

Comparable genetic alteration profiles between gastric cancers with current and past *Helicobacter pylori* infection

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Supplementary Table S1. Frequency of SNPs

SNP/dbSNP	gene	Chromosome	Region	Type	Nucleotide change	Amino acid change	Cases in this study N (Frequency)	Cases in ToMMo 4.7K JPN N (Frequency)	<i>p</i> value
SNP	<i>PIK3CA</i>	chr3	178938877	SNV	c.2119G>A	p.Glu707Lys	36 (0.500)	0 (0)	< 2.2 x 10 ⁻¹⁶
	<i>TP53</i>	chr17	7578283	SNV	c.566C>T	p.Ala189Val	1 (0.014)	0 (0)	0.007
	<i>ATM</i>	chr11	108236200	SNV	c.9136A>G	p.Ser3046Gly	1 (0.014)	1 (1.05 x 10 ⁻⁴)	0.015
	<i>KDR</i>	chr4	55980324	SNV	c.767T>C	p.Ile256Thr	1 (0.014)	5 (5.24 x 10 ⁻⁴)	0.044
	<i>MLH1</i>	chr3	37067242	SNV	c.1153C>T	p.Arg385Cys	1 (0.014)	7 (7.33 x 10 ⁻⁴)	0.058
	<i>MET</i>	chr7	116411986	SNV	c.3025C>T	p.Pro1009Ser	1 (0.014)	7 (7.33 x 10 ⁻⁴)	0.058
	<i>KDR</i>	chr4	55946163	SNV	c.4016C>T	p.Thr1339Ile	1 (0.014)	12 (1.26 x 10 ⁻³)	0.093
	<i>MET</i>	chr7	116340263	SNV	c.1125C>G	p.Asn375Lys	1 (0.014)	13 (1.36 x 10 ⁻³)	0.100
	<i>NOTCH1</i>	chr9	139399426	SNV	c.4717A>G	p.Thr1573Ala	1 (0.014)	13 (1.36 x 10 ⁻³)	0.100
	<i>KIT</i>	chr4	55593461	SNV	c.1618G>C	p.Val540Leu	1 (0.014)	41 (4.29 x 10 ⁻³)	0.271
	<i>TP53</i>	chr17	7579882	SNV	c.31G>C	p.Glu11Gln	1 (0.014)	67 (7.02 x 10 ⁻³)	0.401
	<i>CDKN2A</i>	chr9	21971161	SNV	c.197A>G	p.His66Arg	1 (0.014)	82 (8.60 x 10 ⁻³)	0.466
dbSNP	<i>KDR</i>	chr4	55972974	SNV	c.1416A>T	p.Gln472His	43 (0.597)	3819 (0.400)	0.001
	<i>JAK3</i>	chr19	17945696	SNV	c.2164G>A	p.Val722Ile	1 (0.014)	0 (0)	0.007
	<i>STK11</i>	chr19	1223125	SNV	c.1062C>G	p.Phe354Leu	6 (0.083)	407 (0.043)	0.130
	<i>KIT</i>	chr4	55593464	SNV	c.1621A>C	p.Met541Leu	5 (0.069)	431 (0.045)	0.262
	<i>MLH1</i>	chr3	37067240	SNV	c.1151T>A	p.Val384Asp	4 (0.056)	304 (0.032)	0.294
	<i>MET</i>	chr7	116340262	SNV	c.1124A>G	p.Asn375Ser	4 (0.056)	353 (0.037)	0.343

Supplementary Table S2. The list of samples with gene amplification.

Infection status	Sample	Gene	Fold change	Reference
Current	B-GC1	<i>ERBB2</i>	7.7	this study
	B-GC38	<i>PIK3CA</i>	7.9	this study
	B-GC73	<i>ERBB2</i>	6.7	this study
	B-GC88	<i>KRAS</i>	4.8	this study
	S17	<i>ERBB2</i>	3.6	[23]
	S23	<i>ERBB2</i>	10.5	[23]
	S36	<i>ERBB2</i>	5.4	[23]
Past	B-GC43	<i>KRAS</i>	3.3	this study
	B-GC45	<i>ERBB2</i>	5.2	this study
	B-GC91	<i>MET</i>	4.8	this study

Supplementary Table S3. The primer for quality check of DNA

Gene	Forward Primer (5' -> 3')	Reverse primer (5' -> 3')	Amplified region	Amplicon length(bp)	Reference
<i>RPPH1</i>	GGAGGGAAGCTCATCAGTGG	CGTTCTCTGGGAACCTCACCT	chr14:20811419-20811563	145	[27]

Supplementary Table S4. The primer for detection of *H. pylori*

Gene	GenBank number	Forward Primer (5' -> 3')	Reverse primer (5' -> 3')	Amplicon length(bp)	Reference
<i>jhpr3</i>	NC000921	AAGGATACTGCCTCCGTAAG	ACAATCCGAACTGAGAGGTG	158	[8]

Supplementary Table S5. Baseline characteristics of 90 patients

Characteristic	<i>H. pylori</i> infection status		<i>p</i> value
	Current group (N = 55)	Past group (N = 35)	
Age at surgery, mean (SD)	67.8 (11.7)	73.4 (9.1)	0.033
Gender, N (%)			0.267
Male	38 (69.1)	20 (57.1)	
Female	17 (30.9)	15 (42.9)	
Pathology of GC, N (%)			0.394
Differentiated type	29 (52.7)	15 (42.9)	
pap	2 (3.6)	2	
tub	27 (49.1)	13	
Undifferentiated type	26 (47.3)	20 (57.1)	
por	24 (43.6)	18 (51.4)	
sig	1 (2.0)	0 (0)	
muc	1 (2.0)	2 (5.7)	

Supplementary Table S6. Primers used for dideoxy sequencing

Gene	Target variation	Forward Primer (5' -> 3')	Reverse primer (5' -> 3')	Amplified region	Amplicon length(bp)	Reference
<i>ABL1</i>	c.1107del	CGTGTGAAGTCCTCGTGT	CCCCTACCTGTGGATGAAGTTT	chr9:133748216-133748431	216	This study
<i>ABL1</i>	c.1131_1132insG	ATCTCGTCAGCCATGGAGTA	AATGTGTTGCCAGCACTGAG	chr9:133748378-133748551	174	This study
<i>ABL1</i>	c.1281delC	GGTAGCTGATTTTGGCCCTGA	GGAAAGCAAGAAAGAGGCCA	chr9:133750303-133750515	213	This study
<i>ATM</i>	c.9136A>G	GAAAGGAGTGGAAAGAGGCA	AGAGTGAAAGCAGAGATGTCC	chr11:108236115-108236438	324	This study
<i>BRAF</i>	c.1406G>C	ACGGGACTCGAGTGTGATT	GCGAACAGTGAATATTTCTTTGA	chr7:140481274-140481479	206	This study
<i>CDH1</i>	c.1203_1204insC	AATCCTTTAGCCCCCTGAGA	TCACTGGATTTGTGGTGACG	chr16:68847139-68847369	231	This study
<i>CDH1</i>	c.228delA	TCTCCACAAAGTTCCGTCT	AATGTCAACGGTACCAAGGC	chr16:68835486-68835881	396	This study
<i>CDKN2A</i>	c.197A>G	ACACAAGCTTCCTTCCGTC	ACCAGCGTGTCCAGGAAG	chr9:21971074-21971273	200	This study
<i>CTNNB1</i>	c.101G>A	GCTGATTGATGGAGTTGGAC	TTGGGAGGTATCCACATCCT	chr3:41266016-41266186	171	This study
<i>EGFR</i>	c.2506delC	GAATTCGGATGCAGAGCTTC	ATTCTTTCTTCCGCACCC	chr7:55259346-55259547	202	This study
<i>ERBB2</i>	c.2434G>A	GCAAACCCCTATGTCACAA	TCTGCATGGTACTCTGTCTCGT	chr17:37881199-37881447	249	This study
<i>ERBB2</i>	c.955G>A	CTTGTTTTGTAGCTGTTGGTG	CCTTGTATATAGGCCAGTCTCT	chr2:212578210-212578442	233	This study
<i>ERBB4</i>	c.1817A>G	GGGTCCTGACAACTGTACAAAG	CCAGCAAGAATGCTTACCTT	chr2:212530031-212530203	173	This study
<i>ERBB4</i>	c.542delA	GCAGACACCATTCAITGGC	GCATAACTATTTCAGCCAC	chr2:212652683-212652834	152	This study
<i>ERBB4</i>	c.719G>A	TTCTCTGGTGGCAGACTTT	TAGGGAAGGAAAGGAGAGCA	chr2:212589750-212589968	219	This study
<i>FBXW7</i>	c.1514G>A	TGCAGAGTTGTTAGCGTTT	ATTAGTATGCCCTGAAACG	chr4:153247176-153247388	213	This study
<i>FBXW7</i>	c.1393C>T,c.1394G>A	TGGGACATACAGGTGGAGTAGT	CTACACAGAAAGGCCCAAA	chr4:153249289-153249525	237	This study
<i>FGFR1</i>	c.352_355delGAGG, c.348delC, c.355delG	TCCGTGTTTCTGGAACCTG	CTCTAAACCAATGCCAG	chr8:38285808-38286038	231	This study
<i>FGFR2</i>	c.1672delG	TGATGCCACAGAGAAAGACC	GGAAAGCCAGCCATTCTAA	chr10:123257932-123258118	187	This study
<i>FLT3</i>	c.2011_2012insG	CTAGCCTGGCTTCTCTATA	CCACTGGGTTTGTAGAGTTC	chr13:28602174-28602562	389	This study
<i>GNAS</i>	c.2531G>A	TCTGAGCCCTTCTCCAAAC	GGGGTGAATGTCAGAAACC	chr20:57484301-57484536	236	This study
<i>JAK2</i>	c.1847_1851delGTGTC	TGGACAACAGTCAAACAA	GACACCTAGCTGTGATCCTGAA	chr9:5073651-5073877	227	This study
<i>KDR</i>	c.767T>C	TCTGAGTCCGCTCATGGA	GCAAACTTCACTGGGGCTTA	chr4:55980229-55980410	182	This study
<i>KDR</i>	c.4016C>T	TCACTCCGATGCACAGACA	ACTTCTGCTGGTGGAAAGA	chr4:55946019-55946252	234	This study
<i>KIT</i>	c.1618G>C, c.1630delA	TGTAGAGCAAAATCCATCC	CATACATGGGTTTCTGTGGG	chr4:55593379-55593594	216	This study
<i>KRAS</i>	c.59G>T	GGCTGTGCTGAAAATGACTGA	GAATGGTCTGCACCAAGTAA	chr12:25398164-25398330	167	[29]
<i>KRAS</i>	c.183A>C	CCAGACTGTGTTTCTCCCTTCT	AACCCACCTATAATGGTGAATATC	chr12:25380161-25380371	211	This study
<i>KRAS</i>	c.34G>A, c.35G>T, c.35G>A	CGTCTGCAGTCAACTGGAAAT	GAATGGTCTGCACCAAGTAA	chr12:25398164-25398501	338	[29], [23]
<i>MET</i>	c.1125C>G	ACAAATAGGAGCCAGCCTGA	GTGGGGAACTGATGTGACTT	chr7:116340131-116340360	230	This study
<i>MET</i>	c.3025C>T	GCCCATGATAGCCGCTTTA	TGTCACAACCCACTGAGGTA	chr7:116411854-116412103	250	This study
<i>MLH1</i>	c.1151T>A,c.1153C>T	AGACTTTGCTACCAGGACTTGC	CTTTGTGTATCCCCCTCCA	chr3:37067126-37067448	323	[29], [23]
<i>NOTCH1</i>	c.4717A>G, c.4723G>C	ACCAGTACTGCAAGGACCACTT	TCACGCTTGAAGACCACTGT	chr9:139399317-139399545	229	This study
<i>NRAS</i>	c.34G>T	GATGTGGCTGCCAAATTAAC	TACCTCTATGGTGGGATCA	chr1:115258667-115258840	174	This study
<i>PDGFRA</i>	c.2515delC	CTTGCAGGGGTGATGCTATT	AAAGTGAAAGGAGGATGAGCC	chr4:55151940-55152177	238	This study
<i>PIK3CA</i>	c.2091G>A, c.2119G>A	TCCTATGTGCTGCATGTGG	TCTGCTTGATCCAAGGACC	chr3:178938826-178939049	224	This study
<i>PIK3CA</i>	c.1031T>G	GCATTTCCACAGTACACCA	TGGATGTTCTCTAACCATCTG	chr3:178921447-178921696	250	This study
<i>PIK3CA</i>	c.3140A>G	CTCAATGATGCTGGCTCTG	CTATGCAATCGGTCTTTGCC	chr3:178951951-178952237	287	This study
<i>PIK3CA</i>	c.1624G>A,c.1633G>A	CTGTGAATCCAGAGGGGAAA	CATGCTGAGATCAGCCAAA	chr3:178935934-178936201	268	[29], [23]
<i>PTEN</i>	c.737delC,c.752G>T	TGCAGATCTCAGTTTGTGG	TGGATATTTCTCCAAATGAAAG	chr10:89717605-89717810	206	This study
<i>PTPN11</i>	c.182A>G, c.214G>A	AATCCGACGTGGAAGATGAG	CATTTCTGCACACTAGGGCAC	chr12:112888037-112888378	342	[23]
<i>RET</i>	c.1940delT	AGCCATGAGGCAGAGCATATA	CCTCCGGAAGGTCACTCTCA	chr10:43609843-43610082	240	This study
<i>SMAD4</i>	c.1525T>G	TGTCCTCTGATGCTTCCA	AAGGTTGTGGGCTGCAATC	chr18:48604591-48604829	239	This study
<i>SMAD4</i>	c.1081C>T, c.1082G>A	TGGATGTTCAAGTAGGAGAGAC	CATGGGAAAACATAACCTTGA	chr18:48591829-48592058	230	This study
<i>SMARCB1</i>	c.1129C>T, c.1130G>A	CAGCCAGATCCAGTTTTT	TGCCAGAAGATGGAGGAGA	chr22:24176112-24176439	328	[29]
<i>SMO</i>	c.970G>A	AGTACAGAGTGACCCCTCAA	ACAGTGAAGACAAAGGGGAGT	chr7:128845946-128846188	243	This study
<i>TP53</i>	c.811G>A, c.814G>A, c.818G>A, c.832C>T,	TCCTTACTGCCTCTTGCTTCTC	TGAGGCATAACTGCACCCCTT	chr17:7576964-7577195	232	This study
<i>TP53</i>	c.376T>C, c.380C>T, c.388C>G, c.404G>A	GTTTCTTTGCTGCCGCTTTC	TCATGTGCTGTGACTGCTTG	chr17:7578422-7578637	216	[23]
<i>TP53</i>	c.523C>T, c.524G>A, c.535C>T, c.566C>T, c.565G>A, c.536A>G	TGTGCAGCTGTGGGTTGATT	TCCACTCGGATAAGATGCTG	chr17:7578256-7578504	249	This study
<i>TP53</i>	c.844C>T, c.853G>A, c.857A>T	GCCTCTTGCTTCTTTTCC	GCTTCTTGCTGCTTGTCTT	chr17:7576997-7577187	191	This study
<i>TP53</i>	c.730G>T, c.733G>A, c.742C>T, c.743G>A	AAAAAGGCCTCCCTGCTTG	GGTGGATGGGTAGTAGTATGGAAG	chr17:7577386-7577683	298	[29]
<i>TP53</i>	c.31G>C	TCAGACACTGGCATGGTGT	ATTTTCGCTTCCACAGGTC	chr17:7579756-7580044	289	This study
<i>TP53</i>	c.637C>T,c.641A>G, c.659A>G, c.660T>G	CCTCTGATTCCTCACTGATTGC	GGGAGGTCAAATAAGCAGCAG	chr17:7578070-7578317	248	[29]
<i>TP53</i>	c.294_298delTTCCC	AGATGAAGCTCCAGAAATGC	GCCAGGCATTGAAGTCTCAT	chr17:7579265-7579507	243	This study

