

SUPPLEMENTARY MATERIALS

Text 1

23S ribosomal gene sequence of *H. pylori* (GenBank Accession: No.U27270)

Suquence 1 2142,2143,2144 wild strain

AGCCCGAGTAAACGGCGGCCGTAACTATAACGGCCTAAGGTAGCGAAATTCTTGTGGTTAAATACCGACCTGC
ATGAATGGCGTAACGAGATGGAGCTGTCAACCAGAGATTCACTGAAATTGAGTGGAGGTGAAAATTCTCC
TACCCGCGCAAGACGGAAAGACCCGTGGACCTTACTACAACCTAGCACTGCTAATGGGAATATCATGCGCAG
GATAGGTGGGAGGTTGAAGTAAGGGCTTGGCTTATGGAGTCATCCTGAGATACCACCCCTGATGTTCTG
TTAGCTAACGGCCTGTGTTATCCACAGGCAGGACAATGCTGGTGGTAGTTGACTGGGGCGGTGCTCCTAA
AAAGTAACGGAGGCTGCAAAGGTTGGCTATTGCGGTTGAAATCGCAAGTTGAGTGTAAATGGC(294bp)ACA
AGCCAGCCTGACTGTAAGACATACAAGTCAAGCAGAGACGAAAGTCGG(505bp)

Suquence2 A2142G mutation strain 2

TAAACGGCGGCCGTAACTATAACGGCCTAAGGTAGCGAAATTCTTGTGGTTAAATACCGACCTGCATGAATGG
CGTAACGAGATGGAGCTGTCTCAACCAGAGATTCACTGAAATTGAGTGGAGGTGAAAATTCTCCTACCCGCG
GCAAGACGGAAAGACCCGTGGACCTTACTACAACCTAGCACTGCTAATGGGAATATCATGCGCAGGATAGGTG
GGAGGCTTGAAGTAAGGGCTTGGCTTATGGAGTCATCCTGAGATACCACCCCTGATGTTCTGTTAGCTAA
CTGGCCTGTGTTATCCACAGGCAGGACAATGCTGGTGGTAGTTGACTGGGGCGGTGCTCCTAAAAAGTAAC
GGAGGCTTGCAAAGGTTGGCTATTGCGGTTGAAATCGCAAGTTGAGTGTAAATGGCA

Suquence3 A2143G mutation strain 3

TCCTACCCGCGCAAGACGGAAAGACCCGTGGACCTTACTACAACCTAGCACTGCTAATGGGAATATCATGCGC
AGGATAGGTGGAGGCTTGAAGTAAGGGCTTGGCTTATGGAGTCATCCTGAGATACCACCCCTGATGTTTC
TGTTAGCTAACGGCCTGTGTTATCCACAGGCAGGACAATGCTGGTGGTAGTTGACTGGGGCGGTGCTCCT
AAAAAGTAACGGAGGCTTGCAAAGGTTGGCTATTGCGGTTGAAATCGCAAGTTGAGTGTAAATGGCA

Suquence 4 A2144G mutation strain

TCCTACCCGCGCAAGACGGAAAGACCCGTGGACCTTACTACAACCTAGCACTGCTAATGGGAATATCATGCGC
AGGATAGGTGGAGGCTTGAAGTAAGGGCTTGGCTTATGGAGTCATCCTGAGATACCACCCCTGATGTTTC
TGTTAGCTAACGGCCTGTGTTATCCACAGGCAGGACAATGCTGGTGGTAGTTGACTGGGGCGGTGCTCCT
AAAAAGTAACGGAGGCTTGCAAAGGTTGGCTATTGCGGTTGAAATCGCAAGTTGAGTGTAAATGGCA

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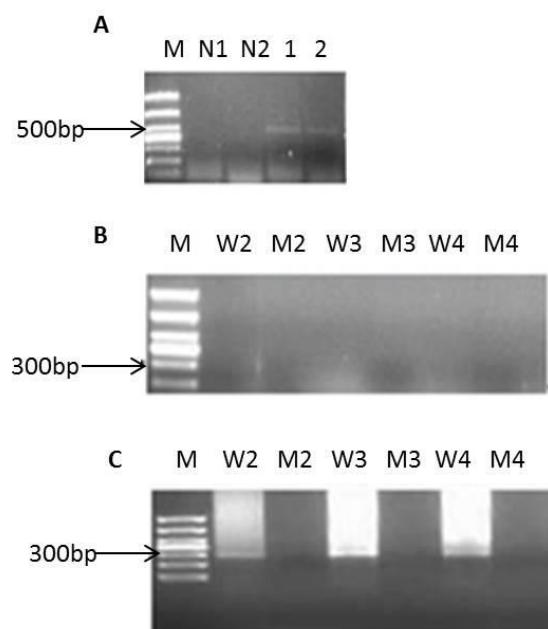


Figure 1 The PCR products of wild-type *Helicobacter pylori* strain in saliva

A: PCR product with the external primers (M: 1000bp DNA Marker, N1 and N2: *H. pylori* negative sample, 1 and 2: wild-type strains); B: PCR products with the different inner primers; C: The products amplified by Nested-ASP-PCR [M: 1000bp DNA Marker (1000, 750, 500, 400, 300, 200, 100), W2: 2142 wild primers (2142A), M2: 2142 mutation primers (2142G), W3: 2143 wild primers (2143A), M3: 2143 mutation primers (2143G), W4: 2144 wild primers (2144A), M4: 2144 mutation primers (2144G)]

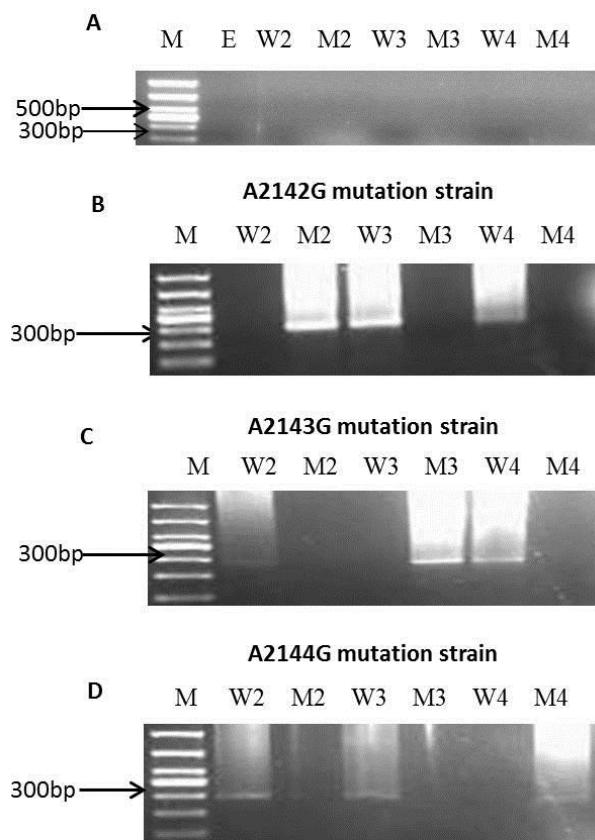


Figure 2 The PCR products of *Helicobacter pylori* clinical strains in saliva with 2142, 2143 and 2144 positions mutation assayed by Nested-ASP-PCR

A: *H. pylori* negative control; B: A2142G mutation strain; C: A2143G mutation strain, D: A2144G mutation strain. [M: 1000bp DNA Marker (1000, 750, 500, 400, 300, 200, 100), E: outer PCR primers, W2: 2142 wild primers (2142A), M2: 2142 mutation primers (2142G), W3: 2143 wild primers (2143A), M3: 2143 mutation primers (2143G), W4: 2144 wild primers (2144A), M4: 2144 mutation primers (2144G)]

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Table 1 The 23SrRNA point mutation genotype with gastric mucosa and saliva of each patient

T S \	NO	WT	2142M	2143M	2144M	WT+2142M	WT+2143M	WT+2144M	2142+2143M	2142+2144M	2143+2144M	2142M+2143 M+2144M
NO	7	10		1			1		6	1	2	8
WT	4	10						1	2		1	4
2142M		1	1									3
2143M	1								1		1	3
2144M												
WT+2142M												
WT+2143M									1			
WT+2144M												
2142+2143M		2								1	1	
2142+2144M		1										1
2143+2144M	1											
2142M+2143 M+2144M	1	4							1		2	9

T-gastric tissue, S-saliva, NO- no detection, WT-wild type, M- muation type, █ - the mutation in gastric tissue or saliva, █ -the mutation in in gastric tissue and saliva simultaneously, █- the mutation consistency individuals of them.