease. The outcome of infection is affected by many factors, including strain, host genotype characteristics and organism density within the stomach.

H. pylori infection has a worldwide distribution. More than half of the world's population is infected. However, the prevalence of *H. pylori* infection varies widely according to different geographic areas, age, race, and socioeconomic status (35-37). In developing countries with poor socioeconomic condition, 70% to 90% of the population is infected. In the other hand, in developed countries, the prevalence of infection is lower, ranging from 25% to 50%. In Thailand, the prevalence of *H. pylori* infection has been reported to be upto 50% in children at the age of 8 to 9 years, whereas the seroprevalence in person older than 30 years is 75% (38, 39). It appears to be no substantial reservoir of *H. pylori* aside from the human stomach. The major question of transmission is how *H. pylori* travel from the stomach of one person to that of another. Possible routes of transmission include, fecal-oral (40, 41), oral-oral and gastro-oral (42, 43).

3. CLINICAL DISEASE

H. pylori colonizes the stomach of human. This ability may be due in part to the production of the urease, which splits urea into ammonia and creates an alkaline microenvironment around the microorganism. *H. pylori* appears to specifically adhere to stomach mucosa (1), and the ammonia and possible toxins it produces may cause injury to the adjacent gastric epithelium. This leads to inflammation and is associated with clinical manifestations such as pain, gas, painful digestion, foul breath, vomiting and nausea. Tissue damage leads to ulcer in the stomach and duodenum. On the other hand, many persons harbor *H. pylori* in their stomachs and remain asymptomatic. Most persons who are infected with *H. pylori* never suffer from any symptoms related to the infection; however *H. pylori* causes chronic active and chronic persistent gastritis in adults and children. Infection with *H. pylori* also causes duodenal and gastric ulcers. Infected persons have a 2-to-6 fold increased risk of developing gastric cancer and mucosal-associated-lymphoid-type (MALT) lymphoma compared with their uninfected counterparts. The role of *H. pylori* in non-ulcer dyspepsia remains unclear (1, 44, 45).

4. DIAGNOSIS OF *H. PYLORI* INFECTION

The numerous tests and strategies have been developed to detect *H. pylori*. Infection of the stomach with *H. pylori* can be diagnosed by both invasive and noninvasive techniques (Table 1). The invasive methods require endoscopy and biopsy. These consist of histological examination, culture, urease test and polymerase chain reaction. Noninvasive methods do not require endoscopy and biopsy. These include serologic test, urea breath test and detection of *H. pylori* antigen in stool specimen. The choice of test used for diagnosis of *H. pylori* infection will depend in most cases, on the clinical information sought and the local availability and cost of individual test.

4.1 Invasive methods

4.1.1 Histology

The histological identification of *H. pylori* infection is now a widely used mean of diagnosis. Different techniques of staining (Giemsa, Warthin Starry, Hematoxylin-Eosin) are available for detection of *H. pylori*. Biopsy samples are obtained from the grossly normal appearing gastric mucosa. Prepyloric antrum has been the preferred site of biopsy. The sensitivity and specificity of histologic analysis approach 95 % to 100 % (46).

4.1.2 Urease test

A rapid urease test is an initial test of choice for the diagnosis of *H. pylori* at endoscopy in many units. It is the most rapid way to diagnose *H. pylori*. Urease activity can be measured directly in the gastric biopsy or after the microorganism has been isolated. Its low cost, ease, and excellent specificity make the rapid urease test a valuable diagnostic tool. The activity of the *H. pylori* urease enzyme splits the urea test reagent (or media agar) to form ammonia. Ammonia increases pH, which is detected by the indicator phenol red. There are numerous types of Rapid Urease Tests (RUT) on the market such as gel tests (CLOtest[®]) or paper tests (PyloriTek[®]). In pretreatment, the sensitivity of RUTs ranges from 80 % to 95 %, while the specificity

range is 95 % to 100 % (47, 48). The sensitivity is dependent on the number of bacteria present in the gastric biopsy.

4.1.3 Polymerase Chain Reaction (PCR)

This technique is reputed to be highly sensitive and specific. The PCR consists of amplifying DNA sequences specific for *H. pylori* in gastric biopsy specimens. Factors affecting test accuracy include the choice of primers and target DNA, specimen preparation, bacterial density and technical issues regarding the PCR procedure. PCR test for *H. pylori* have been described for a number of genomic targets, such as urease gene, and virulence genes (such as *cagA*, *vacA*, *iceA*), or mutations causing macrolide resistance (49, 50).

4.1.4 Culture of *H. pylori*

Culturing *H. pylori* is difficult, timeconsuming, and expensive, and is an impractical mean of establishing the diagnosis of infection. Culture is used in controlled clinical trials of treatment of the infection. Currently, the emergence of resistant strains has rendered culture necessary (2), because it is the only method, which allows antimicrobial susceptibility testing for the isolates. To succeed in culturing *H. pylori*, special care must be taken during handling and processing of the gastric biopsy specimen (2). *H. pylori* lose its viability quickly when exposed to the environment, and biopsies should be cultured immediately to maximize the recovery of bacteria. *H. pylori* is a fastidious bacteria (2). Gastric biopsy can be transported in saline if it is to be processed within 3 hours, but transport medium must be used if the transport time will be longer. The clinical specimen should also be kept on ice before inoculation. Although, the sensitivity of culture in experienced laboratories is greater than 95 %. Culture of gastric biopsy specimens typically provides the greatest yield of *H. pylori*. Several transport media have been suggested, including normal saline, 20% glucose, and Stuart transport medium. Saline is a simple acceptable short term transport medium (51). If the culture is to be delayed more complex media such as supplemented brain heart infusion broth, horse serum, should be used (52). The transport media containing glycerol are suitable for long-term storage of biopsy specimen at -70°C , or the specimens can be immediately frozen at -70°C without a

fluid medium (53). Over the years, there have been a number of reports on the media that can be used for the successful culture of *H. pylori*. Originally, Marshall *et al.*, (1) used brain heart infusion chocolate agar supplemented with 7 % horse blood. Subsequently, a variety of selective media and nonselective media, or a combination of both have been proposed for use in the primary isolation of *H. pylori* (1, 54, 55), but the optimal method of recovery still remains to be established. Numerous agar media including brain heart infusion agar, brucella agar, Columbia agar, Wilkins Chalgren agar, or Shirrow's agar supplemented with horse blood, horse serum, or sheep blood have been used to cultivate *H. pylori*. Primary isolation of *H. pylori* from gastric biopsy specimens on enriched media with and without antibiotic must be freshly prepared and incubated at 37 °C for 7 to 10 days under microaerophilic conditions (5-10% CO₂, 5-10% O₂, 80-90% N₂). Colonies of *H. pylori* are small, translucent and smooth. Identification involves microscopic examination and detection of enzyme (urease, catalase, and oxidase). Isolates were identified as *H. pylori* on the basis of positive urease, catalase and oxidase reactions.

4.2 Noninvasive Methods

4.2.1 Serological test

Infection with *H. pylori* stimulates a humoral immune reaction that persists as the result of continuous exposure to the bacteria. Because the antibody titers persist for many years, the test cannot be used to discriminate between past and current infection. In response to *H. pylori* infection, the immune system typically mounts a response through production of immunoglobulins to *H. pylori*-specific antigens (56). These antibodies can be detected in serum or whole – blood. Serologic test offers a fast, easy and relatively inexpensive mean of identifying patients who have been infected with *H. pylori* (56, 57). However, this method is not a useful means for confirming eradication of *H. pylori*. Serological test can only diagnose the infection and not any specific condition such as peptic ulcer or gastric cancer. Serological test was the first noninvasive method based on the detection of a specific anti- *H. pylori* IgG antibody in patient's serum (58). Persistent antibodies will lead to false- positive results. Numerous formats have been developed for the detection of specific

antibodies to *H. pylori*. These consist of latex agglutination, capillary, and enzyme-linked immunosorbent assay (ELISAs) (59).

4.2.2 Urea breath test (UBT)

H. pylori is a strong producer of urease, an enzyme that splits urea into ammonia and CO₂. The UBT is based on this principle. Carbon-labeled urea is given to a patient. The label used can be a ¹³C or a radioactive ¹⁴C (60). If *H. pylori* is present, its urease activity hydrolyses the labeled urea and the isotope is expelled as ¹³CO₂ or ¹⁴CO₂. If *H. pylori* is not present the labeled urea passes through the stomach intact and ¹³CO₂ or ¹⁴CO₂ will not be found in breath samples. ¹³C-labeled ureas has the advantage of being non radioactive and thus safer for children and pregnant females. At certain intervals after ingestion breath samples are collected and the amount of radio-labeled CO₂ is measured. Sensitivity of UBT is in the range of 90%, whereas specificity is approximated to 100% (61).

4.2.3 Stool antigen testing

Stool antigen testing is a relatively new methodology that uses an enzyme immunoassay to detect the presence of *H. pylori* antigen in stool specimen (62, 63). It is a cost effective and reliable means of diagnosis of active infection and confirming cure, and has a sensitivity and specificity comparable to those of other noninvasive tests (64). The *Helicobacter pylori* stool antigen (HpSA) test may be useful for the primary diagnosis of *H. pylori* infection. Its specificity is similar to other standard tests but its sensitivity is lower. It was found that HpSA was positive in 66.7 % of gastric ulcer disease and 80 % of duodenal ulcer disease (63).

Table 1 Summary of methods for detection of *H. pylori* (48, 60, 65, 66).

Method	Sensitivity (%)	Specificity (%)	Advantages	Disadvantages
Invasive Histology	93-99	95-99	Widely available; detection best with special stains; can evaluate underlying mucosal damage; gold standard	Expensive ; at least two biopsies required ; observer error; recent antibiotics or proton pump inhibitor use can lead to false negative results
Culture of biopsy specimen	77-92	100	<i>In vitro</i> antibiotic susceptibility can be determined	Expensive; organism requires special transfer and culture technique; requires up to 1 wk for results; recent antibiotics or proton pump inhibitor use can lead to false-negative results
Rapid urease test CLOtest hpFast PylorTek	89-98	93-98	Rapid results ; easy to perform ; less expensive than other invasive techniques	Formalin, simethicone, local anesthetic spray, recent antibiotics, bismuth, or proton pump inhibitor use can lead to false-negative results; poor technique or handling will affect results
Noninvasive Urea breath test ¹³ C ¹⁴ C	90-100	89-100	Inexpensive ; represents entire mucosa (not subject to biopsy sampling bias)	Antibiotics or proton pump inhibitor use can lead to false-negative results; presence of ulcer disease not determined; can be difficult to collect in children younger than 2 year of age
Serology (ELISA) HM-CAP Pylori.STAT Rapid serology FlexSure QuixVue	44-99	89-95	Inexpensive ; good for screening or epidemiologic studies in older children but not for diagnosis	Possible cross-reactivity with similar bacteria; remains positive for a variable period after successful treatment; not accurate in children younger than 6 yr of age; currently available rapid office-based tests require serum
Stool antigen testing (HpSA)	85-94	97.7	Inexpensive, more accurate test of choice in children	Stool must be collected

5. TREATMENT OF *H. PYLORI* INFECTION

H. pylori is the cause of active chronic gastritis, a necessary factor in the peptic ulcer and a risk factor in the development of gastric cancer (67, 68). Treatment of *H. pylori* infection decreases these diseases. Maastricht guidelines (69) strongly recommended eradication therapy for unequivocally diagnose *H. pylori* positive patients with duodenal or gastric ulcer, low grade MALT gastric lymphoma, gastritis with severe early gastric cancer. Several eradication regimens have been applied, varying in the choice of antibiotic agents, dose and duration of treatment.

The most common antibiotics used for the treatment of *H. pylori* infections are clarithromycin, metronidazole, tetracycline and amoxicillin. Other antibiotics, such as fluoroquinolones or furazolidone have been used by some authors only. However, an antibiotic alone is not able to eradicate *H. pylori*. Some anti-ulcer compounds must be used, such as bismuth salts (subcitrate or subsalicylate), H₂ antagonists (ranitidine, ebrotidine, etc), proton pump inhibitors (omeprazole, lansoprazole, pantoprazole), or more recently, ranitidine bismuth citrate. These compounds play a role by increasing the pH allowing antibiotics to act against *H. pylori* (70-73).

Monotherapy with antibiotics is unsuccessful in the treatment of *H. pylori* because of the low efficacy of currently available drugs and the rapid emergency of bacterial resistance to them. In recent years, triple therapies is first line therapy for the eradication of *H. pylori* infection (6, 9, 74-79). Triple therapy, including proton pump inhibitors (PPI), ranitidine bismuth citrate, plus 2 antibiotics (clarithromycin plus amoxicillin, tetracycline or metronidazole).

Clarithromycin

Clarithromycin is a macrolide antibiotic that inhibits bacterial protein synthesis. Its antibacterial spectrum is similar to that of erythromycin, but it is more acid-stable, better absorbed, and more effective against *H. pylori*. As with metronidazole, resistance can develop when clarithromycin is given alone (80). Clarithromycin commonly causes an alteration of taste sensation that can be

sufficiently unpleasant to cause the cessation of treatment. It is also the most expensive of the antimicrobial drugs used to treat *H. pylori* infection.

Tetracycline

H. pylori is also very sensitive to tetracycline which inhibits bacterial protein synthesis and, like amoxicillin, appears to act lumenally or topically. It is active at low pH. It should not be given to pregnant women or children because it causes permanent staining of developing teeth.

Metronidazole

Metronidazole is a mainstay of triple therapy for *H. pylori* infection. The organism ordinarily is highly sensitive to metronidazole. Metronidazole is actively secreted into the gastric juice and saliva, and therefore is active after absorption, with a half-life of 8 to 12 hours. Its activity is relatively independent of pH (81). Mutant organisms with defective nitroreductase activity are resistant to metronidazole (82), and rates of resistance are very high in areas of the world where it is used frequently for other reasons such as gynecological infections and parasitic infections (83). The side effects of metronidazole include neuropathy and, when alcohol is consumed, flushing and gastrointestinal symptoms. Tinidazole is a related drug with similar properties and side effects.

Amoxicillin

H. pylori is very sensitive *in vitro* and *in vivo* to amoxicillin. It acts by inhibiting the synthesis of bacterial cell walls. It has topical or intraluminal activity, and although stable in an acid environment, it is most active at a neutral pH (84). Unlike ampicillin, a related compound, amoxicillin is actively secreted from blood into the gastric juice, (81) and intravenous amoxicillin can therefore eradicate *H. pylori* infection (85). Bacterial resistance to amoxicillin has been rarely reported. The side effects of amoxicillin include diarrhea, allergic reactions, and pseudomembranous colitis.

6. ANTIBIOTIC RESISTANCE OF *H. PYLORI*

H. pylori is susceptible to most antibiotics *in vitro*, but when used alone, eradication of the organism from the gastric mucosa is not obtained. Factors implicated in treatment failure, include a lack of penetration by pH, lack of compliance by the patients, lack of correlation between *in vitro* susceptibility test and *in vivo* efficacy, and the presence of *H. pylori* strains with primary or acquired resistance to the antibiotics used.

In recent years, standard therapy regimens for treating *H. pylori* infection are multiple antibiotics in combination with proton pump inhibitors (PPI). Antibiotics that are frequently included in triple therapy (6, 9, 74, 76, 86, 87) regimens are clarithromycin, metronidazole, tetracycline and amoxicillin. In addition to the lack of compliance of the patient with the treatment, emergence of antibiotic resistance has become an increasing problem leading to the therapy failure. The prevalence of antibiotic-resistant *H. pylori* varies among different geographical areas but generally has been increasing worldwide (Table 2).

EPIDEMIOLOGY OF ANTIBIOTIC RESISTANCE IN *H. PYLORI*

Reports on the isolations of *H. pylori* with antibiotic resistance are increasing worldwide, with a high frequency in particular geographical area. The most common acquired resistance of *H. pylori* is to: metronidazole, clarithromycin, tetracycline and amoxicillin (11, 13-17, 22, 88). Prevalence of *H. pylori* resistant to antibiotic previously reported and shown in Table 2. Resistance to tetracycline is very low (11, 17, 18, 89, 90), or even absent, in most countries, such as in Spain (0 %) (90), the UK (0.5%) (89), and North Wales (0.27%) (11). However, a higher rate of tetracycline resistance was also found in Brazil (7 %) (91), Bangladesh (15 %) (10), and China (58.8 %) (21). Resistance increases with the use of antibiotic due to selective pressure. Resistance to amoxicillin is rare. Very high resistance rates to amoxicillin have been reported in some studies with a range 18 % to 71.9 % (20, 21, 91). Metronidazole resistance is more prevalent in developing countries (10) as it is widely prescribed to patients with giardiasis, amoebiasis and protozoan infections, and in women probably as a consequence of metronidazole use for gynecological conditions (92).

Metronidazole resistance varies from 21.12 % to 80 %. (10, 11, 14, 16-22, 93-95). The prevalence of primary clarithromycin resistance is increasing world wide. Prevalence rates vary from 1.7 % to 46.4 % (10-20, 22, 89-91, 94-100). A strict policy of antibiotic use is necessary to limit the spread of antibiotic resistance and surveillance programmes should be implemented at regional levels.



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Table 2 Prevalence of antibiotic resistance amongst *H. pylori* in different geographic areas.

Country/region	Year (collected)	No.of test isolates	Percentage of antibiotic resistance				Reference
			CH	MZ	TC	AC	
Netherlands	1997-1998	231	1.7	21.2	0	0	(18)
Bulgaria	1989-2000	115	12.4	15.8	ND	0	(15)
North Wales	2000-2003	363	7	24	0.27	0	(11)
Belgium	2000-2001	555	16	18	ND	0	(96)
France	1994-1999	150	21	43	ND	0	(97)
Poland	1998-2000	98	23.5	ND	ND	ND	(98)
UK	1994-1999	1064	4.4	40.3	0.5	0	(89)
Germany	1998*	172	2	21	ND	0	(99)
Spain	1991-1995	282	3.5	19.9	0	0	(90)
European multicentre	1997-1998	1,274	9.9	33.1	ND	0.8	(14)
Brazil	2000*	90	7	42	7	29	(91)
Austria	1997-2000	117	20.3	16	ND	0	(100)
Mexico	1995-1997	195	24	80	ND	18	(20)
Lebanon	2002*	45	4	29.5	2	0	(19)
Israel	2000-2001	138	46.4	60.7	0	0.72	(17)
U.S.A	1993-1999	3624	10.1 (360/3571)	36.9 (1063/2883)	ND	1.4 (48/3486)	(16)
Bangladesh	1999-2001	120	10	77.5	15	6.6	(10)
Singapore	1993-1996	495	ND	62.7	ND	ND	(93)
Korea	1996-2000	224	5.4	41.9	ND	ND	(94)
Korea	1994-1999	456	5.9	40.6	5.3	0	(95)
Japan	1996-2003	149	34.7	12.5	ND	0	(12)
Japan	1995-2000	593	11	9	ND	0.3	(13)
Thailand	2001-2002	79	19	30.4	5.1	13.9	(22)
China	1998-1999	153	ND	77.8	58.8	71.9	(21)

CH, clarithromycin; MZ, metronidazole; TC, tetracycline; AC, amoxicillin; and ND, not determined; * year published

7. AMOXICILLIN RESISTANCE

BETA-LACTAM ANTIBIOTIC

Beta-lactam belongs to a family of antibiotic, which is characterized by a beta-lactam ring. Penicillins, cephalosporins, monobactams and carbapenems are members of this antibiotic family (Figure 1). They are potent, broad-spectrum bactericidal agents of low toxicity with widespread clinical use. All beta-lactam antibiotics are bactericidal, and act by inhibiting the synthesis of the peptidoglycan layer of bacterial cell walls. The peptidoglycan layer is important for cell wall structural integrity, especially in Gram-positive organisms (101). The final transpeptidation step in the synthesis of the peptidoglycan is facilitated by transpeptidase known as penicillin-binding proteins (PBPs) (102). Beta-lactam antibiotics are analogues of D-alanyl-D-alanine the terminal amino acid residues on the precursor NAM/NAG-peptide subunits of the nascent peptidoglycan layer. The structural similarity between beta-lactam antibiotics and D-alanyl-D-alanine facilitates their binding to the active site of PBPs (103). The beta-lactam nucleus of the molecule irreversibly binds to (acylates) the serine residue of the PBP active site (103). This irreversible inhibition of the PBPs prevents the final cross-linking (transpeptidation) of the nascent peptidoglycan layer, disrupting cell wall synthesis. Inhibition of PBPs may also lead to the activation of autolytic enzymes in the bacterial cell (104).

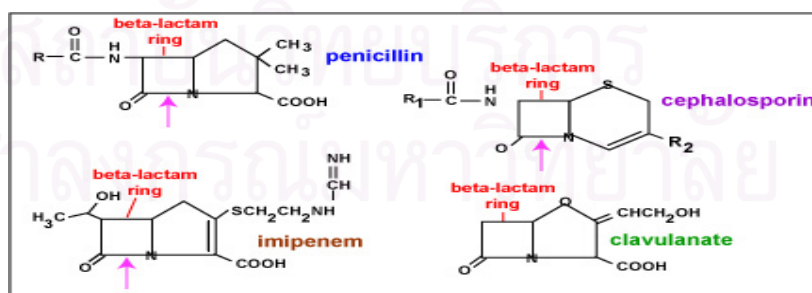


Figure 1 Chemical structure of beta-lactam antibiotics.

AMOXICILLIN

Amoxicillin is a penicillin derivative belonging to a group of beta-lactam antibiotics. This chemical modification of penicillin extends the clinical properties of antibiotic, resulting in broader spectrum activity agents Gram-negative bacteria, more complete gastrointestinal absorption and little or no effect on the interaction with food (105). The drug acts as a bactericidal agent and binds to beta-lactam receptor proteins, which are involved in cell-wall synthesis and destruction (104). Amoxicillin is often used in *H. pylori* eradication.

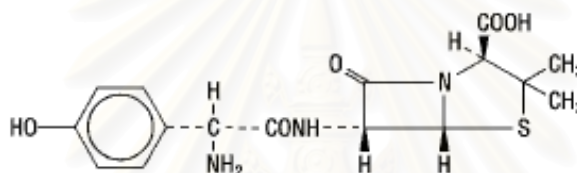


Figure 2 Chemical structure of amoxicillin.

MECHANISM OF BETA-LACTAM RESISTANCE

Resistance to beta-lactam antibiotics by Gram-negative bacteria is most commonly due to the production of beta-lactamase, either chromosomally-encoded or, more often, plasmid-mediated (106). Other important mechanisms of resistance include alterations in PBPs, decreased permeation of the antibiotic into the bacterial cell, or combinations of these resistance strategies (107). Active efflux pumps which excrete drugs, including multidrug efflux pumps, can also confer resistance to beta-lactams (108).

The major bacterial beta-lactam resistance mechanisms (Figure 3) belong to one of the following categories:

1. Enzymatic inactivation (Beta-lactamase)

Many bacteria become resistant to antibiotics by producing various beta-lactamases that are able to inactivate some forms of these drugs. Beta-lactamases break the beta-lactam ring of the antibiotics, thus destroying the drugs (24).

2. Alteration of the target site

PBPs are a group of enzymes (peptidoglycan transpeptidases) which are target sites of beta-lactam antibiotics. Changing the structure of PBPs greatly reduces affinity for binding of bacteria to these antibiotics (24).

3. Reduction in permeability

Antibiotic efflux pumps are a common way for bacteria to resist the action of numerous classes of antibiotics. Most of these pumps use protons as the motive force for efflux. A similar mechanism of resistance involves the alteration of the porin binding proteins in the Gram-negative outer membrane to limit the access of drugs to the periplasmic space (24).

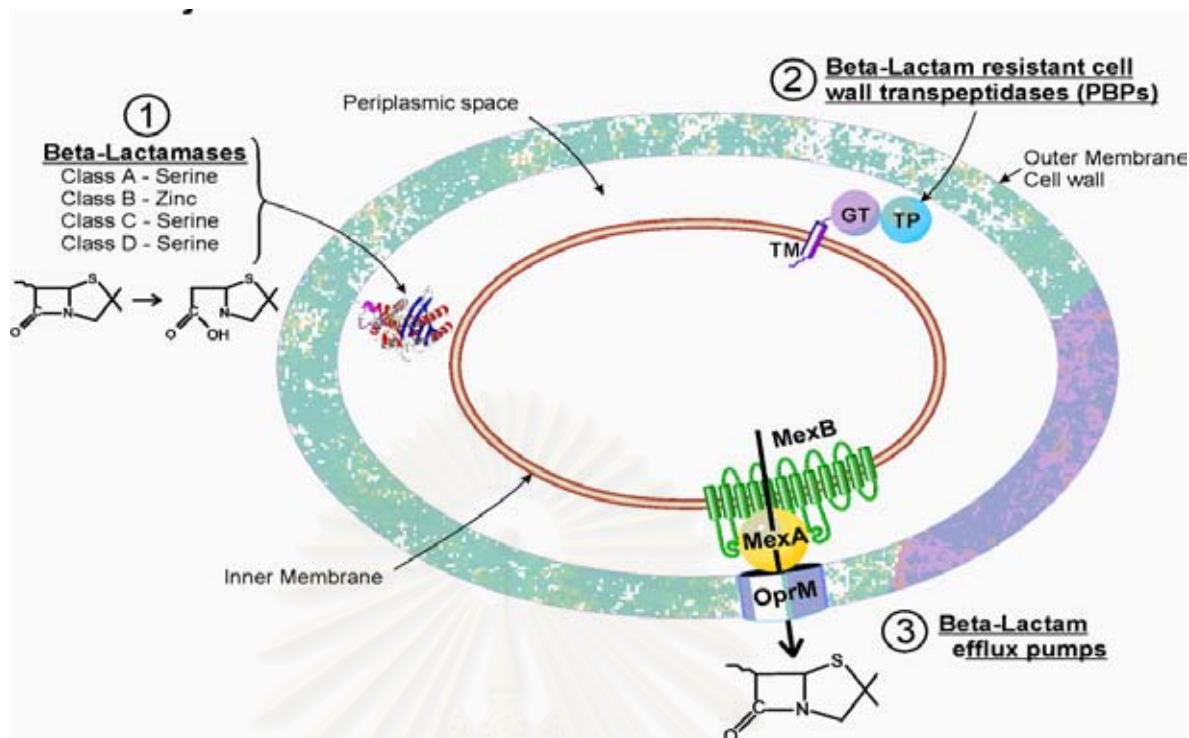


Figure 3 The major bacterial beta-lactam resistance mechanisms.

AMOXICILLIN RESISTANCE IN *H. PYLORI*

Amoxicillin is the only beta-lactam used to treat *H. pylori* infection. The molecular mechanisms of *H. pylori* strain resistance to amoxicillin are unclear. Resistance to beta-lactams in Gram-negative bacteria is most often, due to the production of beta-lactamase. However, beta-lactamase activity was not detected in *H. pylori* isolates resistant to amoxicillin (25-27, 29, 30), suggesting that this is not the mechanism in *H. pylori*. Another mechanism of bacterial resistance to amoxicillin is modification of the bacterial cell wall target, i.e., PBPs.

PBPs are a set of enzymes found in the cytoplasmic membrane of bacteria that are required for the biosynthesis of the bacterial cell wall (109, 110). PBPs catalyze the final steps of the polymerization (transglycosylation) and cross-linking (transpeptidation) of peptidoglycan, an essential component of the bacterial cell wall. PBPs are membrane-bound enzymes and targets of beta-lactam antibiotic (109). Covalent binding of beta-lactams to PBPs results in the inability of the bacterium to

built a complete cell wall, leading to cell lysis. Initial studies with *H. pylori* indicated the presence of three high-molecular-weight PBPs, designated PBP1A, PBP2 and PBP3 (29). Later a fourth, low-molecular-weight PBP, PBP4 was identified (111).

Modification of PBPs leading to decreased affinity for antibiotics accounts for a relatively low level resistance and a stepwise increase over time in MIC values. Dore *et al.*, (28) found that one of four PBPs that are normally present in amoxicillin susceptible *H. pylori* strain was missing in the amoxicillin resistance *H. pylori* strain, suggesting that modification of PBP may be responsible for the amoxicillin resistance. It has been reported that *H. pylori* resistant to amoxicillin was associated with alteration in the *pbp1* gene (25-27, 30). Kwon *et al.*, (30) found that ten amino acid changes in PBP1 of amoxicillin-resistant *H. pylori* clinical isolate (MIC 64 µg/ml). These amino acids include position 406 from glutamic acid to alanine, 417 from serine to threonine, 515 from methionine to isoleucine, 535 from aspartic acid to asparagine, 543 from serine to arginine, 556 from threonine to serine, 562 from asparagine to tyrosine, 648 from lysine to glutamine, 649 from arginine to lysine and 656 from arginine to proline. In addition, Okamoto *et al.*, (27) reported four amino acid changes in PBP1 of amoxicillin-resistant *H. pylori* clinical isolate (MIC 8 µg/ml), including at the position 69 from alanine to valine, 556 from threonine to serine, 562 from asparagine to tyrosine, 593 from threonine to alanine and an insertion of amino acid at the position 464 as glutamic acid. Paul *et al.*, (25) demonstrated that mutations in PBP1 at the position 414 from serine to arginine, 484 from tyrosine to cysteine, 541 from threonine to isoleucine and 600 from proline to threonine (25) of amoxicillin-resistant strain from laboratory mutant. Gerrits *et al.*, (26) suggested that alteration in PBP1 in amoxicillin-resistant isolate at the position 414 from serine to arginine conferred resistance.

CHAPTER IV

MATERIALS AND METHODS

The chemical agents used in this study were molecular biology grade. Name list of all media, chemical reagents materials, instruments and reagents were shown in Appendix I.

1. BACTERIAL STRAINS

Helicobacter pylori were isolated from Gastric biopsies from 357 patients who underwent upper gastrointestinal endoscopy at King Chulalongkorn Memorial Hospital between August 2003 and June 2004. Four gastric biopsy specimens were obtained from the antrum of each patient and placed in transport medium (1ml of 0.85 % sterile normal saline). All specimens were transported to the laboratory on ice and processed within 2 hours.

2. ISOLATION OF *H. PYLORI* ISOLATES

Two pieces of gastric biopsies from each patient were ground and cultured on selective and non-selective media modified from Tee *et al.*, (112). Non-selective medium is Columbia blood agar containing 7% sheep blood and 7% horse serum. Selective medium is Columbia blood agar with antibiotic supplement containing vancomycin (10 mg/L), cefsulodin (5 mg/L), trimethoprim (5 mg/L), and amphotericin B (5 mg/L). Plates were incubated at 37 ° C under microaerophilic conditions (10 % CO₂, 5 % O₂ and 85 % N₂) produced by a gas generating system (CampyGen, Oxoid, England) in anaerobic jar for 5-10 days.

3. IDENTIFICATION OF *H. PYLORI* ISOLATES

Colonies were identified as *H. pylori* by typical morphology on Gram-stained smear and positive urease, catalase and oxidase test. *H. pylori* NCTC 11637 was used as a positive control.

4. BIOCHEMICAL TESTS

4.1 Catalase test

The enzyme catalase breaks down hydrogen peroxide into oxygen. This results in the visible formation of bubbles of oxygen. Catalase activity is detected by putting a loop full of colonies into a drop of 3% (V/V) hydrogen peroxide on a glass slide. If the microorganism is catalase-positive, bubbles will appear due to the liberation of oxygen.

4.2 Oxidase test

The oxidase test detects the presence of cytochrome oxidase. This enzyme can oxidize the substrate N, N,N',N'-tetramethyl-*p*-phenylenediamine dihydrochloride (Sigma, U.S.A) and to produce a purple color. To test for oxidase, transfer colonies with a loop onto filter paper soaked with oxidase reagent. A dark purple color will appear within 10 seconds if the microorganism has an enzyme, cytochrome oxidase.

4.3 Urease test

The purpose of the urease test is to detect whether an microorganism possesses the enzyme urease which hydrolyzes urea. The urea agar contains phenol red indicator, which turns pink at an alkaline pH. When urea is hydrolyzed, it releases ammonia, which causes an alkaline reaction and a vivid pink color develops. Urease activity is detected by inoculating a loop full of the organism onto slope of the urea agar slant. A positive pink color occurs in a few minutes.

5. PRESERVATION OF *H. PYLORI* ISOLATES

H. pylori isolates were subcultured on Columbia blood agar with 7% sheep blood and 7% horse serum (GibcoBRL, U.S.A) at 37 °C under microaerophilic conditions for 3 days and were transferred by loop into 1 ml Brain heart infusion broth (Oxoid, England) containing 20% glycerol (V/V) (18). The strains were kept at -70 °C until used.

6. ANTIMICROBIAL SUSCEPTIBILITY TEST

All *H. pylori* isolates were tested for amoxicillin susceptibility. The minimal inhibitory concentration (MIC) of amoxicillin was examined by the epsilometer test (Etest, AB Biodisk, Solna, Sweden) and an agar dilution. The MIC is the lowest concentration of antimicrobial agents required to inhibit the growth of a microorganism *in vitro*.

6.1 Epsilometer test (E-test)

The E-test is a plastic strip containing a predefined, continuous and exponential antibiotic gradient on one side and graded continuous MIC scale (0.016 to 256 µg/ml). Columbia blood agars with a depth of 4 mm in plastic plate (90 mm) were used to determine the MIC by E-test. The media and E-test amoxicillin strips must be allowed to reach room temperature prior to use. The inoculum was prepared by the direct colony suspension method. *H. pylori* strains were grown on Columbia blood agar, at 37°C under microaerophilic conditions for 3 days. Subsequently, the selected colonies were transferred into brain heart infusion broth (Oxoid, USA). Suspension of *H. pylori* were adjusted turbidity to a McFarland standard no 3 (9×10^8 CFU/ml) and 1 ml of the suspensions were added onto Columbia blood agar (17). The suspensions were spreaded by bent rod, and the excess suspensions were removed. The inoculated agar plates were allowed to air dry for 15 minutes at room temperature prior to apply amoxicillin E-test strips (AB Biodisk, Solna, Sweden). E-test strips were placed on the agar surface by sterile forceps. After an incubation period of 3 days at 37°C under microaerophilic conditions produced by a

gasgenerating system (CampyGen Pack, Oxoid). The MIC was defined by the point of complete inhibition of all growth, including hazes and isolated colonies. Amoxicillin resistance was reported when the MIC value was greater than 0.5 µg/ml (12-15, 113, 114).

6.2 Agar dilution

H. pylori strains which were resistant to amoxicillin were confirmed by the agar dilution. Amoxicillin resistance in *H. pylori* was determined when the MIC value was greater than 0.5 µg/ml. Stock solutions of amoxicillin (Sigma Chemical Co., St Louis, MO, USA) were prepared at 10 mg/ml. Agar dilution plates were prepared using Columbia blood agar containing 7% (V/V) sheep blood, 7% (V/V) horse serum supplemented with twofold serial dilutions of amoxicillin. Fresh *H. pylori* isolates (2 to 3 days cultures) were prepared in Brain heart infusion broth (Oxoid, USA.) and adjusted to a no.3 McFarland standard (9×10^8 CFU / ml) (17). Mark the plates so that the orientation is obvious. Transfer diluted bacterial suspensions to the wells of an inoculum replicating apparatus. Use the apparatus to transfer the inocula to the series of agar plates, including a control plate without antimicrobial agent. Allow the inoculum spots to dry at room temperature before inverting the plates for incubation. The plates were incubated at 37 °C under microaerophilic conditions for 3 days. The MIC was investigated as the lowest amoxicillin concentration preventing visible growth.

7. DETERMINATION OF BETA-LACTAMASE PRODUCTION

The production of beta-lactamase by *H. pylori* strains was tested by the chromogenic cephalosporin method (115). Several colonies of *H. pylori* were selected and smear over the paper impregnated with nitrocefin solution of 500 µg/ml (Oxoid, England), a chromogenic cephalosporin. The presence of beta-lactamase was indicated by a change in the color of filter paper disc from yellow to pink. Activity was determined absent if no color change had occurred after 2 hours of incubation at room temperature. *Neisseria gonorrhoeae* beta-lactamase positive (Laboratory strain) was used as positive control.

8. AMPLIFICATION OF *pbp 1* GENE

8.1 DNA Extraction

The extraction of *H. pylori* DNA was performed by QIAamp DNA Mini kit (QIAGEN, Germany). The DNA was purified according to the manufacturer's directions. *H. pylori* colonies were scraped from the culture plate with inoculation loop and suspended with 180 µl of ALT. Twenty microliters of proteinase K were added, mixed by vortexing, and incubated at 56 °C until bacterial cell were completely lysed. The samples were then added by 200 µl of buffer AL. After well mixing the suspensions were heated at 70 °C for 10 min, and briefly centrifuged to remove drops from inside the lid. The samples were added by 200 µl of ethanol and mixed by pulse-vortexing for 15 sec. The supernatants were then transferred into spin columns and centrifuged at 8,000 rpm for 1 min. Place the QIAamp spin columns in a clean 2 ml collection tube and discard the tube containing the filtrate. QIAamp spin columns were carefully opened and 500 µl of buffer AW1 were added and centrifuged at 8,000 rpm for 1 min. The filtrates were then discarded. QIAamp spin columns were washed with 500 µl of AW2 and centrifuged at 14,000 rpm for 3 minutes. QIAamp spin columns were placed in a clean 1.5 microcentrifuge tube and added with 200 µl of buffer AE. The samples were incubated at room temperature for 1 minute and centrifuged at 8,000 rpm for 1 minute. Extracted DNA were stored at -20 °C.

8.2 DNA amplification by polymerase chain reaction (PCR)

8.2.1 Primer

Primers for amplification of *pbp1* were designed with primer3 program (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). The sequence data appear in GenBank under accession no. AE 000573. A fragment of 2,200 bp was amplified by using PBP1-F1 and PBP1-R1 primers (Table 3).

8.2.2 Amplification of the *pbp1* gene by PCR

Primer PBP1-F1 and PBP1-R1 were used for amplification of the entire *pbp1* gene in a 50 µl PCR reaction mixture. All PCR reagents were purchased from Furmentas, USA. The PCR mixture was as followed; 10X PCR buffer (20mM Tris-HCl (pH 8.8), 10 mM KCl, 10mM (NH₄)₂ SO₄), 1.5mM MgCl₂, 200 µM dNTP mixture (dNTPs; dATP, dCTP, dGTP, dTTP), 20 pmol of each primer, 2 U *Pfu* DNA polymerase, and 5 µl of DNA template. The reactions were run for 30 cycles through a temperature profile of 94 °C 1 minute (denaturation), 55 °C for 90 seconds (annealing), 72 °C 2 minutes (extension) and final extension at 72 °C for 10 minutes.

8.3 Analysis of PCR product

The PCR products were analyzed on 1 % agarose gels (Pronalisa, Spain) in TBE buffer containing 0.5 µg/ml ethidium bromide (Sigma, USA) was prepared. Ten microliters of PCR products were mixed with 3 µl of gel loading buffer (20 % ficoll, 0.05 % bromophenol blue). The electrophoresis was carried out at 80 volts for 50 minutes. The amplified products were visualized on of UV light transilluminator. A 1 Kb DNA ladder was used as a DNA size marker.

9. DETECTION OF POINT MUTATIONS IN *pbp 1* GENE BY DNA SEQUENCING

9.1 Purification of PCR product

The PCR products of 2,200 bp were purified by QIAquick PCR Purification Kit as described by the manufacturer (QIAGEN, GmbH, Germany). The QIAquick system is combination of spin-column technology with the selective binding properties of a uniquely- designed silica-gel membrane. DNA was absorbed to the silica- membrane in the presence of high salt while contaminants pass through the column. The PCR products were added 5 volumes of buffer PB (Contains guanidine hydrochloride and isopropanol) to 1 volume of PCR sample. After well mixing, the PCR sample were then transferred into QIAquick spin column in a provided 2 ml

collection tube and centrifuged at 13,000 rpm for 30-60 sec. Discard flow – through and place the QIAquick column back into the same tube. Collection tubes were re-used to reduce plastic waste. QIAquick spin column was carefully opened and added 750 µl of buffer PE (washing buffer) and centrifuged at 13,000 rpm for 30-60 sec. QIAquick spin columns were placed in a clean 1.5 microcentrifuge tube and added with 50 µl of buffer EB (10 mM Tris-Cl, pH 8.5) The samples were incubated at room temperature for 1 minute and centrifuged at 13,000 rpm for 30-60 sec. The purified PCR product were stored at -20 °C. The concentration of DNA was determined by spectrophotometer (BIO RAD, U.S.A).

9.2 Primers for DNA sequencing

Primers for DNA sequenced of *pbp1* were designed with primer3 program (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi) base on the sequence data in GenBank under accession no. AE 000573. A fragment of 2,200 bp was amplified using PBP1-F1 and PBP1-R1 primers. The primers used for sequencing are shown in Table 3.

Table 3 Sequences of the oligonucleotides used as primers for DNA sequencing the *pbp1* gene of *H. pylori* (GenBank under accession number AE000573).

Primers	Sequence (5' to 3')	Locations
PBP1-F1	CCT ACG GTT TCT AAA CCC CTT T	6766-6745
PBP1-F2	GCG CGC TAT GAT TAA AAA CG	6335-6316
PBP1-F3	ACG GGT TAA AAA CTC AAG GCTA	5817-5796
PBP1-F4	AAC CTT GCA AGA AGC CTT GA	5369-5350
PBP1-F5	TTG GTT CAT TGG CTT TAC CC	4946-4927
PBP1-R1	ATC AAG CGG TGA GTA TCC TTG T	4567-4588
PBP1-R2	GAG CCA AAC TCC CTG TGC	5005-5022
PBP1-R3	GCG CGG TAT CAG GGA TTT	5461-5478
PBP1-R4	GCT CGT TAG AAG AAA TCC AGC CTA	5923-5946
PBP1-R5	CGT GTG AGC ACC ATG TTT TT	6243-6262

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9.3 Preparation of sequencing reactions

PCR products were sequenced using primers shown in Table 3 with ABI prime Big Dye terminator cycle sequencing ready reaction kit (PE Applied Biosystem, Foster, Ca). The sequence reaction required 4 μ l of Big Dye® Terminator as demonstrated by manufacturer, with 3.2 pmole of primer and 50 ng of purified PCR product template in a total volume of 10 μ l. The sequencing cycle was examined using 25 cycles of denaturation at 96 °C for 30 sec, annealing at 50 °C for 10 sec and extension at 60 °C for 4 min and hold at 4 °C until ready to purify. The PCR product was purified with ethanol / EDTA precipitation before capillary electrophoresis was run for sequencing analysis.

9.4 Analysis

The nucleotide sequence and the deduced protein sequence were analyzed with the software available over the Internet at the National Center for Biotechnology Information ([http:// www.ncbi.nlm.nih.gov/BLAST](http://www.ncbi.nlm.nih.gov/BLAST)), Multalin (www.toulouse.inra.fr/multalin.html) and ExPASy (www.expasy.org/).

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CHAPTER V

RESULTS

1. BACTERIAL STRAINS

Gastric biopsy samples were obtained from 357 patients who underwent upper gastrointestinal endoscopy at King Chulalongkorn Memorial Hospital between August 2003 and June 2004. There were 134 men and 223 women with mean age 48 years (range, 16-93 years). Of all patients, 289 had non-ulcer dyspepsia, 56 had gastric ulcer, and 12 had duodenal ulcer (Table 4).

Fifty *Helicobacter pylori* isolates were obtained from 357 patients (14 %, 50/357). All clinical isolates included 33 strains (11.4% , 33/289) from non-ulcer dyspepsia patients , mean age 49 years, range 26-79 years, male / female : 9/24, 14 strains (25% , 14/56) from gastric ulcer patients, mean age 57 years, range 35-89 years, male / female : 9/5, and 3 strains (25%, 3/12) from duodenal ulcer patients, mean age 53 years, range 38-73 years, male / female : 3 / 0 (Table 4, Appendix IV: Table 7).

A total of fifty *H. pylori* isolates were identified as *H. pylori* based on morphological and biochemical tests. Colonies grown on Columbia blood agar were examined for morphology and biochemical characteristics. Colonies of *H. pylori* are small translucent to gray (Figure 4). Gram stain of *H. pylori* colonies shows a range of shapes from short rods to curved rod and occasionally S-shaped spirals (Figure 5). Isolates were identified as *H. pylori* on the basis of positive urease, catalase and oxidase reactions (Figure 6-8).

Table 4 *H. pylori* isolates and patient groups.

Patient group*	Fifty <i>H. pylori</i> isolates		
	No.of <i>H. pylori</i> isolates (%)	Age	Gender
		Mean/Range	Male/Female
NUD (n=289)	33 (11.4)	49/26-79	9/24
GU (n=56)	14 (25)	57/35-89	9/5
DU (n=12)	3 (25)	53/38-73	3/0

*NUD, non-ulcer dyspepsia; GU, gastric ulcer; DU, duodenal ulcer



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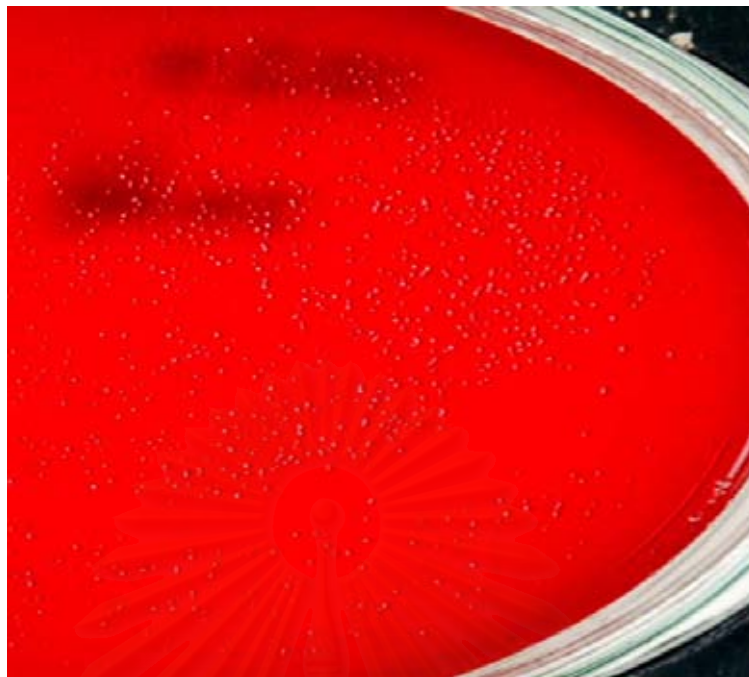


Figure 4 Colonies of *H. pylori* on Columbia blood agar plate.

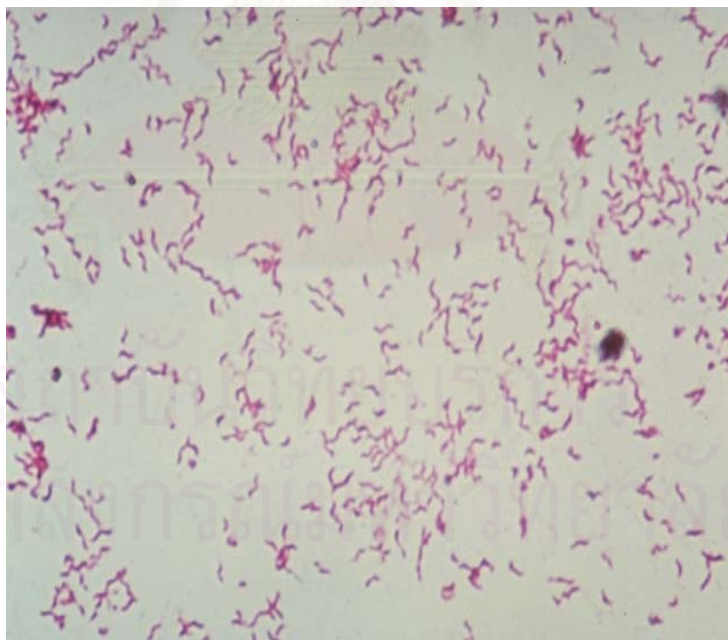


Figure 5 Gram stain of *H. pylori*.



Figure 6

Urease test: *H. pylori* is positive for urease test

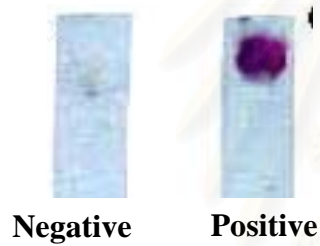


Figure 7 Oxidase test:

***H. pylori* is positive for oxidase test**

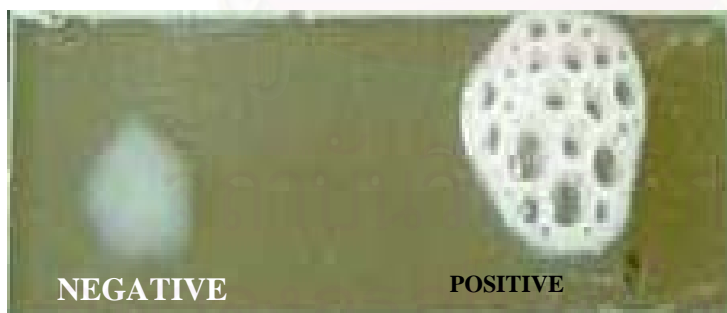


Figure 8 Catalase test: *H. pylori* is positive for catalase test

2. DETERMINATION OF THE AMOXICILLIN SUSCEPTIBILITY OF *H. PYLORI*

The MIC results for the 50 *H. pylori* isolates are shown in Table 7 (Appendix IV) and Figure 9. For MICs determined by the E-test, strains were considered resistant when the MIC was $> 0.5 \mu\text{g/ml}$ for amoxicillin (13-15, 113, 114). Distribution of MICs of amoxicillin for the 50 *H. pylori* isolates are shown in Figure 9. It was demonstrated that MICs of *H. pylori* isolates ranged from < 0.016 to $0.75 \mu\text{g/ml}$. MIC required to inhibit 50 % (MIC₅₀) and 90% (MIC₉₀) of isolates are $< 0.016 \mu\text{g/ml}$ and $0.016 \mu\text{g/ml}$, respectively.

Of the 50 isolates, 49 (98%) were susceptible to amoxicillin (MICs range = < 0.016 - $0.25 \mu\text{g/ml}$) and only one isolate was resistant (MIC = $0.75 \mu\text{g/ml}$). Of these isolates, 70 % (35/50) had the MIC of $< 0.016 \mu\text{g/ml}$, 24% (12/50) had the MIC of $0.016 \mu\text{g/ml}$, and two isolates had the MIC of 0.047 and $0.25 \mu\text{g/ml}$ respectively. The remaining one isolate (2 %), HP-1144, was resistant to amoxicillin (MIC $0.75 \mu\text{g/ml}$). The MIC of amoxicillin-resistant *H. pylori* was confirmed by the agar dilution method. There was a slightly higher MIC of HP-1144 (MIC= $1 \mu\text{g/ml}$) by agar dilution comparing by E-test.

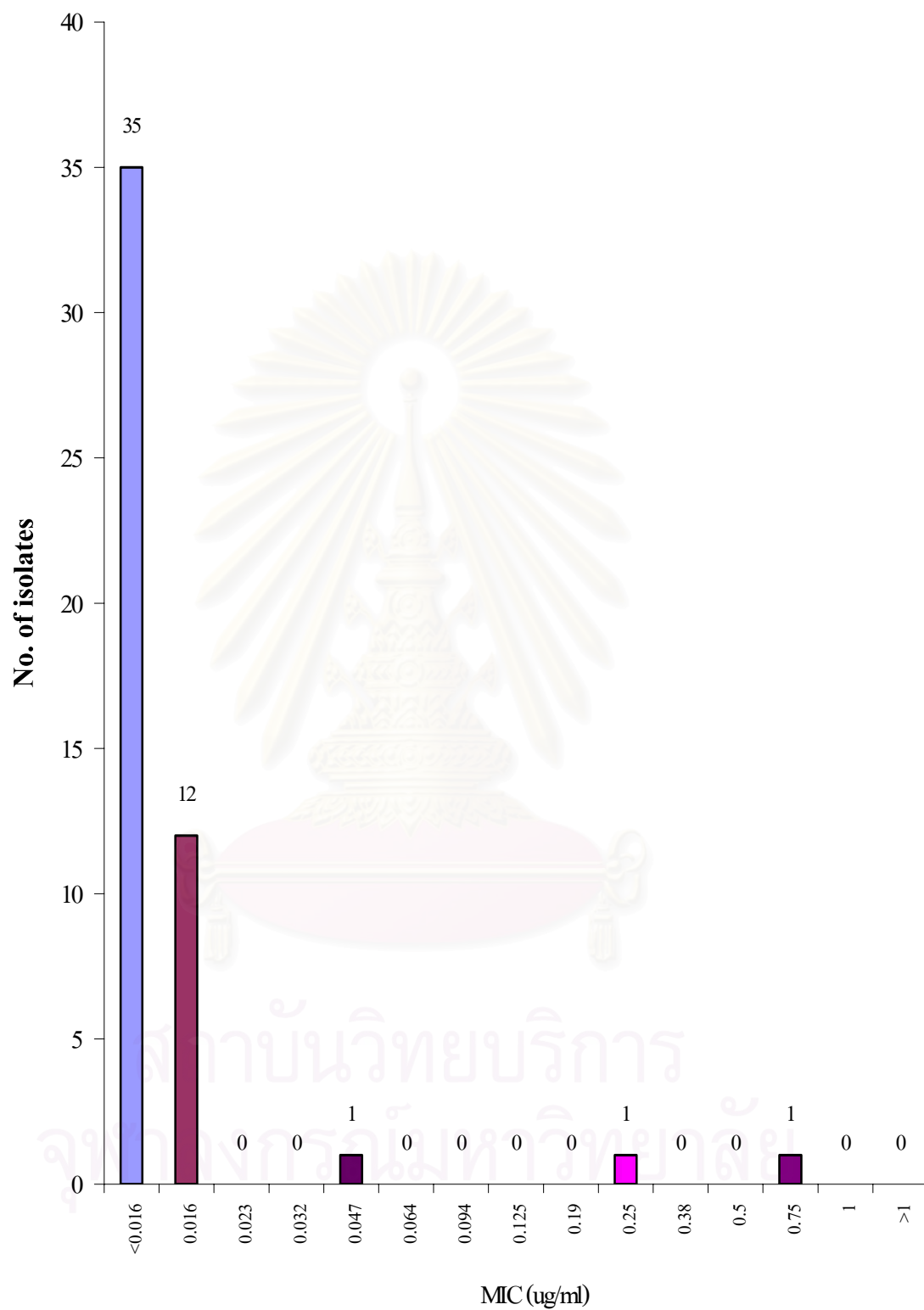


Figure 9 Distribution of amoxicillin MICs determined by the E-test.

3. DETECTION OF BETA-LACTAMASE

In this study, only one *H. pylori* isolate was resistant to amoxicillin (MIC 0.75 µg/ml). It was tested for production of beta-lactamase using the chromogenic cephalosporin method. However, the activity of beta – lactamase was not found in amoxicillin-resistant *H. pylori* strain, HP-1144.



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4. AMPLIFICATION OF *pbp1* GENE

Six *H. pylori* isolates were screened for the presence of *pbp1* gene by PCR with primers PBP-F1 and PBP-R1. Of the 6 isolates, 5 were susceptible to amoxicillin (MICs range = < 0.016 – 0.25 µg/ml) and one isolate, HP-1144, was resistant (MIC = 0.75µg/ml). These susceptible strains included *H. pylori* with different MIC; *H. pylori* NCTC 11637 (MIC = 0.016 µg/ml), HP-1174 (MIC= <0.016 µg/ml), HP-1163 (MIC= 0.016 µg/ml), HP-870 (MIC= 0.047 µg/ml), HP-1028 (MIC= 0.25 µg/ml) and HP-1144 (MIC= 0.75 µg/ml). PCR products of 2200 bp were present in all strains, including *H. pylori* NCTC 11637 (lane 3), amoxicillin- susceptible *H. pylori* strains (lane 4-7) and amoxicillin – resistant *H. pylori* strain (lane 8) as shown in Figure 10.

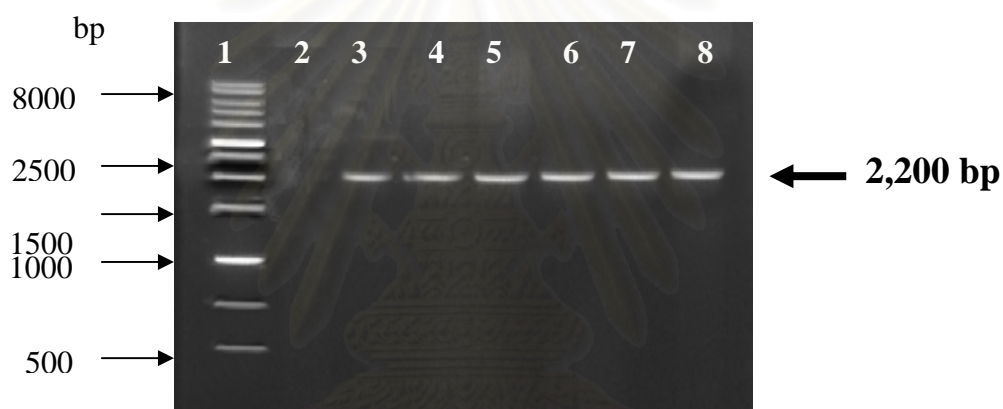


Figure 10 Agarose gel electrophoresis of PCR products of *pbp1* gene (2200 bp) from *H. pylori* isolates.

Lane 1: 1 Kb DNA marker

Lane 2: Double distilled water

Lane 3: *H. pylori* NCTC 11637 (MIC =0.016 µg/ml)

Lane 4: HP-1174 (MIC < 0.016 µg/ml)

Lane 5: HP-1163 (MIC= 0.016 µg/ml)

Lane 6: HP-870 (MIC =0.047 µg/ml)

Lane 7: HP-1028 (MIC =0.25 µg/ml)

Lane 8: HP-1144 (MIC =0.75 µg/ml)

5. DETECTION OF POINT MUTATION IN *pbp1* GENE BY DNA SEQUENCING

Nucleotide sequences of *pbp1* gene from the 6 *H. pylori* isolates including a resistant isolate (HP-1144, MIC 0.75 µg/ml) and susceptible isolates (*H. pylori* NCTC 11637, HP-1174, HP-1163, HP-870 and HP-1028) were determined by sequencing and amino acid changes in PBP1 are shown in Table 5 and Appendix IV (Figure 11-12). The comparison of the PBP1 sequences of all six stains with *H. pylori* 26695 from Genbank was investigated. The results demonstrated that there was diversity of amino acid substitutions in PBP1 (Table 5) both amoxicillin-susceptible and amoxicillin - resistant *H. pylori* isolates. Alignments of the PBP1 from amoxicillin – resistant, amoxicillin-susceptible isolates and *H. pylori* 26695 did not highlight any clustering of amino acid substitutions in PBP1 of amoxicillin resistant isolate (Table 5).

Comparison of the PBP1 sequences of all six strains revealed amino acid substitutions. There were 10-18 amino acid substitutions in PBP1 among all isolates sequenced. One amino acid deletion at position 400 and forty-two amino acid substitutions were found in both amoxicillin- susceptible and amoxicillin-resistant isolates. Of the 42 amino acid substitutions, 27 were found in sensitive strains (positions 13, 16, 45, 114, 120, 242, 243, 322, 332, 352, 374, 392, 406, 408, 414, 432, 469, 534, 547, 556, 589, 593, 595, 611, 653, 654 and 656) and 15 shared by both amoxicillin-resistant and sensitive *H. pylori* isolates (positions 17, 35, 79, 125, 148, 324, 479, 504, 508, 509, 515, 535, 543, 648 and 649) (Table 5). However, the variability of nucleotide substitutions and amino acid substitutions sequence in the PBP1 did not relate to the amoxicillin MICs, suggesting that these amino acid changes did not directly relate to the functional activity of PBP1. Amino acid substitutions in PBP1 in amoxicillin-sensitive isolates suggested there is genetic diversity of *pbp1* gene of *H. pylori*.

It has been demonstrated that transpeptidase domain of PBP1 of *H. pylori* 26695 has a catalytic center consisting of motif 1 (SXXK at 368 – 371), motif 2 (SLN at 433 – 435) and motif 3 (KTG at 555 – 557) when aligned with the sequence of *E. coil* PBP1a(102). In this study, the resistant isolate, HP-1144, had no amino acid substitution in these 3 motifs but one amoxicillin-susceptible isolate, HP-1028, with

the MIC of 0.25 $\mu\text{g/ml}$ had mutation in the KTG motif changing from KTG to KSG (Table 6).



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Table 5 Amino acid changes in PBP1 in amoxicillin-susceptible and amoxicillin-resistant *H. pylori* isolates.

Strains	MICs μg/ml	Amino acid at position :																					
		13	16	17	35	45	79	114	120	125	148	242	243	322	324	332	352	374	392	400	406	408	414
Susceptible strains																							
26695*	0.016	F	V	M	I	V	I	Y	T	F	I	G	A	N	D	M	K	V	T	N	E	N	S
HP-1174	<0.016	.	.	I	T	.	V	T	.	L	L	.	.	.	Y
HP-1163	0.016	.	I	I	.	I	.	.	.	L	L	.	.	D	A	.	V	S	.
HPC	0.016	.	I	I	.	I	.	.	.	L	L	.	.	D
HP-870	0.047	V	I	V	L	.	S	S
HP-1028	0.25	.	I	A	L	I	E	L	.	**	.	.	R
Resistant strain																							
HP-1144	0.75	.	.	I	T	.	V	.	.	L	L	.	.	.	Y

*; GenBank accession no.AE000573, HPC; *H. pylori* NCTC 11637, **; deletion of amino acid

.; Same as for 26695

Table 5 Amino acid changes in PBP1 in amoxicillin-susceptible and amoxicillin-resistant *H. pylori* isolates (Continued).

Strains	MICs μg/ml	Amino acid at position :																				
		432	469	479	504	508	509	515	534	535	543	547	556	589	593	595	611	648	649	653	654	656
Susceptible strains																						
26695*	0.016	H	V	D	N	D	V	M	M	D	S	I	T	S	T	G	A	K	R	S	E	R
HP-1174	<0.016	.	.	E	D	N	I	I	.	N	N	Q	K	.	.	.
HP-1163	0.016	L	I	N	R	T
HPC	0.016	I	N	R	T
HP-870	0.047	.	G	E	D	N	.	.	.	G	A	S	.	Q	K	G	K	P
HP-1028	0.25	.	.	E	D	.	.	I	.	N	.	.	S	G	.	.	S	P
Resistant strain																						
HP-1144	0.75	.	.	E	D	N	I	I	.	N	N	Q	K	.	.	.

*; GenBank accession no.AE000573, HPC; *H. pylori* NCTC 11637, **; deletion of amino acid

•; Same as for 26695

Table 6 Sequences of the three conserved amino acid motifs of PBP1.

Strains	Change in amino acids of conserved PBP1 sites making up active penicillin-binding site of PBP.		
	Motif 1 Position 368-371	Motif 2 Position 433-435	Motif 3 Position 555-557
HP-26695	SAIK	SLN	KTG
HPC	SAIK	SLN	KTG
HP-1163	SAIK	SLN	KTG
HP-1174	SAIK	SLN	KTG
HP-870	SAIK	SLN	KTG
HP-1028	SAIK	SLN	KSG
HP-1144	SAIK	SLN	KTG

HPC; *H. pylori* NCTC 11637

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CHAPTER VI

DISCUSSION

Helicobacter pylori infection is responsible for most cases of peptic ulcer disease and successful treatment of the infection results in cure of the disease. Triple therapy, in with a bismuth or proton pump inhibitor is combined with two antibiotics from clarithromycin, metronidazole, amoxicillin and tetracycline, is the most widely used regimen. Eradication rates of approximately 90 % are obtained by using these regimens (9). However, antibiotic resistance has been reported and is one of the major causes of treatment failure.

The prevalence of amoxicillin resistance varies with geographical regions. Amoxicillin resistance has been reported to be rare, however, recent data have shown an increasing rate of amoxicillin resistance in Bangladesh (6.6%) (10), Thailand (13.9%) (22), Mexico (18%) (20) and China (71.9%) (21). This study shows low rate of *H. pylori* resistant to amoxicillin (2%). The prevalence of amoxicillin resistance rate was higher in previous studies from Brazil (29%) (91), Mexico (18%) (20), Bangladesh (6.6%) (10) and China (71.9%) (21). The difference in rates of resistance is due to the geographical origin of population and the cutoff values used for amoxicillin resistance. Variability occurs between laboratories with amoxicillin – resistant breakpoints described from as low as 0.5 µg/ml to as high as 8 µg/ml (11, 13-15, 19, 113, 116, 117). Similar results have been reported in the studies from Korea (0%) (95), Philippines (0%) (118) Japan (0.3%) (13) , USA (1.4%) (16), Israel (0.72%) (17) and European multicentre (0.8%) (14). However, the present study, amoxicillin resistance rate (2%) in *H. pylori* isolate from Thai patients was lower than in the study by Tangmankongworakoon *et al.*,(13.9%) (22). The difference may be partly from the different group of patients and testing parameters (medium, size of inoculums, incubation time). We had only 50 *H. pylori* isolates, therefore, more isolates are needed to clearly demonstrated the prevalence of amoxicillin resistance.

In this study, MIC₅₀ and MIC₉₀ of amoxicillin showed that amoxicillin was potent against *H. pylori* as the MIC₉₀ was 0.016 µg/ml and only one low-level resistant isolate was found (MIC 0.75 µg/ml). This suggests that amoxicillin is

potential alternative agent for the treatment of clarithromycin-resistant and metronidazole-resistant *H. pylori* in Thai patients and further clinical studies are need to confirm these data *in vivo*.

Alterations in PBPs resulting in reduced binding ability can lead to resistance to beta-lactam. Previous studies demonstrated that resistance to amoxicillin in *H. pylori* was associated with mutation in the *pbp1* gene (25-27, 30). Similar findings were observed in *Streptococcus pneumoniae* (119-121), *S. mitis* (122) and *Neisseria gonorrhoeae* (123). Seventeen distinct PBP1 mutations have been reported to be associated with amoxicillin resistance in *H. pylori*, i.e., at the position 69 from alanine to valine, 406 from glutamic acid to alanine, 414 from serine to arginine, 417 from serine to threonine, 484 from tyrosine to cysteine, 515 from methionine to isoleucine, 535 from aspartic acid to asparagine, 541 from threonine to isoleucine, 543 from serine to arginine, 556 from threonine to serine, 562 from asparagine to tyrosine, 593 from threonine to alanine, 600 from proline to threonine, 648 from lysine to glutamine, 649 from arginine to lysine and 656 from arginine to proline and one amino acid insertion at position 464 (25-27, 30). However, the results from these studies obtained from only 1-2 *H. pylori* isolates (MICs range= 8 µg/ml to 64 µg/ml).

When compared with amino acid sequence of PBP1 of *H. pylori* 26695 from GenBank, the result from this study showed forty-two different amino acid substitutions in both amoxicillin-sensitive and resistant isolates at positions 13, 16, 17, 35, 45, 79, 114, 120, 125, 148, 242, 243, 322, 324, 332, 352, 374, 392, 406, 408, 414, 432, 469, 479, 504, 508, 509, 515, 534, 535, 543, 547, 556, 589, 593, 595, 611, 648, 649, 653, 654, 656 and one amino acid deletion at position 400. Fifteen amino acid changes were shared among resistant and susceptible strains. All mutations in the resistant isolate were found in susceptible isolates (positions 17, 35, 79, 125, 148, 324, 479, 504, 508, 509, 515, 535, 543, 648 and 649). The results are different from the study by Okamoto *et al.*, (27) which demonstrated five mutations in PBP1 of amoxicillin-resistant clinical isolate (MIC 8 µg/ml), including amino acid substitutions at the position 69, 556, 562, 593 and one amino acid insertion at position 464. Our study found amino acid substitutions at the position 556 and 593 in susceptible isolates. Kwon *et al.*,(30) demonstrated that high-level beta-lactam

resistance in clinical *H. pylori* isolate (MIC 64 µg/ml) was associated with alterations in PBP1, resulting in the following amino acid substitutions at the positions 406, 417, 515, 535, 543, 556, 562, 648, 649 and 656. Our study demonstrated that amino acid substitutions in PBP1 at the positions 406, 515, 535, 543, 556, 648, 649 and 656 were also found in amoxicillin-susceptible isolates. Gerrit *et al.* (26) reported that amino acid substitution at the position 414 in PBP1 was responsible for amoxicillin resistance. In contrast, our study found that amino acid substitution at position 414 was present in amoxicillin-susceptible isolate (HP-1028). Amino acid substitutions at position 414, 484, 541 and 600 in an amoxicillin-resistant strain were also reported by Paul *et al.* (25) However, none of these mutations was found in amoxicillin-resistant isolate, HP-1144.

The transpeptidase domain of PBP1 of *H. pylori* 26695 has a catalytic centre consisting of motif 1 (SXXK at 368-371), motif 2 (SLN at 433-435) and motif 3 (KTG at 555-557) when aligned with the sequence of *E. coli* PBP1a (102). It has been reported that the amoxicillin-resistant isolates had a KSG sequence in motif 3 instead of the KTG sequence conserved in other strains (27, 30). In contrast, we did not find mutations in these motifs in amoxicillin-resistant isolate but mutation in KTG motif was occurred in amoxicillin-susceptible strain. The susceptible strain HP-1028 (MIC = 0.25µg/ml) has a KSG sequence in motif 3 instead of KTG sequence conserved in other strains. Therefore, alteration in KTG motif may not the sole contributor to the mechanism of amoxicillin resistance. Other mechanisms of resistance must be involved such as decreased permeation of the antibiotic in to the bacterial cell, alterations in OMPs and active efflux pumps.

HP-1028 with the MIC of 0.25 µg/ml, had mutations in KTG motif and amino acid substitution at position 414. Although these mutations were not found in our resistant strain (HP-1144), it may be associated with increased amoxicillin MIC as this isolate had the MIC 15.6 times more than the MIC of most strains (MIC₉₀ = 0.016 µg/ml).

It has been demonstrated that beta-lactam resistance in *H. pylori* was not mediated by beta-lactamase (25-30). Similar to other studies, beta-lactamase activity was not detected in amoxicillin-resistant isolate (HP-1144).

The present study showed that mutations in the *pbp1* gene may not be associated with low-level amoxicillin resistance in HP-1144, an amoxicillin-resistant clinical isolate, as amino acid substitutions found in this isolate were also present in sensitive strains. Other mechanisms of resistance must play a role in this amoxicillin-resistant isolate, including decreased permeation of the antibiotic into the bacterial cell, alterations in OMPs and active efflux pumps.

When compared the PBP1 sequences of HP-1144 and HP-1174 (MIC <0.016 µg/ml), the results showed that all except one amino acid at position 114 were identical. Therefore, amino acid substitution at position 114 may be involved in the mechanism of amoxicillin resistance. For further study, site-directed mutagenesis should be done to investigate the role of mutation at position 114.

The limitation of this study is that we had only one amoxicillin-resistant isolate with low-level amoxicillin resistance. Much more amoxicillin-resistant clinical *H. pylori* isolates are required to gain more results on the PBP1 mutations associated with amoxicillin resistance. Interestingly, our results showed that mutations in PBP1 at positions 406, 414, 515, 535, 543, 556, 593, 648, 649 and 656 which others investigators reported to be linked to amoxicillin resistance were present in our amoxicillin susceptible isolates. Although there were no particular amino acid substitution associated with amoxicillin resistance in this study, a number and types of amino acid changes may cause structural changes in PBP1 leading to decreased affinity of PBP1 for amoxicillin.

CHAPTER VII

CONCLUSION

In recent years, standard therapy regimens for treating *Helicobacter pylori* infection are multiple antibiotics in combination with proton pump inhibitors (PPI). Antibiotics that are frequently included in triple therapy (6, 9, 74, 76, 86, 87) regimens are clarithromycin, metronidazole, tetracycline and amoxicillin. Amoxicillin is an important component of combination therapies for *H. pylori* eradication and there is an increasing rate of amoxicillin resistance in many countries.

Fifty *H. pylori* isolates were obtained from 357 patients (14%, 50/357) who underwent upper gastrointestinal endoscopy at King Chulalongkorn Memorial Hospital between August 2003 and June 2004. The minimum inhibitory concentration (MIC) of amoxicillin was examined by the E-test. Of the 50 isolates, 49 (98%) were susceptible to amoxicillin and only one isolate was resistant (2%) (MIC 0.75 µg/ml). MIC₅₀ and MIC₉₀ were <0.016 and 0.016 µg/ml, respectively. This suggests that amoxicillin is potential alternative agent for the treatment of clarithromycin-resistant and metronidazole-resistant *H. pylori* in Thai patients and further clinical studies are needed to confirm these data *in vivo*.

Mutations in the *pbp1* gene were analyzed by PCR and DNA sequencing. The DNA sequences of *pbp1* were determined by sequencing both amoxicillin – susceptible and amoxicillin – resistant *H. pylori* isolates. Of the 6 isolates, 5 were susceptible to amoxicillin (MICs range = < 0.016 – 0.25 µg/ml) and one isolate, HP-1144, was resistant to amoxicillin (MIC = 0.75µg/ml). When compared with amino acid sequence of PBP1 of *H. pylori* 26695 from GenBank, there were forty-two different amino acid substitutions in both amoxicillin-sensitive and resistant isolates and one amino acid deletion. Fifteen amino acid changes were shared among resistant and susceptible strains. All mutations in the resistant isolate, HP-1144, were found in susceptible isolates.

Interestingly, our results showed that mutations in PBP1 at positions 406, 414, 515, 535, 543, 556, 593, 648, 649 and 656 which others investigators reported to be linked to amoxicillin resistance were present in our amoxicillin susceptible isolates. Beta-lactamase activity was not detected in HP-1144.

Therefore, mutation in PBP1 and production of beta-lactamase may not be associated with amoxicillin resistance in HP-1144. Other mechanisms must be involved in amoxicillin resistance such as decreased membrane permeability, alterations in OMPs and efflux pump.



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APPENDICES

สถาบันวิทยบริการ
จุฬาลงกรณ์มหาวิทยาลัย

APPENDIX I

REAGENTS, MATERIALS AND INSTRUMENTS

A. REAGENTS

Absolute ethanol	(Merck, Germany)
Agarose	(Biorad, USA)
Brain heart infusion agar	(Oxoid, England)
EDTA	(Amresco, USA)
Ethidium bromide	(Amresco, USA)
Glacial acetic acid	(Merck, Germany)
Horse serum	(GibcoBRL, USA)
Miniral oil	(Sigma, USA)
Columbia agar base	(Oxoid, England)
Urea agar base	(BBL, U.S.A.)
Bacto agar	(Difco, USA)
NaCl	(Merck, Germany)
NaHCO ₃	(Merck, Germany)
Na ₂ HPO ₄ *2H ₂ O	(Sigma, USA)
Tris	(Amresco, USA)

B. MATERIALS

Anaerobic jar	(BBL, USA)
Gas pack	(Oxoid, England)

C. INSTRUMENTS

Water bath	(Memmert, USA)
Perkin Elmer GeneAmp PCR system 9600	(Perkin Elmer, USA)
Camera Gel Doc TM MZL	(BIO-RAD, USA)
Incubator	(BIO-RAD, USA)
Microcentrifuge	(Eppendorf, USA)
Spectrophotometer	(BIO-RAD, USA)



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APPENDIX II

MEDIA, SOLUTION AND IDENTIFICATION PROCEDURES

1. Columbia agar with 7 % sheep blood

Columbia agar base	39 g/L
Horse serum	70 ml/L
Sheep blood	70 ml/L
Distilled water	860 ml

The medium was sterilized by autoclaving at 121°C, 15 pounds/inch² pressure, for 15 minutes. The sterile medium was cooled to 45°C to 50°C. Add blood and horse serum after cooling base medium. Dispense 20 ml per petri dish. Cool and store at 4°C until used.

Do not add any heat labile components (Sheep blood or antibiotic solutions) to the sterilizer.

2. Columbia agar with 7 % Sheep blood and antibiotics

Columbia agar base	39 g/L
Horse serum	70 ml/L
Sheep blood	70 ml/L
Vancomycin (1 ml of stock)	10 mg/L
Trimethoprim (0.5 ml of stock)	5 mg/L
Cefsoludin (0.5 ml of stock)	5 mg/L
Amphotericin B (0.5 ml of stock)	5 mg/L
Distilled water	860 ml

The medium was sterilized by autoclaving at 121°C, 15 pounds/inch² pressure, for 15 minutes. The sterile medium was cooled to 45°C to 50°C. Add blood, horse serum and antibiotic solution after cooling base medium. Dispense 20 ml per petri dish. Cool and store at 4°C until used.

Do not add any heat labile components (Sheep blood or antibiotic solutions) to the sterilizer.

3. Antibiotic solution preparation

Vancomycin, final concentration 10 mg/L

- Prepare a stock solution; dissolve 0.028 g in 5.78 ml distilled water

Cefsoludin, final concentration 5 mg/L

- Prepare a stock solution, dissolve 0.014 g in 2.82 ml distilled water.

Trimethoprim, final concentration 5 mg/L

- Prepare a stock solution, dissolve 0.018 g in 3.7 ml distilled water.

Amphotericin, final concentration 5 mg/L

- Prepare a stock solution, dissolve 0.014 g in 2.84 ml distilled water.

4. Urease test

Solution A: for	20 ml
Urea agar base (BBL)	2.9 g
Urea	4 g
Distilled water	20 ml

Dissolve in 20 ml of distilled water. Adjust to pH 6.2 Sterilize by filtration (use a 0.22 μm filter).

Solution B: for	80 ml
Bacto agar (Difco)	0.5 g
Distilled water	80 ml

Add the ingredient to 80 ml of distilled water; heat with stirring until the agar is dissolved. Sterilize by autoclaving at 121°C, 15 ponds/inch² pressure, for 15 minutes. Mix solution A, 20 ml with solution B, 80 ml. Aliquot into sterile 1.5 microtube (1 ml/tube). Test the sterility of Urease medium by incubate tubes at 37°C for 24 hours. Store tubes in refrigerator at 4°C until used.

5. Brain heart infusion with 20 % glycerol

Brain heart infusion	37 g/L
Glycerol	200 ml
Distilled water	800 ml

Sterilize by autoclaving at 121°C, 15 pounds/inch² pressure, for 15 minutes. Aliquot into sterile screw cap tubes (1 ml/tube). Store tubes in refrigerator at 4°C until used.

6. Sterile saline solution

Sodium Chloride	8.5 g/L
Distilled water	1 L

Sterilize by autoclaving at 121°C, 15 pounds/inch² pressure, for minutes. Store at room temperature.



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APPENDIX III

REAGENTS AND PREPARATION

1. 5x Tris-borate buffer (TBE)

Tris base	54 g/L
Boric acid	27.5 g/L
0.5 M EDTA (pH 8.0)	20 ml

Adjust volume to 1 liter with distilled water. The solution was mixed and sterilized by autoclaving at 121°C for 15 min.

2. 0.5 M EDTA (pH 8.0)

Disodium ethylene diamine tetra-aceate 2H ₂ O	186.1 g/L
Distilled water	1 L

Adjust pH to 8.0 and volume to 1 liter. Store at room temperature for no longer than 1 year.

3. 10x TE buffer

Tris	12.11 g/L
0.5 M EDTA	20 ml

Adjust to pH 8.0 by adding conc. HCl. Adjust volume to 1,000 ml and sterilized by autoclaving at 121°C for 15 min.

4. 1 % Agarose gel

Agarose	0.2 g
1x TBE	20 ml

Dissolve by heating in microwave oven and occasional mix unit no granules of agarose are visible.

5. 5x Loading buffer 100 ml

Tris HCl	0.6 g
EDTA	1.68 g
SDS	0.5 g

Bromphenol Blue	0.1 g
Sucrose	40 g

Adjust volume to 100 ml with distilled water. Mix the solution, aliquot into 1.5 microtubes and store at 4°C.

Reagent for DNA Extraction

Protease K

Reconstituted of protease K (lyophilized) with 1.25 ml protease solvent, stored at -20°C

1.2 Buffer AL (Ready to used)

1.3 Buffer AW1

Buffer AW1 is supplied as a concentrate. Before using for the first time, add the 25 ml of ethanol (96-100%) to buffer AW1 concentrate as indicated on the bottle.

1.4 Buffer AW2

Buffer AW2 is supplied as a concentrate. Before using for the first time, add the 30 ml of ethanol (96-100%) to buffer AW2 concentrate as indicated on the bottle.

1.5 Buffer AE (Ready to used)

Reagent for PCR product purification

Buffer PB (Ready to used)

Buffer PE

Buffer PE is supplied as a concentrate. Before using for the first time, add the 55 ml of ethanol (96-100%) to buffer PE concentrate as indicated on the bottle.

APPENDIX IV

Table 7 *H. pylori* isolates, demographic information of patients and amoxicillin MICs ($\mu\text{g/ml}$) .

Number	<i>H. pylori</i> strains	Age	Sex*	Diagnosis*	MIC by E-test ($\mu\text{g/ml}$)
1	HP-826	63	F	NUD	< 0.016
2	HP-827	29	F	NUD	< 0.016
3	HP-846	62	F	GU	< 0.016
4	HP-847	26	F	NUD	< 0.016
5	HP-858	56	F	NUD	< 0.016
6	HP-870	64	F	NUD	0.047
7	HP-874	28	M	NUD	< 0.016
8	HP-876	51	M	NUD	< 0.016
9	HP-890	70	M	GU	0.016
10	HP-903	60	F	NUD	0.016
11	HP-904	38	F	NUD	< 0.016
12	HP-911	65	M	NUD	< 0.016
13	HP-927	69	F	GU	0.016
14	HP-976	89	M	GU	< 0.016
15	HP-977	67	F	NUD	< 0.016
16	HP-989	28	F	NUD	< 0.016
17	HP-991	54	M	GU	< 0.016
18	HP-992	36	F	NUD	< 0.016
19	HP-994	63	M	GU	< 0.016
20	HP-1001	32	F	NUD	< 0.016
21	HP-1002	73	M	DU	< 0.016
22	HP-1007	49	M	DU	0.016
23	HP-1014	65	M	NUD	0.016
24	HP-1027	42	F	NUD	< 0.016
25	HP-1028	23	F	NUD	0.25
26	HP-1029	79	M	NUD	0.016

Table 7 *H. pylori* isolates, demographic information of patients and amoxicillin MICs ($\mu\text{g/ml}$) (Continued).

Number	<i>H. pylori</i> strains	Age	Sex*	Diagnosis*	MIC by E-test ($\mu\text{g/ml}$)
27	HP-1037	64	F	NUD	< 0.016
28	HP-1038	26	F	NUD	< 0.016
29	HP-1045	34	M	NUD	< 0.016
30	HP-1051	60	F	NUD	< 0.016
31	HP-1052	45	F	NUD	< 0.016
32	HP-1059	61	F	NUD	<0.016
33	HP-1076	45	M	GU	0.016
34	HP-1081	53	F	NUD	0.016
35	HP-1101	84	F	GU	0.016
36	HP-1107	53	M	NUD	<0.016
37	HP-1111	38	F	NUD	< 0.016
38	HP-1112	36	F	NUD	< 0.016
39	HP-1123	71	M	NUD	<0.016
40	HP-1129	40	M	GU	< 0.016
41	HP-1135	39	F	NUD	< 0.016
42	HP-1140	54	F	NUD	< 0.016
43	HP-1142	38	M	DU	0.016
44	HP-1144	74	M	NUD	0.75
45	HP-1146	35	M	GU	< 0.016
46	HP-1162	53	M	GU	< 0.016
47	HP-1163	60	F	GU	0.016
48	HP-1164	42	F	NUD	< 0.016
49	HP-1173	52	M	GU	< 0.016
50	HP-1174	60	F	GU	< 0.016

* M, man; F, female; NUD, non-ulcer dyspepsia; GU, gastric ulcer; and DU, duodenal ulcer

Figure 11 Alignment of amino acid sequences of PBPI.

	1				50
26695	MLKKIFYGFI	VLFLIVMGLL	AIIIAQVWVT	TDKDI AKIKD	YRPGVASQIL
HPC	MLKKIFYGFI	VLFLIIIIGLL	AIIIAQVWVT	TDKDI AKIKD	YRPGIASQIL
HP-1163	MLKKIFYGFI	VLFLIIIIGLL	AIIIAQVWVT	TDKDI AKIKD	YRPGIASQIL
HP-1174	MLKKIFYGFI	VLFLIVIGLL	AIIIAQVWVT	TDKDT AKIKD	YRPGVASQIL
HP-1144	MLKKIFYGFI	VLFLIVIGLL	AIIIAQVWVT	TDKDT AKIKD	YRPGVASQIL
HP-870	MLKKIFYGFI	VLVLIIIVGLL	AIIIAQVWVT	TDKDI AKIKD	YRPGVASQIL
HP-1028	MLKKIFYGFI	VLFLIIMGLL	AIIIAQVWVT	TDKDI AKIKD	YRPGVASQIL
Consensus	MLKKIFYGFI	VLFLI! .GLL	AIIIAQVWVT	TDKDi AKIKD	YRPG! ASQIL
	51				100
26695	DRKGRLIANI	YDKEFRFYAR	FEEI PPRFIE	SLLAVEDTLF	FEHGGINLDA
HPC	DRKGRLIANI	YDKEFRFYAR	FEEI PPRFIE	SLLAVEDTLF	FEHGGINLDA
HP-1163	DRKGRLIANI	YDKEFRFYAR	FEEI PPRFIE	SLLAVEDTLF	FEHGGINLDA
HP-1174	DRKGRLIANI	YDKEFRFYAR	FEEI PPRFVE	SLLAVEDTLF	FEHGGINLDA
HP-1144	DRKGRLIANI	YDKEFRFYAR	FEEI PPRFVE	SLLAVEDTLF	FEHGGINLDA
HP-870	DRKGRLIANI	YDKEFRFYAR	FEEI PPRFIE	SLLAVEDTLF	FEHGGINLDA
HP-1028	DRKGRLIANI	YDKEFRFYAR	FEEI PPRFIE	SLLAVEDTLF	FEHGGINLDA
Consensus	DRKGRLIANI	YDKEFRFYAR	FEEI PPRF! E	SLLAVEDTLF	FEHGGINLDA
	101				150
26695	IMRAMIKNAK	SGRYTEGGST	LTQQFVKNMV	LTREKTLTRK	LKEAII SiRI
HPC	IMRAMIKNAK	SGRYTEGGST	LTQQLVKNMV	LTREKTLTRK	LKEAII SLRI
HP-1163	IMRAMIKNAK	SGRYTEGGST	LTQQLVKNMV	LTREKTLTRK	LKEAII SLRI
HP-1174	IMRAMIKNAK	SGRTTEGGST	LTQQLVKNMV	LTREKTLTRK	LKEAII SLRI
HP-1144	IMRAMIKNAK	SGRYTEGGST	LTQQLVKNMV	LTREKTLTRK	LKEAII SLRI
HP-870	IMRAMIKNAK	SGRYTEGGST	LTQQLVKNMV	LTREKTLTRK	LKEAII SiRI
HP-1028	IMRAMIKNAK	SGRYTEGGSA	LTQQLVKNMV	LTREKTLTRK	LKEAII SiRI
Consensus	IMRAMIKNAK	SGRYTEGGST	LTQQLVKNMV	LTREKTLTRK	LKEAII SiRI
	151				200
26695	EKVLSKEEIL	ERYLNQTFFG	HGYYGVTAS	LGYFKKPLDK	LTLKEITMLV
HPC	EKVLSKEEIL	ERYLNQTFFG	HGYYGVTAS	LGYFKKPLDK	LTLKEITMLV
HP-1163	EKVLSKEEIL	ERYLNQTFFG	HGYYGVTAS	LGYFKKPLDK	LTLKEITMLV
HP-1174	EKVLSKEEIL	ERYLNQTFFG	HGYYGVTAS	LGYFKKPLDK	LTLKEITMLV
HP-1144	EKVLSKEEIL	ERYLNQTFFG	HGYYGVTAS	LGYFKKPLDK	LTLKEITMLV
HP-870	EKVLSKEEIL	ERYLNQTFFG	HGYYGVTAS	LGYFKKPLDK	LTLKEITMLV
HP-1028	EKVLSKEEIL	ERYLNQTFFG	HGYYGVTAS	LGYFKKPLDK	LTLKEITMLV
Consensus	EKVLSKEEIL	ERYLNQTFFG	HGYYGVTAS	LGYFKKPLDK	LTLKEITMLV
	201				250
26695	ALPRAPSFYD	PTKNLEFSLS	RANDILRRLY	SLGWISSNEL	KGALNEVPIV
HPC	ALPRAPSFYD	PTKNLEFSLS	RANDILRRLY	SLGWISSNEL	KGALNEVPIV
HP-1163	ALPRAPSFYD	PTKNLEFSLS	RANDILRRLY	SLGWISSNEL	KGALNEVPIV
HP-1174	ALPRAPSFYD	PTKNLEFSLS	RANDILRRLY	SLGWISSNEL	KGALNEVPIV
HP-1144	ALPRAPSFYD	PTKNLEFSLS	RANDILRRLY	SLGWISSNEL	KGALNEVPIV
HP-870	ALPRAPSFYD	PTKNLEFSLS	RANDILRRLY	SLGWISSNEL	KSSLNEVPIV
HP-1028	ALPRAPSFYD	PTKNLEFSLS	RANDILRRLY	SLGWISSNEL	KGALNEVPIV
Consensus	ALPRAPSFYD	PTKNLEFSLS	RANDILRRLY	SLGWISSNEL	KgaLNEVPIV

	251				300
26695	YNQTSTQNI	PYVVDEV	LDQLDGL	GYTIKLT	DYQRLALE
HPC	YNQTSTQNI	PYVVDEV	LDQLDGL	GYTIKLT	DYQRLALE
HP-1163	YNQTSTQNI	PYVVDEV	LDQLDGL	GYTIKLT	DYQRLALE
HP-1174	YNQTSTQNI	PYVVDEV	LDQLDGL	GYTIKLT	DYQRLALE
HP-1144	YNQTSTQNI	PYVVDEV	LDQLDGL	GYTIKLT	DYQRLALE
HP-870	YNQTSTQNI	PYVVDEV	LDQLDGL	GYTIKLT	DYQRLALE
HP-1028	YNQTSTQNI	PYVVDEV	LDQLDGL	GYTIKLT	DYQRLALE
Consensus	YNQTSTQNI	PYVVDEV	LDQLDGL	GYTIKLT	DYQRLALE
	301				350
26695	RFHQKILE	IAKEKPK	SNEDEDN	SMIVTDT	KILALVGG
HPC	RFHQKILE	IAKEKPK	SDEDEDN	SMIVTDT	KILALVGG
HP-1163	RFHQKILE	IAKEKPK	SDEDEDN	SMIVTDT	KILALVGG
HP-1174	RFHQKILE	IAKEKPK	SNEYEDN	SMIVTDT	KILALVGG
HP-1144	RFHQKILE	IAKEKPK	SNEYEDN	SMIVTDT	KILALVGG
HP-870	RFHQKILE	IAKEKPK	SNEDEDN	SMIVTDT	KILALVGG
HP-1028	RFHQKILE	IAKEKPK	SNEDEDN	SIIVTDT	KILALVGG
Consensus	RFHQKILE	IAKEKPK	S#EdEDN	SmIVTDT	KILALVGG
	351				400
26695	YKSAFNRA	QAKRQFG	KPFVYQI	NGYSTTS	DTARNFEN
HPC	YKSAFNRA	QAKRQFG	KPFVYQI	NGYSTTS	DTARNFEN
HP-1163	YKSAFNRA	QAKRQFG	KPFVYQI	NGYSTTS	DAARNFEN
HP-1174	YKSAFNRA	QAKRQFG	KPFVYQI	NGYSTTS	DTARNFEN
HP-1144	YKSAFNRA	QAKRQFG	KPFVYQI	NGYSTTS	DTARNFEN
HP-870	YKSAFNRA	QAKRQFG	KPFVYQI	NGYSTTS	DTARNFEN
HP-1028	YEKSAFNRA	QAKRQFG	KPFVYQI	NGYSTTS	DTARNFEN
Consensus	YkSAFNRA	QAKRQFG	KPFvYQI	NGYSTTS	DtARNFEN
	401				450
26695	YSKNSEQN	WHPSNYS	LGLVTLQ	SHSLNLAT	LSDQLGFE
HPC	YSKNSEQN	WHPSNYS	LGLVTLQ	SHSLNLAT	LSDQLGFE
HP-1163	YSKNSEQN	WHPSNYS	LGLVTLQ	SLSLNLAT	LSDQLGFE
HP-1174	YSKNSEQN	WHPSNYS	LGLVTLQ	SHSLNLAT	LSDQLGFE
HP-1144	YSKNSEQN	WHPSNYS	LGLVTLQ	SHSLNLAT	LSDQLGFE
HP-870	YSKNSEQN	WHPSNYS	LGLVTLQ	SHSLNLAT	LSDQLGFE
HP-1028	YSKNSEQN	WHPRNYS	LGLVTLQ	SHSLNLAT	LSDQLGFE
Consensus	YSKNSeQn	WHpsNYS	LGLVTLQ	ShSLNLAT	LSDQLGFE
	451				500
26695	YQSLSDMG	NLPKDLS	GSPFAISP	AEKYSLE	GTMLKPM
HPC	YQSLSDMG	NLPKDLS	GSPFAISP	AEKYSLE	GTMLKPM
HP-1163	YQSLSDMG	NLPKDLS	GSPFAISP	AEKYSLE	GTMLKPM
HP-1174	YQSLSDMG	NLPKDLS	GSPFAISPI	AEKYSLE	GTMLKPM
HP-1144	YQSLSDMG	NLPKDLS	GSPFAISPI	AEKYSLE	GTMLKPM
HP-870	YQSLSDMG	NLPKDLS	GSPFAISPI	AEKYSLE	GTMLKPM
HP-1028	YQSLSDMG	NLPKDLS	GSPFAISPI	AEKYSLE	GTMLKPM
Consensus	YQSLSDMG	NLPKDLS	GSPFAISPI#	AEKYSLE	GTMLKPM

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501
26695 SITNQQNDVK TFTPMEtKKI TSKEQAFLL SVLMDAVENG TGSLARiKGL
HPC SITNQQNDVK TFTPMEtKKI TSKEQAFLL SVLINAVENG TGRLARTKGL
HP-1163 SITNQQNDVK TFTPMEtKKI TSKEQAFLL SVLINAVENG TGRLARTKGL
HP-1174 SITDQQNNIK TFTPPIETKKI TSKEQAFLL SVLMDAVENG TGSLARiKGL
HP-1144 SITDQQNNIK TFTPPIETKKI TSKEQAFLL SVLMDAVENG TGSLARiKGL
HP-870 SITDQQNDVK TFTPMEtKKI TSKEQAFLL SVLMDAVENG TGSLARiKGL
HP-1028 SITDQQNDVK TFTPPIETKKI TSKEQAFLL SVLMDAVENG TGSLARiKGL
Consensus SIT#QQN#iK TFTPMEtKKI TSKEQAFLL SVLm#AVENG TGsLARiKGL

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551
26695 EIAGKTGTSN NNIDAWFIGF TPTLQSVIWF GRDDNTPIsK GATGGVVSAP
HPC EIAGKTGTSN NNIDAWFIGF TPTLQSVIWF GRDDNTPIsK GATGGVVSAP
HP-1163 EIAGKTGTSN NNIDAWFIGF TPTLQSVIWF GRDDNTPIsK GATGGVVSAP
HP-1174 EIAGKTGTSN NNIDAWFIGF TPTLQSVIWF GRDDNTPIsK GATGGVVSAP
HP-1144 EIAGKTGTSN NNIDAWFIGF TPTLQSVIWF GRDDNTPIsK GATGGVVSAP
HP-870 EIAGKTGTSN NNIDAWFIGF TPTLQSVIWF GRDDNTPIgK GAAGSVVSAP
HP-1028 EIAGKsGTSN NNIDAWFIGF TPTLQSVIWF GRDDNTPIgK GATGGVVSAP
Consensus EIAGKtGTSN NNIDAWFIGF TPTLQSVIWF GRDDNTPIsK GAtGgVVSAP

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601
26695 VYSYEMRNIL AIEPSLKRKE DVPKGLRKEI VDKIPYYSTP NSITPTPKRT
HPC VYSYEMRNIL AIEPSLKRKE DVPKGLRKEI VDKIPYYSTP NSITPTPKRT
HP-1163 VYSYEMRNIL AIEPSLKRKE DVPKGLRKEI VDKIPYYSTP NSITPTPKRT
HP-1174 VYSYEMRNIL AIEPSLKRKE DVPKGLRKEI VDKIPYYSTP NSITPTPQKT
HP-1144 VYSYEMRNIL AIEPSLKRKE DVPKGLRKEI VDKIPYYSTP NSITPTPQKT
HP-870 VYSYEMRNIL AIEPSLKRKE DVPKGLRKEI VDKIPYYSTP NSITPTPQKT
HP-1028 VYSYEMRNIL SIEPSLKRKE DVPKGLRKEI VDKIPYYSTP NSITPTPKRT
Consensus VYSYEMRNIL aIEPSLKRKE DVPKGLRKEI VDKIPYYSTP NSITPTPkRT

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651
26695 DDSEERLLF
HPC DDSEERLLF
HP-1163 DDSEERLLF
HP-1174 DDSEERLLF
HP-1144 DDSEERLLF
HP-870 DDGKEPLLF
HP-1028 DDSEEP LLF
Consensus DDseErLLF

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Abbreviation: A, alanine; C, cysteine; D, aspartic acid; E, glutamic acid; F, phenylalanine; G, glycine; H, histidine; I, isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; W, tryptophan; Y, tyrosine; 26695, *H. pylori* 26695; HP, *H. pylori*; HPC, *H. pylori* NCTC 11637

Figure 12 Alignment of nucleotide sequences of *pbp1* gene.

	1				50
26695	ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTATTTT	TGATTGTCAT
HPC	ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTATTTT	TGATCATCAT
HP-1163	ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTATTTT	TGATCATCAT
HP-1174	ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTATTTT	TAATTGTCAT
HP-1144	ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTATTTT	TAATTGTCAT
HP-1028	ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTATTTT	TGATTATCAT
HP-870	ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTAGTTT	TGATTATCGT
Consensus	ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTAtTTT	TgAttatCaT
	51				100
26695	GGGGTTATTA	GCCATTCTTA	TCGCTCAAGT	TTGGGTAACT	ACGGATAAAG
HPC	AGGGTTGTTA	GCCATTCTTA	TCGCTCAAGT	TTGGGTAACT	ACGGATAAAG
HP-1163	AGGGTTGTTA	GCCATTCTTA	TCGCTCAAGT	TTGGGTAACT	ACGGATAAAG
HP-1174	AGGGTTATTA	GCCATTCTTA	TCGCTCAAGT	TTGGGTAACT	ACGGATAAAG
HP-1144	AGGGTTATTA	GCCATTCTTA	TCGCTCAAGT	TTGGGTAACT	ACGGATAAAG
HP-1028	GGGGTTGTTA	GCCATTCTTA	TCGCTCAAGT	TTGGGTAACT	ACGGATAAAG
HP-870	AGGGTTGTTA	GCCATTCTTA	TCGCTCAAGT	TTGGGTAACT	ACAGATAAAG
Consensus	aGGGTTgTTA	GCCATTCTTA	TCGCTCAAGT	TTGGGTAACT	ACgGATAAagG
	101				150
26695	ATATTGCTAA	AATTAAAGAT	TATCGCCCAG	GCGTCGCTTC	ACAGATTtTA
HPC	ATATTGCTAA	GATTAAAGAT	TATCGCCCgG	GTATCGCTTC	ACAGATTCTA
HP-1163	ATATTGCTAA	GATTAAAGAT	TATCGCCCgG	GTATCGCTTC	ACAGATTCTA
HP-1174	ATACTGCTAA	AATTAAAGAT	TATCGCCCgG	GCGTCGCTTC	ACAGATTtTA
HP-1144	ATATTGCTAA	AATTAAAGAT	TATCGCCCgG	GCGTCGCTTC	ACAGATTtTA
HP-1028	ATATTGCTAA	GATTAAAGAT	TATCGCCCgG	GCGTCGCTTC	ACAGATTtTA
HP-870	ATATTGCTAA	AATTAAAGAT	TATCGCCCgG	GTGTCGCTTC	ACAGATTtTA
Consensus	ATAtTGCTAA	aATTAAAGAT	TATCGCCCgG	GcgTCGCTTC	ACAGATTtTA
	151				200
26695	GACCGAAAAG	GGCGTTTGAT	CGCTAATATC	TATGATAAAG	AATTtCGTTT
HPC	GACCGAAAAG	GGCGTTTGAT	CGCTAATATC	TATGATAAAG	AATTCCGTTT
HP-1163	GACCGAAAAG	GGCGTTTGAT	CGCTAATATC	TATGATAAAG	AATTCCGTTT
HP-1174	GACCGAAAAG	GGCGTTTGAT	CGCTAATATC	TATGACAAGG	AATTCCGTTT
HP-1144	GACCGAAAAG	GGCGTTTGAT	CGCTAATATC	TATGACAAGG	AATTCCGTTT
HP-1028	GACCGAAAAG	GGCGTTTGAT	CGCTAATATC	TATGATAAAG	AATTtCGTTT
HP-870	GACAGAAAAG	GGCGTTTGAT	CGCTAATATt	TACGATAAAG	AATTtCGTTT
Consensus	GACcGAAAAG	GGCGTTTGAT	CGCTAATATc	TatGAtAAGg	AATTtCGTTT
	201				250
26695	TTATGCGCGT	TTTGAAGAAA	TCCCCCCACG	ATTTATTGAA	AGCCTTTTAg
HPC	TTATGCGCGT	TTTGAAGAAA	TCCCCCCACG	ATTTATTGAA	AGCCTTTTAg
HP-1163	TTATGCGCGT	TTTGAAGAAA	TCCCCCCACG	ATTTATTGAA	AGCCTTTTAg
HP-1174	TTATGCACGT	TTTGAAGAAA	TCCCCCCACG	ATTTGTTGAA	AGCCTTTTAg
HP-1144	TTATGCACGT	TTTGAAGAAA	TCCCCCCACG	ATTTGTTGAA	AGCCTTTTAg
HP-1028	TTATGCGCGT	TTTGAAGAAA	TCCCCCCACG	ATTTATTGAA	AGCCTTTTAg
HP-870	TTATGCGCGT	TTTGAAGAAA	TCCCCCCACG	ATTTATTGAA	AGCCTTTTAg
Consensus	TTATGCgCGT	TTTGAAGAAA	TCCCCCCACG	ATTTAttGAA	AGCCTTTTAg

	251				300
26695	CGGTAGAAGA	CACCCTCTTT	TTTGAACATG	GGGGGATCAA	TTTAGACGCT
HPC	CGGTAGAAGA	CACCCTCTTT	TTTGAACATG	GGGGGATCAA	TTTAGACGCT
HP-1163	CGGTAGAAGA	CACCCTCTTT	TTTGAACATG	GGGGGATCAA	TTTAGACGCT
HP-1174	CGGTAGAAGA	CACCCTCTTT	TTTGAACATG	GGGGGATCAA	TTTAGACGCT
HP-1144	CGGTAGAAGA	CACCCTCTTT	TTTGAACATG	GGGGGATCAA	TTTAGACGCT
HP-1028	CGGTAGAAGA	CACCCTCTTT	TTTGAGCATG	GGGGGATCAA	TTTAGACGCT
HP-870	CAGTAGAAGA	CACCCTCTTT	TTTGAGCATG	GGGGGATCAA	TTTAGACGCT
Consensus	CgGTAGAAGA	CACCCTCTTT	TTTGAaCATG	GGGGGATCAA	TTTAGACGCT

	301				350
26695	ATCATGCGCG	CTATGATTAA	AAACGCTAAA	AGCGGTCGTT	ACACCGAGGG
HPC	ATCATGCGCG	CTATGATTAA	AAACGCTAAA	AGCGGTCGTT	ACACTGAAGG
HP-1163	ATCATGCGCG	CTATGATTAA	AAACGCTAAA	AGCGGTCGTT	ACACTGAAGG
HP-1174	ATCATGCGCG	CTATGATTAA	AAATGCTAAA	AGCGGTCGTA	CCACCGAGGG
HP-1144	ATCATGCGCG	CTATGATTAA	AAATGCTAAA	AGCGGTCGTT	ACACCGAGGG
HP-1028	ATCATGCGCG	CTATGATTAA	AAACGCTAAA	AGCGGTCGTT	ACACTGAAGG
HP-870	ATCATGCGTG	CTATGATTAA	AAACGCTAAA	AGCGGTCGTT	ACACCGAGGG
Consensus	ATCATGCGcG	CTATGATTAA	AAAcGCTAAA	AGCGGTCGtT	aCACcGAGgG

	351				400
26695	GGGTAGCACC	CTAACCCAAC	AATTCGTTAA	AAACATGGTG	CTCACACGAG
HPC	GGGCAGCACT	CTAACCCAAC	AACTCGTTAA	AAACATGGTG	CTCACGCGAG
HP-1163	GGGCAGCACT	CTAACCCAAC	AACTCGTTAA	AAACATGGTG	CTCACGCGAG
HP-1174	GGGTAGCACC	CTAACCCAAC	AACTCGTTAA	AAACATGGTG	CTCACACGAG
HP-1144	GGGTAGCACC	CTAACCCAAC	AACTCGTTAA	AAACATGGTG	CTCACACGAG
HP-1028	GGGTAGCGCC	CTAACCCAAC	AACTCGTTAA	AAACATGGTG	CTCACACGAG
HP-870	GGGTAGCACC	CTAACCCAAC	AACTCGTTAA	AAACATGGTG	CTCACACGAG
Consensus	GGGtAGCaCc	CTAACCCAAC	AAcTCGTTAA	AAACATGGTG	CTCACaCGAG

	401				450
26695	AAAAAACCCT	AACCAGAAAA	CTCAAAGAAG	CGATCATTTC	TATACGCATT
HPC	AAAAAACATT	AACCAGAAAA	CTCAAAGAAG	CTATCATTTC	TTTACGCATT
HP-1163	AAAAAACATT	AACCAGAAAA	CTCAAAGAAG	CTATCATTTC	TTTACGCATT
HP-1174	AAAAAACATT	AACCAGAAAA	CTCAAAGAAG	CTATCATTTC	TTTACGCATT
HP-1144	AAAAAACATT	AACCAGAAAA	CTCAAAGAAG	CTATCATTTC	TTTACGCATT
HP-1028	AAAAAACGCT	AACCAGAAAA	CTCAAAGAAG	CGATCATTTC	CATACGCATT
HP-870	AAAAAACCCT	AACCAGAAAA	CTCAAAGAAG	CTATCATTTC	CATACGCATT
Consensus	AAAAAAC.cT	AACCAGAAAA	CTCAAAGAAG	CtATCATTTC	tATACGCATT

	451				500
26695	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	GAGCGTTATT	TGAACCAAAC
HPC	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	GAGCGTTATT	TGAACCAAAC
HP-1163	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	GAGCGTTATT	TGAACCAAAC
HP-1174	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	GAGCGTTATT	TGAACCAAAC
HP-1144	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	GAGCGTTATT	TGAACCAAAC
HP-1028	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	GAGCGTTATT	TGAACCAAAC
HP-870	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	GAGCGCTATT	TGAACCAAAC
Consensus	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	GAGCGtTATT	TGAACCAAAC

	501				550
26695	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	TTAGGGTATT
HPC	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	TTAGGGTATT
HP-1163	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	TTAGGGTATT
HP-1174	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	TTAGGGTATT
HP-1144	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	TTAGGGTATT
HP-1028	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	TTAGGGTATT
HP-870	TTTTTTTGGG	CATGGGTATT	ATGGCGTCAA	AACCGCAAGT	TTAGGGTATT
Consensus	TTTTTTTGGG	CATGGGTATT	ATGGCGTgAA	AACCGCAAGT	TTAGGGTATT

	551				600
26695	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGCTAGTC
HPC	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGtTAGTC
HP-1163	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGtTAGTC
HP-1174	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGtTAGTC
HP-1144	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGtTAGTC
HP-1028	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGtTAGTC
HP-870	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGtTAGTC
Consensus	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGtTAGTC

	601				650
26695	GCCTTGCCTA	GGGCTCCGAG	TTTTTATGAT	CCTACCAAAA	ATTTAGAATT
HPC	GCCTTGCCTA	GGGCTCCGAG	TTTTTATGAT	CCTACCAAAA	ATTTAGAATT
HP-1163	GCCTTGCCTA	GGGCTCCGAG	TTTTTATGAT	CCTACCAAAA	ATTTAGAATT
HP-1174	GCCTTGCCCA	GAGCTCCGAG	TTTTTATGAC	CCTACCAAAA	ATTTAGAATT
HP-1144	GCCTTGCCCA	GAGCTCCGAG	TTTTTATGAC	CCTACCAAAA	ATTTAGAATT
HP-1028	GCCTTGCCTA	GGGCTCCGAG	TTTTTATGAC	CCTACCAAAA	ATTTAGAATT
HP-870	GCCTTGCCTA	GGGCTCCAAG	TTTTTATGAC	CCTACCAAAA	ATTTAGAATT
Consensus	GCCTTGCCtA	GgGCTCCgAG	tTTTTATGAC	CCTACCAAAA	ATTTAGAATT

	651				700
26695	TTCACtCTCT	AGGGCTAATG	ATATTTTAAG	GCGGTtGTAT	TCTTTAGGcT
HPC	TTCACtCTCT	AGAGCTAATG	ATATTTTAAG	GCGGTtGTAT	TCTTTAGGcT
HP-1163	TTCACtCTCT	AGAGCTAATG	ATATTTTAAG	GCGGTtGTAT	TCTTTAGGcT
HP-1174	TTCACtTTCT	AGGGCTAATG	ATATTTTAAG	GCGGTtGTAT	TCTTTGGGtT
HP-1144	TTCACtTTCT	AGGGCTAATG	ATATTTTAAG	GCGGTtGTAT	TCTTTGGGtT
HP-1028	TTCACtCTCT	AGGGCTAATG	ATATTTTAAG	GCGGTtGTAT	TCTTTGGGtT
HP-870	TTCACtCTCT	AGGGCTAATG	ATATTTTAAG	GCGGTtGTAT	TCTTTAGGcT
Consensus	TTCACtCTCT	AGgGCTAATG	ATATTTTAAG	GCGGTtGTAT	TCTTTaGGcT

	701				750
26695	GGATtTCTTC	TAACGAGCTC	AAAGGCGCTC	TCAATGAAGT	GCCAATtGTT
HPC	GGATtTCTTC	TAACGAGCTC	AAAGGCGCTC	TCAATGAAGT	GCCAATcGTC
HP-1163	GGATtTCTTC	TAACGAGCTC	AAAGGCGCTC	TCAATGAAGT	GCCAATcGTC
HP-1174	GGATCTCTTC	TAACGAGCTC	AAAGGCGCTC	TCAATGAAGT	GCCAATcGTC
HP-1144	GGATCTCTTC	TAACGAGCTC	AAAGGCGCTC	TCAATGAAGT	GCCAATcGTC
HP-1028	GGATCTCTTC	TAACGAGCTC	AAAGGCGCTC	TCAATGAAGT	GCCAATcGTC
HP-870	GGATtTCTTC	TAACGAGCTC	AAATcCTCTC	TCAATGAAGT	GCCAATcGTC
Consensus	GGATtTCTTC	TAACGAGCTC	AAAgGcGCTC	TCAATGAAGT	GCCAATcGTc

	751		800
26695	TATAACCAAA	CCTCCACGCA	AAACATCGCC
HPC	TATAACCAAA	CTTCCACGCA	AAATATCGCT
HP-1163	TATAACCAAA	CTTCCACGCA	AAATATCGCT
HP-1174	TATAACCAAA	CTTCCACGCA	AAATATCGCC
HP-1144	TATAACCAAA	CTTCCACGCA	AAATATCGCC
HP-1028	TATAACCAAA	CTTCCACGCA	AAATATCGCC
HP-870	TATAACCAAA	CTTCCACGCA	AAATATCGCT
Consensus	TATAACCAAA	CtTCCACGCA	AAAtATCGCc
	801		850
26695	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT
HPC	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT
HP-1163	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT
HP-1174	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT
HP-1144	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT
HP-1028	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT
HP-870	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT
Consensus	GTTGAAGCAA	TTGGATCAAT	TAGACGGGTT
	851		900
26695	TAAAGCTCAC	GATAGATTTG	GATTACCAAC
HPC	TAAAGCTCAC	GATAGATTTG	GATTACCAAC
HP-1163	TAAAGCTCAC	GATAGATTTG	GATTACCAAC
HP-1174	TCAAGCTCAC	GATAGATTTG	GATTACCAAC
HP-1144	TCAAGCTCAC	GATAGATTTG	GATTACCAAC
HP-1028	TCAAGCTCAC	GATAGATTTG	GATTACCAAC
HP-870	TAAACTCAC	GATAGATTTG	GATTACCAAC
Consensus	TaAAGcTCAC	GATAGATTTG	GATTACCAAC
	901		950
26695	CGTTTTGGGC	ATCAAAAAAT	CTTAGAAAAA
HPC	CGTTTTGGGC	ATCAAAAAAT	CTTAGAAAAA
HP-1163	CGTTTTGGGC	ATCAAAAAAT	CTTAGAAAAA
HP-1174	CGTTTTGGGC	ACCAAAAAAT	CTTAGAAAAA
HP-1144	CGTTTTGGGC	ACCAAAAAAT	CTTAGAAAAA
HP-1028	CGTTTTGGGC	ACCAAAAAAT	CTTAGAAAAA
HP-870	CGTTTTGGGC	ATCAAAAAAT	CTTAGAAAAA
Consensus	CGTTTTGGGC	AtCAAAAAAT	CTTAGAAAAA
	951		1000
26695	AACTAACGCG	TCTAATGAAG	ATGAAGACAA
HPC	AACTAACGCC	TCTGATGAAG	ATGAAGACAA
HP-1163	AACTAACGCC	TCTGATGAAG	ATGAAGACAA
HP-1174	AACTAACGCA	TCTAATGAAT	ATGAAGACAA
HP-1144	AACTAACGCA	TCTAATGAAT	ATGAAGACAA
HP-1028	AACTAACGCA	TCTAATGAAG	ATGAAGATAA
HP-870	AACTAACGCC	TCTAATGAAG	ATGAAGACAA
Consensus	AACTAACGC.	TCTaATGAAG	ATGAAGAcAA

	1001		1050
26695	TTACAGACAC GAGCACCGGT AAGATTTT TAG CTTTAGTGGG GGGGATTGAT		
HPC	TTACAGACAC GAGCACCGGT AAGATTTT TAG CTTTAGTGGG GGGGATTGAT		
HP-1163	TTACAGACAC GAGCACCGGT AAGATTTT TAG CTTTAGTGGG GGGGATTGAT		
HP-1174	TTACAGACAC GAGCACCGGT AAGATTTT TAG CTTTAGTGGG GGGGATTGAT		
HP-1144	TTACAGACAC GAGCACCGGT AAGATTTT TAG CTTTAGTGGG GGGGATTGAT		
HP-1028	TTACAGACAC GAGTACCGGT AAGATTTT TAG CTTTAGTGGG GGGGATTGAT		
HP-870	TTACAGACAC AAGCACCGGT AAGATTTT TAG CTCTAGTGGG GGGGATTGAT		
Consensus	TTACAGACAC gAGcACCGGT AAGATTTT TAG CTtTAGTGGG GGGGATTGAT		
	1051		1100
26695	TATAAAAAA GCGCTTTCAA TCGCGCCACG CAAGCCAAAC GGCAGTTTGG		
HPC	TATAAAAAA GCGCTTTCAA TCGCGCCACG CAAGCCAAAC GGCAGTTTGG		
HP-1163	TATAAAAAA GCGCTTTCAA TCGCGCCACG CAAGCCAAAC GGCAGTTTGG		
HP-1174	TATAAAAAA GCGCTTTCAA TCGCGCCACG CAAGCCAAAC GGCAGTTTGG		
HP-1144	TATAAAAAA GCGCTTTCAA TCGCGCCACG CAAGCCAAAC GGCAGTTTGG		
HP-1028	TATGAAAAA GCGCTTTCAA TCGCGCCACG CAAGCCAAAC GGCAGTTTGG		
HP-870	TATAAAAAA GCGCTTTCAA TCGCGCCACG CAAGCCAAAC GGCAGTTTGG		
Consensus	TATaAAAAA GCGCTTTCAA TCGCGCCACG CAAGCCAAAC GGCAGtTTTGG		
	1101		1150
26695	GAGCGCGATA AAGCCTTTTG TGTATCAGAT CGCTTTTGAT AATGGCTATT		
HPC	GAGCGCGATA AAGCCTTTTG TGTATCAAAAT CGCTTTTGAT AATGGCTATT		
HP-1163	GAGCGCGATA AAGCCTTTTG TGTATCAAAAT CGCTTTTGAT AATGGCTATT		
HP-1174	GAGCGCGATC AAGCCTTTTG TGTATCAAAAT CGCTTTTGAT AATGGCTATT		
HP-1144	GAGCGCGATC AAGCCTTTTG TGTATCAAAAT CGCTTTTGAT AATGGCTATT		
HP-1028	GAGCGCGATA AAGCCTTTTC TGTATCAAAAT CGCTTTTGAT AATGGCTATT		
HP-870	GAGCGCAATA AAGCCTTTTG TGTATCAAAAT CGCTTTTGAT AATGGCTATT		
Consensus	GAGCGCgATa AAGCCTTTTg TGTATCAaAT CGCTTTTGAT AATGGCTATT		
	1151		1200
26695	CCACGACTTC TAAAATCCCT GATACCGCGC GAAACTTTGA AAATGGCAAT		
HPC	CCACCACTTC CAAAATCCCT GATACCGCGC GAAACTTTGA AAATGGCAAT		
HP-1163	CCACCACTTC CAAAATCCCT GATGCCGCGC GAAACTTTGA AAATGGCAAT		
HP-1174	CCACGACTTC CAAAATCCCT GATACCGCAC GAAACTTTGA AAATGGCAAT		
HP-1144	CCACGACTTC CAAAATCCCT GATACCGCAC GAAACTTTGA AAATGGCAAT		
HP-1028	CCACCACTTC TAAAATCCCT GATACCGCGC GAAACTTTGA AAATGGC---		
HP-870	CCACCACTTC TAAAATCCCT GATACCGCGC GAAATTTTGA AAATGGCAAT		
Consensus	CCACcACTTC tAAAATCCCT GATACCGCgC GAAAcTTTGA AAATGGCaat		
	1201		1250
26695	TATAGTAAAA ACAGTGAACA AAACCACGCA TGGCACCCCA GCAATTATTC		
HPC	TATAGTAAAA ACAGCGAACA AAACCACGCA TGGCACCCCA GCAATTATTC		
HP-1163	TATAGTAAAA ACAGCGTACA AAGCCACGCA TGGCACCCCA GCAATTATTC		
HP-1174	TATAGTAAAA ACAGCGAACA AAACCACGCA TGGCACCCCA GCAATTATTC		
HP-1144	TATAGTAAAA ACAGCGAACA AAACCACGCA TGGCACCCCA GCAATTATTC		
HP-1028	TATAGTAAAA ACAGCGAACA AAACCACGCA TGGCACCCCA GCAATTATTC		
HP-870	TATAGTAAAA ACAGCGAACA AAACCACGCA TGGCACCCCA GCAATTATTC		
Consensus	TATAGTAAAA ACAGcGAACA AAACCACGCA TGGCACCCcA GcAATTATTC		

	1251				1300
26695	TCGCAAGTTT	TTAGGGCTTG	TAACCTTGCA	AGAAGCCTTG	AGCCATTTCGT
HPC	TCGCAAGTTT	TTAGGGCTTG	TAACCTTGCA	AGAAGCCTTA	AGCCATTTCGT
HP-1163	TCGCAAGTTT	TTAGGGCTTG	TAACCTTGCA	AGAAGCCTTA	AGCCTTTTCGT
HP-1174	TCGCAAGTTT	TTAGGGCTTG	TAACCTTGCA	AGAAGCTTTG	AGCCATTTCGT
HP-1144	TCGCAAGTTT	TTAGGGCTTG	TAACCTTGCA	AGAAGCTTTG	AGCCATTTCGT
HP-1028	TCGCAAGTTT	TTAGGGCTTG	TAACCTTGCA	AGAAGCTTTG	AGCCATTTCGT
HP-870	TCGCAAGTTT	TTAGGGCTTG	TAACCTTGCA	AGAAGCTTTG	AGCCATTTCGT
Consensus	TCGCAAGTTT	TTAGGGCTTG	TAACCTTGCA	AGAAGCtTTg	AGCCATTTCGT
	1301				1350
26695	TAAATCTAGC	CACGATCAAT	TTAAGCGATC	AGCTTGGCTT	TGAAAAAATT
HPC	TAAATCTAGC	CACGATCAAT	TTAAGCGATC	AGCTTGGCTT	TGAAAAAATT
HP-1163	TAAATCTAGC	CACGATCAAT	TTAAGTGATC	AGCTTGGCTT	TGAAAAAATT
HP-1174	TAAATCTAGC	CACGATCAAT	TTAAGCGATC	AGCTTGGCTT	TGAAAAAATT
HP-1144	TAAATCTAGC	CACGATCAAT	TTAAGCGATC	AGCTTGGCTT	TGAAAAAATT
HP-1028	TAAATCTAGC	CACGATCAAT	TTAAGCGATC	AGCTTGGCTT	TGAAAAAATT
HP-870	TAAATCTGGC	CACGATCAAT	TTAAGCGATC	AGCTTGGCTT	TGAAAAAATT
Consensus	TAAATCTaGC	CACGATCAAT	TTAAGCGATC	AGCTTGGCTT	TGAAAAAATT
	1351				1400
26695	TATCAATCTT	TAAGCGATAT	GGGGTTTTAA	AACCTCCCTA	AGGACTTGTC
HPC	TATCAATCTT	TAAGCGATAT	GGGGTTTTAA	AACCTCCCTA	AGGACTTGTC
HP-1163	TATCAATCTC	TAAGCGATAT	GGGGTTTTAA	AACCTCCCTA	AGGACTTGTC
HP-1174	TATCAATCTT	TAAGCGATAT	GGGGTTTTAA	AACCTCCCTA	AAGACTTGTC
HP-1144	TATCAATCTT	TAAGCGATAT	GGGGTTTTAA	AACCTCCCTA	AAGACTTGTC
HP-1028	TATCAATCTT	TAAGCGATAT	GGGGTTTTAA	AACCTCCCTA	AAGACTTGTC
HP-870	TATCAATCTT	TAAGCGATAT	GGGGTTTTAA	AATCTCCCTA	AAGACTTGTC
Consensus	TATCAATCTT	TAAGCGATAT	GGGGTTTTAA	AaCtCCCTA	AaGACTTGTC
	1401				1450
26695	TATtGTGTTA	GGGAGCTTTG	CTATCTCACC	CATTGATGCA	GCTGAAAAGT
HPC	TATCGTGTTA	GGGAGCTTTG	CTATCTCACC	CATTGATGCG	GCTGAAAAGT
HP-1163	TATCGTGTTA	GGGAGCTTTG	CTATCTCACC	CATTGATGCG	GCTGAAAAGT
HP-1174	TATtGTATTA	GGGAGCTTTG	CTATCTCACC	GATTGAAGCG	GCTGAAAAGT
HP-1144	TATtGTATTA	GGGAGCTTTG	CTATCTCACC	GATTGAAGCG	GCTGAAAAGT
HP-1028	TATtGTGTTA	GGGAGCTTTG	CTATCTCACC	GATTGAAGCG	GCTGAAAAGT
HP-870	TATtGTGTTA	GGAAGCTTTG	CTATCTCACC	GATTGAAGCG	GCTGAAAAGT
Consensus	TATtGTgTTA	GgGAGCTTTG	CTATCTCACC	gATTGAaGCg	GCTGAAAAGt
	1451				1500
26695	ATTCTTTATT	TTCTAATTAC	GGCACCATGC	TCAAACCCAT	GCTCATTGAA
HPC	ATTCTTTATT	TTCTAATTAC	GGCACCATGC	TCAAACCCAT	GCTCATTGAA
HP-1163	ATTCTTTATT	TTCTAATTAC	GGCACCATGC	TCAAACCCAT	GCTCATTGAA
HP-1174	ATTCTTTATT	TTCTAATTAC	GGCACCATGC	TCAAACCCAT	GCTCATTGAA
HP-1144	ATTCTTTATT	TTCTAATTAC	GGCACCATGC	TCAAACCCAT	GCTCATTGAA
HP-1028	ATTCTTTATT	TTCTAATTAC	GGCACCATGC	TCAAACCCAT	GCTCATTGAA
HP-870	ATTCTTTATT	TTCTAATTAC	GGCACCATGC	TCAAACCCAT	GCTCATTGAA
Consensus	ATTCTTTATT	TTCTAATTAC	GGCACCATGC	TCAAACCCAT	GCTCATTGAA

	1501		1550
26695	AGCATCACTA	ACCAACAAAA	CGATGTCAA
HPC	AGCATCACTA	ACCAACAAAA	CGATGTCAA
HP-1163	AGCATCACTA	ACCAACAAAA	CGATGTCAA
HP-1174	AGCATTACCG	ATCAGCAAAA	CAATATCAA
HP-1144	AGCATTACCG	ATCAGCAAAA	CAATATCAA
HP-1028	AGCATCACTG	ACCAACAAAA	CGATGTCAA
HP-870	AGCATCACTG	ACCAACAAAA	CGATGTCAA
Consensus	AGCATcACTg	AcCAaCAAAA	CgATgTCAA
	1551		1600
26695	CAAAAAGATC	ACCTCCAAAG	AACAGGCTTT
HPC	CAAAAAGATC	ACCTCCAAAG	AACAGGCTTT
HP-1163	CAAAAAGATC	ACCTCCAAAG	AACAGGCTTT
HP-1174	CAAAAAGATC	ACCTCCAAAG	AACAGGCTTT
HP-1144	CAAAAAGATC	ACCTCCAAAG	AACAGGCTTT
HP-1028	CAAAAAGATC	ACCTCCAAAG	AACAGGCTTT
HP-870	CAAAAAGATC	ACCTCTAAAG	AGCAAGCTTT
Consensus	CAAAAAGATC	ACCTCcAAAG	AaCAGGCTTT
	1601		1650
26695	TGGATGCGGT	AGAAAATGGC	ACAGGGAGTT
HPC	TAAATGCGGT	AGAAAACGGC	ACAGGGCGTT
HP-1163	TAAATGCGGT	AGAAAACGGC	ACAGGGCGTT
HP-1174	TGAATGCGGT	AGAAAACGGC	ACAGGAAATT
HP-1144	TGAATGCGGT	AGAAAACGGC	ACAGGAAATT
HP-1028	TGAATGCGGT	AGAAAATGGC	ACGGGGAGTT
HP-870	TGAATGCGGT	AGAAAATGGC	ACAGGGAGTT
Consensus	TgaATGCGGT	AGAAAAtGGC	ACaGGgagTT
	1651		1700
26695	GAAATCGCCG	GTAAAACCGG	GACTTCTAAC
HPC	GAAATCGCCG	GTAAAACCGG	GACTTCTAAC
HP-1163	GAAATCGCCG	GTAAAACCGG	GACTTCTAAC
HP-1174	GAAATTGCCG	GTAAAACCGG	GACTTCTAAC
HP-1144	GAAATTGCCG	GTAAAACCGG	GACTTCTAAC
HP-1028	GAAATCGCCG	GTAAAAGCGG	GACTTCTAAC
HP-870	GAAATTGCCG	GTAAAACCGG	GACTTCTAAC
Consensus	GAAATcGCCG	GTAAAACCGG	GACTTCTAAC
	1701		1750
26695	CATTGGCTTT	ACCCCCACCT	TGCAAAGCGT
HPC	CATTGGCTTT	ACCCCCACCT	TGCAAAGCGT
HP-1163	CATTGGCTTT	ACCCCCACCT	TGCAAAGCGT
HP-1174	CATTGGTTTT	ACCCCCACCT	TACAAAGCGT
HP-1144	CATTGGTTTT	ACCCCCACCT	TACAAAGCGT
HP-1028	CATTGGCTTT	ACCCCCACCT	TACAGAGCGT
HP-870	CATTGGCTTT	ACCCCCACCT	TACAAAGCGT
Consensus	CATTGGcTTT	ACCCCCACCT	TaCAaAGCGT

	1751		1800
26695	ATAACACGCC	TATTAGCAAA	GGAGCGACAG GGGGTGTTGT GAGTGCGCCT
HPC	ATAACACGCC	TATTAGCAAA	GGAGCGACAG GAGGCGTTGT GAGTGCACCT
HP-1163	ATAACACGCC	TATTAGCAAA	GGAGCGACAG GAGGCGTTGT GAGTGCACCT
HP-1174	ATAACACGCC	TATTAGCAAA	GGAGCGACAG GAGGCGTTGT GAGTGCACCT
HP-1144	ATAACACGCC	TATTAGCAAA	GGAGCGACAG GAGGCGTTGT GAGTGCACCT
HP-1028	ATAACACGCC	TATTGGCAAA	GGAGCGACAG GAGGCGTTGT GAGCGCGCCT
HP-870	ATAACACACC	TATTGGCAAA	GGAGCGGCAG GAAGCGTTGT GAGTGCGCCT
Consensus	ATAACACgCC	TATTaGCAAA	GGAGCGaCAG GagGcGTTGT GAGtGCgCCT
	1801		1850
26695	GTGTATTCGT	ATTTTCATGCG	TAACATTTTA GCGATTGAAC CTTCTTTAAA
HPC	GTGTATTCGT	ATTTTCATGCG	TAATATTTTA GCGATTGAAC CTTCTTTAAA
HP-1163	GTGTATTCGT	ATTTTCATGCG	TAATATTTTA GCGATTGAAC CTTCTTTAAA
HP-1174	GTGTATTCGT	ATTTTCATGCG	TAACATTTTA GCGATTGAAC CTTCTTTAAA
HP-1144	GTGTATTCGT	ATTTTCATGCG	TAACATTTTA GCGATTGAAC CTTCTTTAAA
HP-1028	GTGTATTCGT	ATTTTCATGCG	TAATATTCTA AGCATTGAAC CTTCTTTAAA
HP-870	GTGTATTCGT	ATTTTCATGCG	TAATATTTTA GCGATCGAAC CTTCTTTAAA
Consensus	GTGTATTCGT	ATTTTCATGCG	TAATATTTtTA gcgAttGAAC CTTCTTTAAA
	1851		1900
26695	AAGAAAGTTT	GATGTCCCCA	AAGGCTTGCG TAAAGAAATC GTGGATAAAA
HPC	AAGAAAGTTT	GATGTCCCCA	AAGGCTTGCG TAAAGAAATC GTGGATAAAA
HP-1163	AAGAAAGTTT	GATGTCCCCA	AAGGCTTGCG TAAAGAAATC GTGGATAAAA
HP-1174	AAGAAAGTTT	GATGTCCCCA	AAGGCTTGCG TAAAGAAATC GTGGATAAAA
HP-1144	AAGAAAGTTT	GATGTCCCCA	AAGGCTTGCG TAAAGAAATC GTGGATAAAA
HP-1028	AAGAAAGTTT	GATGTCCCCA	AAGGCTTGCG TAAAGAAAT T GTGGATAAAA
HP-870	AAGAAAGTTT	GATGTCCCCA	AAGGCTTGCG TAAAGAAATC GTGGATAAAA
Consensus	AAGAAAGTTT	GATGTCCCCA	AAGGCTTGCG TAAAGAAATc GTGGATAAAA
	1901		1950
26695	TCCCCTACTA	TTCAACCCCT	AATTCATCA CCCCACCCC CAAAAGAACA
HPC	TCCCCTACTA	CTCAACTCCT	AATTCATCA CCCCACCCC CAAAAGAACA
HP-1163	TCCCCTACTA	CTCAACTCCT	AATTCATCA CCCCACCCC CAAAAGAACA
HP-1174	TCCCCTACTA	CTCAACCCCT	AACTCCATCA CCCCACCCC CAAAAAACA
HP-1144	TCCCCTACTA	CTCAACCCCT	AACTCCATCA CCCCACCCC CAAAAAACA
HP-1028	TCCCCTACTA	TTCAACCCCT	AATTCATCA CCCCACCCC CAAAAGAACA
HP-870	TCCCCTACTA	CTCAACCCCT	AATTCATCA CCCCACCCC AAAAAAACC
Consensus	TCCCCTACTA	cTCAACcCCT	AATTCcATCA CCCCcACCCC caAAAgAACa
	1951		1980
26695	GACGATAGCG	AGGAACGCTT	GTTGTTCTAA
HPC	GACGATAGTG	AGGAACGCTT	GTTGTTCTAA
HP-1163	GACGATAGTG	AGGAACGCTT	GTTGTTCTAA
HP-1174	GACGATAGCG	AGGAGCGCTT	GTTGTTCTAA
HP-1144	GACGATAGCG	AGGAGCGCTT	GTTGTTCTAA
HP-1028	GACGATAGCG	AAGAACCCTT	ATTGTTCTAA
HP-870	GACGATGGCA	AAGAACCCTT	ATTGTTCTAA
Consensus	GACGATaGcg	AgGAaCgCTT	gTTGTTCTAA

Abbreviations: A, adenine; C, cytosine; G, guanine; T, thymine; 26695, *H. pylori* 26695; HP, *H. pylori*; HPC, *H. pylori* NCTC 11637

1. 64 codon on DNA

First Position	Second Position				Third Position
	T	C	A	G	
T	F	S	Y	C	T
	F	S	Y	C	C
	L	S	STOP CODON	STOP CODON	A
	L	S	STOP CODON	W	G
C	L	P	H	R	T
	L	P	H	R	C
	L	P	Q	R	A
	L	P	Q	R	G
A	I	T	N	S	T
	I	T	N	S	C
	I	T	K	R	A
	M	T	K	R	G
G	V	A	D	G	T
	V	A	D	G	C
	V	A	E	G	A
	V	A	E	G	G

Abbreviation: A, alanine; C, cysteine; D, aspartic acid; E, glutamic acid; F, phenylalanine; G, glycine; H, histidine; I, isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; W, tryptophan; Y, tyrosine

BIOGRAPHY

Miss. Punjapon Prasurthsin was born on November 4, 1971 in Ubonrajathanee, Thailand. She graduated with the Bachelor degree of Agronomy from the Faculty of Agriculture, Ubon Rajathanee University in 1994. She is currently a member of Bacteriology Unit, Department of Microbiology, King Chulalongkorn Memorial Hospital and was given the opportunity to pursue her MS degree in the Inter-Department of Medical Microbiology, Faculty of Graduate School, Chulalongkorn University since 2002.



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