

***Helicobacter pylori* chronic infection and mucosal inflammation switches the human gastric glycosylation pathways**

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Supplementary Table 1 – Individual features, histopathological data of gastric biopsies and genetic characteristics of *H. pylori* infecting strains.

Case	Code ^A	Sex	Age	Region	<i>H. pylori</i>	IgG/IgA ^B	<i>cagA</i> ^C	Sialyl-Le ^a	Sialyl-Le ^x	Inflammation	PMN infiltration	Atrophy	RNA analysis group
1	C	M	25	Antrum	-	2.7/0.8	.	-	-	absent/mild	absent/mild	absent/mild	
2	C	F	59	Antrum	+	197.7/2.2	<i>cagA</i> +	+	+	absent/mild	absent/mild	absent/mild	
3	C	F	48	Antrum	+	166.7/3.0	<i>cagA</i> +	-	+	absent/mild	absent/mild	absent/mild	
4	C	M	45	Incisura	+	68.1/1.2	<i>cagA</i> +	+	+	absent/mild	absent/mild	absent/mild	
5	C	M	32	Antrum	+	596/7.5	<i>cagA</i> +	+	+	moderate/severe	absent/mild	absent/mild	Hp+
6	C	M	22	Antrum	-	12.0/0.5	.	-	-	absent/mild	absent/mild	absent/mild	Hp-
7	C	M	64	Antrum	+	1181/1.9	<i>cagA</i> +	+	+	moderate/severe	absent/mild	absent/mild	Hp+
8	C	M	37	Antrum	+	170.6/1.3	<i>cagA</i> +	-	-	absent/mild	absent/mild	absent/mild	
9	C	F	26	Antrum	+	688/2.5	<i>cagA</i> -	-	-	moderate/severe	moderate/se	absent/mild	Hp+
10	C	M	62	Incisura	+	1281/9.8	<i>cagA</i> +	+	+	moderate/severe	moderate/se	moderate/severe	Hp+
11	C	M	20	Antrum	-	6.9/1.3	.	-	-	absent/mild	absent/mild	absent/mild	Hp-
12	C	F	61	Antrum	+	179/5.5	<i>cagA</i> -	+	+	moderate/severe	moderate/se	moderate/severe	Hp+
13	C	F	50	Antrum	+	183/4.9	<i>cagA</i> +	+	+	moderate/severe	moderate/se	absent/mild	Hp+
14	C	F	40	Antrum	+	524/2.9	<i>cagA</i> +	+	+	moderate/severe	absent/mild	moderate/severe	Hp+
15	C	F	46	Antrum	+	74.9/1.9	<i>cagA</i> -	+	+	moderate/severe	absent/mild	absent/mild	Hp+
16	C	M	57	Antrum	+	183/5.2	<i>cagA</i> +	+	+	moderate/severe	moderate/se	moderate/severe	Hp+
17	C	M	53	Antrum	-	8.1/0.7	.	-	-	absent/mild	absent/mild	absent/mild	Hp-
18	C	M	43	Antrum	-	11.6/3.1	.	+	+	absent/mild	absent/mild	absent/mild	Hp-
19	C	F	35	Antrum	+	170.9/3.8	<i>cagA</i> +	+	+	moderate/severe	moderate/se	absent/mild	Hp+
20	C	F	38	Antrum	+	>200/4.0	<i>cagA</i> +	+	+	moderate/severe	moderate/se	absent/mild	Hp+
21	C	F	53	Antrum	+	166.7/2.8	nd	+	+	moderate/severe	moderate/se	absent/mild	
22	C	M	33	Antrum	-	7.6/0.6	.	-	-	absent/mild	absent/mild	absent/mild	Hp-
23	C	F	37	Antrum	+	286/7.7	<i>cagA</i> +	+	+	moderate/severe	moderate/se	absent/mild	Hp+
24	C	F	20	Antrum	+	76.2/0.8	<i>cagA</i> -	+	+	moderate/severe	absent/mild	absent/mild	Hp+
25	C	F	18	Antrum	-	26.7/1.7	.	-	-	absent/mild	absent/mild	absent/mild	Hp-
26	C	F	22	Antrum	+	122.8/0.8	<i>cagA</i> -	+	+	moderate/severe	moderate/se	absent/mild	Hp+
27	S	M	39	Antrum	+	>2000/7.2	<i>cagA</i> +	+	+	moderate/severe	moderate/se	absent/mild	
28	S	M	31	Antrum	-	3.3/0.0	.	-	-	absent/mild	absent/mild	absent/mild	
29	S	F	50	Antrum	-	10.8/1.3	.	-	+	absent/mild	absent/mild	absent/mild	Hp-
30	S	F	46	Antrum	+	502/2.2	<i>cagA</i> +	+	+	moderate/severe	moderate/se	moderate/severe	
31	S	M	35	Antrum	+	1265/2.3	<i>cagA</i> +	+	+	moderate/severe	absent/mild	moderate/severe	
32	S	F	39	Antrum	-	135/3.1	.	-	-	absent/mild	absent/mild	absent/mild	
33	S	M	56	Antrum	-	6.0/0.7	.	-	-	absent/mild	absent/mild	absent/mild	
34	S	M	59	Antrum	+	1902/6.6	<i>cagA</i> +	+	+	moderate/severe	moderate/se	absent/mild	Hp+
35	S	M	59	Antrum	-	4.2/0.5	.	+	+	absent/mild	absent/mild	absent/mild	
36	S	F	37	Antrum	-	24.1/2.0	.	-	-	absent/mild	absent/mild	absent/mild	
37	S	F	50	Antrum	-	4.2/05	.	-	+	absent/mild	absent/mild	absent/mild	Hp-
38	S	M	46	Antrum	+	136/2.7	<i>cagA</i> +	+	+	moderate/severe	absent/mild	absent/mild	
39	S	F	64	Antrum	+	275/7.6	nd	+	+	absent/mild	absent/mild	absent/mild	
40	D	M	39	Antrum	+	123/7.8	<i>cagA</i> +	-	-	absent/mild	absent/mild	absent/mild	
41	D	M	36	Antrum	+	89/2.3	<i>cagA</i> +	+	+	moderate/severe	moderate/se	moderate/severe	
42	D	M	45	Antrum	-	7.1/2.1	.	-	-	absent/mild	absent/mild	absent/mild	
43	D	M	32	Antrum	-	5.0/0.8	.	-	-	absent/mild	absent/mild	absent/mild	
44	D	F	65	Antrum	-	2.1/1.1	.	-	-	absent/mild	absent/mild	absent/mild	
45	D	F	57	Antrum	+	65/5.3	<i>cagA</i> +	-	-	absent/mild	absent/mild	absent/mild	
46	S	F	35	Antrum	+	52.7/1.7	<i>cagA</i> -	+	+	moderate/severe	moderate/se	absent/mild	Hp+
47	N	F	28	Antrum	+	77/2,5	<i>cagA</i> +	+	+	absent/mild	absent/mild	absent/mild	
48	N	F	39	Antrum	+	200/2,4	<i>cagA</i> +	+	+	moderate/severe	moderate/se	absent/mild	
49	N	M	46	Antrum	+	200/0,8	<i>cagA</i> +	+	+	absent/mild	absent/mild	absent/mild	
50	N	F	39	Antrum	+	200/7,5	<i>cagA</i> +	+	-	moderate/severe	moderate/se	moderate/severe	

^A Codification for individual's identification: C-first degree relative of patients with early-onset gastric carcinoma; S-spouses; D-dyspeptic patients and N-neighbors; ^B anti-*H. pylori* IgG/IgA serological values; ^C n.d.- not determined.

Supplementary Table 2 - Primer sequences for qRT-PCR analysis of gene expression.

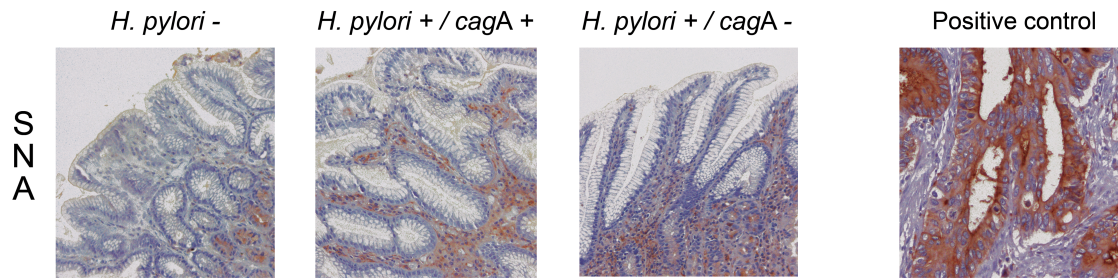
Gene	Accession #	Forward Primer (5' to 3')	Reverse Primer (5' to 3')
<i>B3GALT5</i>	NM_006057	CTCCGTATGCCTCTTCAGGA	GCCTGCCAGTAGTCCAAGAG
<i>B3GNT1</i>	NM_006876	GAAGCGTTGAAGTTCATCC	TGTTTGAAGTGGCGATATAGGA
<i>B3GNT2</i>	NM_006577	TGCCAAAGTCTATGAGGCATC	ACAGAGGCCCATGAACACAT
<i>B3GNT3</i>	NM_014256	AGGCACAGACTCACGGAGAC	GAGCGTGAGGTTGAAGAAGG
<i>B3GNT4</i>	NM_030765	CTAGCCGTCACCGTCTCTTC	TGAAGGCTCCAGCAAGATAGA
<i>B3GNT5</i>	NM_032047	TGCCAAAGTCTATGAGGCATC	ACAGAGGCCCATGAACACAT
<i>ST3GAL1</i>	NM_003033	ATTGAGCCTCCACCTCTGG	CACGATGGGTAGCAGGAAGT
<i>ST3GAL2</i>	NM_006927	TGGTTTGACAGCCACTTTGA	CGGTGGAAGATCCATGTTCT
<i>ST3GAL3</i>	NM_006279	ACACTGCGCATCACCTACC	GAGAGAATCGCGCTCGTACT
<i>ST3GAL4</i>	NM_006278	CGTCCTGGTAGCTTTCAAGG	GCACCCGCTTCTTATCACTC
<i>ST3GAL5</i>	NM_003896	CAACGGAAACCAAGTTCCTCT	CACGATCAATGCCTCCACT
<i>ST3GAL6</i>	NM_006100	CCTAAACACCCAACAACAGGA	CCAGCTAGGTGAACTTCGTGA
<i>FUT2</i>	NM_000511	GATTCAAGCCATGTGGGAGT	GTCCAGTGCCTTTGATGTT
<i>FUT3</i>	NM_000149	CGCTGGATCTGGTTCAACTT	GTATCTGTCCAGGGCTTCCA
<i>FUT4</i>	NM_002033	TGGCCCGCTACAAGTTCTAC	GCCAGAGCTTCTCGGTGATA
<i>FUT6</i>	NM_000150	CTGCTGATGGCTGTGTGTTT	GGGTACACAGTGGGATCGTC
<i>FUT9</i>	NM_006581	CTTACCGCCGTGATTCAGAT	AAACACGAAGGGATTTGTGC
<i>FUT10</i>	NM_032664	TATGTTTCGCGAGCTGATGAC	TGAGGGAGGTCTTTGTTTCG
<i>FUT11</i>	NM_173540	AGTCTGAAGCATCGGGAGTG	TCGAAGCCGTTGAGGTAGTT
<i>IL-8</i>	NM_000584	AAGACATACTCCAAACCTTTCCA	GGTCCACTCTCAATCACTCTCA
<i>IL-6</i>	NM_000600	CTTCCCTGCCCCAGTACC	GGTGAGTGGCTGTCTGTGTG
<i>IL-1β</i>	NM_000576	GCTGAGGAAGATGCTGGTTC	TGAAGGGAAAGAAGGTGCTC
<i>TNF-α</i>	NM_000594	CCTCTTCTCCTTCTGATCGT	ATCACTCCAAAGTGCAGCAG
<i>IFN-γ</i>	NM_000619	CAGCAGCTAAAACAGGGAAGC	CTGGGATGCTCTTCGACCTC
<i>KRT18</i>	NM_000224	GAACGAGAAGGAGACCATGC	AGGCTCCTCACTCTGTCCAG

Supplementary table 3– Sialyl-Le^a and sialyl-Le^x expression and histopathological features.

	Sialyl-Le ^a			Sialyl-Le ^x		
	Negative n (%)	Positive n (%)	p-value ^C	Negative n (%)	Positive n (%)	p-value ^C
<i>H. pylori</i>						
negative (n=17)	15 (88%)	2 (12%)	<0.0001	13 (76%)	4 (24%)	<0.0001
positive (n=33)	5 (15%)	28 (85%)		5 (15%)	28 (85%)	
<i>cagA</i> status^A						
negative (n=6)	1 (17%)	5 (83%)	n.s.	1 (17%)	5 (83%)	n.s.
positive (n=25)	4 (16%)	21 (84%)		4 (16%)	21 (84%)	
Chronic inflammatory infiltrate^B						
absent/mild (n= 9)	4 (44%)	5 (56%)	0.0133	3 (33%)	6 (67%)	n.s.
moderate/severe (n=24)	1 (4%)	23 (96%)		2 (8%)	22 (92%)	
Inflammatory activity^B						
absent/mild (n=16)	4 (25%)	12 (75%)	n.s.	3 (19%)	13 (81%)	n.s.
moderate/severe (n=17)	1 (6%)	16 (94%)		2 (12%)	15 (88%)	
Atrophy^B						
absent/mild (n=25)	5 (20%)	20 (80%)	n.s.	4 (16%)	21 (84%)	n.s.
moderate/severe (n=8)	0 (0%)	8 (100%)		1 (12%)	7 (88%)	

^A For two cases classified as *H. pylori* positive by histology and with high anti-*H. pylori* IgG/IgA antibody titers bacteria did not grow on culture, so *cagA* status could not be determined. ^B Only *H. pylori* infected individuals were included in this analysis. ^C Statistical significance was determined using the Fisher's exact test, n.s.-non significant.

Supplementary Figure 1



Supplementary Figure 1 – Evaluation of α 2,6 sialylated antigens expression in *H. pylori* chronically infected human gastric mucosa (A) Histochemical detection of α 2,6 sialylated antigens using the *Sambucus nigra* lectin (SNA) in paraffin-embedded sections of human gastric mucosa from non-infected individuals (*H. pylori*-) and individuals infected with either *cagA*-positive (*H. pylori*+/*cagA*+) or *cagA*-negative (*H. pylori*+/*cagA*-) strains. A colon carcinoma sample was included as positive control
Magnification 200x