

Supplementary Table

Table S1. Genes were upregulated after glutaraldehyde treatment*

Cellular role category	Fold change	ORF	ORF	Common name and function #
		HP no. †	JHP no. †	
Hypothetical	19.818	HP1004	N/A	Hypothetical protein
Transporter	13.700	HP0653	JHP0598	Nonheme iron-containing ferritin, <i>pfr</i>
Conserved hypothetical	9.218	HP1216	JHP1138	Conserved hypothetical secreted protein, <i>imp/osta</i>
Amino acid biosynthesis	8.968	HP0652	JHP0597	Phosphoserine phosphatase, <i>serB</i>
Hypothetical	7.341	HP1440	JHP1333	Hypothetical protein
Energy metabolism	7.321	HP1238	JHP1159	Formamidase, <i>aimF</i>
Transporter	6.848	HP0715	JHP0653	ABC transporter, ATP-binding protein
Hypothetical	6.673	HP0412	JHP0970	Hypothetical protein
Hypothetical	5.662	HP0365	N/A	Hypothetical protein
Biosynthesis and metabolism	5.015	HP0642	JHP0586	NAD(P)H-flavin oxidoreductase, <i>frxA</i>
Cell envelope	4.959	HP0651	JHP0596	Alpha 1,3-fucosyltransferase, <i>futB</i>
Hypothetical	4.937	HP1502	JHP1395	Hypothetical protein
Chaperone	4.488	HP0109	JHP0101	Chaperone and heat shock protein 70, <i>dnaK</i>
Transporter	4.429	HP0889	JHP0822	Iron(III) dicitrate ABC transporter, permease protein, <i>fecD</i>
Cell envelope	4.414	HP0057	JHP0049	Lipoprotein, putative
Cell envelope	4.397	HP0511	N/A	Lipoprotein Lpp, an urease enhancing factor
Hypothetical	4.282	HP0641	JHP0584	Hypothetical protein
Regulatory	4.232	HP0111	JHP0103	Heat-inducible transcription repressor of Class I heat shock genes, <i>hrcA</i>
Hypothetical	4.160	HP0174	JHP0160	Membrane protein, putative
Cell envelope	4.084	HP0549	JHP0496	Glutamate racemase, <i>glr, murl</i>
DNA metabolism	3.946	HP1383	N/A	Type I R-M system specificity subunit, <i>hsdS6</i>
Protein synthesis and processing	3.808	HP1497	JHP1390	Peptidyl-tRNA hydrolase, <i>pth</i>
Biosynthesis and metabolism	3.731	HP1254	JHP1175	Biotin synthesis protein, <i>bioC</i>
Motility	3.617	HP0752	JHP0689	Flagellar hook-associated protein 2 (HAP2), <i>fliD</i>
Hypothetical	3.527	HP0287	JHP0272	Hypothetical protein
Conserved hypothetical	3.424	HP0926	JHP0860	Conserved hypothetical protein
Conserved hypothetical	3.412	HP0965	JHP0899	Remnant pseudogene of an ancestral ATP/GTP-binding protein
Hypothetical	3.353	HP0754	JHP0691	Hypothetical protein

Biosynthesis and metabolism	3.285	HP0240	JHP0225	Octaprenyl-diphosphate synthase, <i>ispB</i>
Biosynthesis and metabolism	3.221	HP0211	JHP0197	Cysteine-rich protein A, <i>hcpA</i>
DNA/RNA synthesis and processing	3.217	HP0602	JHP0549	Novel 3-methyladenine DNA glycosylase involved in base excision repair, <i>magIII</i>
Hypothetical	3.159	HP1176	N/A	Hypothetical protein
Biosynthesis and metabolism	3.136	HP1461	JHP1354	Cytochrome c551 peroxidase
Motility	3.112	HP1119	JHP1047	Flagellar hook-associated protein 1 (HAP1), <i>flgK</i>
Amino acid biosynthesis	3.040	HP0107	JHP0099	Cysteine synthetase, <i>cysK</i>
Conserved hypothetical	2.825	HP1026	JHP0398	Conserved hypothetical helicase-like protein
Transporter	2.661	HP1082	JHP0343	Multidrug resistance protein, <i>msbA</i>
Hypothetical	2.631	HP0918	JHP0852	Hypothetical protein
Protein synthesis and processing	2.598	HP0223	JHP0209	DNA repair protein, <i>radA</i>
Biosynthesis of cofactors, prosthetic groups, and carriers	2.589	HP0221	JHP0207	NifU-like protein involved in [Fe-S] cluster assembly, <i>nifU</i>

* Genes listed here are according to microarray analysis differed more than 2.5-fold in *H. pylori* NTUH-S1 glutaraldehyde treatment compared to *H. pylori* NTUH-S1 without glutaraldehyde treatment.

† ORFs are according to the whole genome sequences of *H. pylori* 26695 and J99.

Common name and function of each ORF are according to the PyloriGene database (<http://genolist.pasteur.fr/PyloriGene>).

Table S2. Genes were downregulated after glutaraldehyde treatment*

Cellular role category	Fold change	ORF	ORF	Common name and function #
		HP no.†	JHP no.‡	
Central intermediary metabolism	10.870	HP1186	JHP1112	Carbonic anhydrase, <i>cah</i>
Transport and binding protein	7.246	HP1400	JHP1426	Iron(III) dicitrate transport protein, <i>fecA3</i>
Fatty acid and phospholipids metabolism	6.329	HP0690	JHP0638	Acetyl coenzyme A acetyltransferase (thiolase) involved in the TCA cycle, <i>fadA</i>
Amino acid biosynthesis	5.952	HP0691	JHP0637	Succinyl-CoA-transferase subunit A of the succinyl-coenzyme A (CoA) involved in the TCA cycle, <i>yjD</i>
Hypothetical	5.814	HP1175	JHP1102	Integral membrane protein
Amino acid biosynthesis	4.808	HP0695	JHP0633	N-methylhydantoinase
Fatty acid and phospholipids metabolism	4.587	HP0090	JHP0083	Malonyl coenzyme A-acyl carrier protein transacylase, <i>fabD</i>
Fatty acid and phospholipids metabolism	4.348	HP1045	N/A	Acetyl-CoA synthetase, <i>acoE</i>
Transport and binding protein	4.184	HP1512	JHP1405	Nickel-regulated outer membrane protein, <i>frpB-3</i>
Energy metabolism	4.016	HP0193	JHP0179	Fumarate reductase, cytochrome b subunit, <i>frdC</i>
Biosynthesis of cofactors, prosthetic groups, and carriers	3.984	HP1582	JHP1489	Pyridoxal phosphate biosynthetic protein J, <i>pdxJ</i>
Hypothetical	3.788	HP0489	JHP0441	Hypothetical protein
Central intermediary metabolism	3.717	HP0089	JHP0082	S-adenosylhomocysteine nucleosidase involved in S-adenosylmethionine recycling into methionine, <i>pfs</i>
Energy metabolism	3.559	HP0692	JHP0636	Succinyl-CoA-transferase subunit B of the succinyl-coenzyme A (CoA) involved in the TCA cycle, <i>yjE</i>
Transport and binding protein	3.559	HP0299	JHP0284	Dipeptide ABC transporter, permease protein, <i>dppB</i>
Transport and binding protein	3.546	HP0214	JHP0200	Sodium-dependent transporter, <i>huNaDC-1</i>
Hypothetical	3.534	HP0697	JHP0631	Hypothetical protein
Cell envelope	3.390	HP0253	JHP0238	Outer membrane protein, <i>hopG</i>
Energy metabolism	3.175	HP0696	JHP0632	N-methylhydantoinase
Hypothetical	3.115	HP0015	JHP0013	Hypothetical protein
Conserved hypothetical	3.067	HP0709	JHP0648	Conserved hypothetical protein
Energy metabolism	3.040	HP0588	JHP0536	OorD subunit of the 2-oxoglutarate oxidoreductase involved in the TCA cycle, <i>oorD</i>
Amino acid biosynthesis	3.012	HP0096	JHP0088	D-2-hydroxyacid dehydrogenase

Cell envelope	2.994	HP1167	JHP1094	Outer membrane protein, <i>hofH</i>
Cell envelope	2.967	HP0710	JHP0649	Outer membrane protein, <i>homA</i>
Biosynthesis of cofactors, prosthetic groups, and carriers	2.817	HP1118	JHP1046	Gamma-glutamyltranspeptidase, <i>ggt</i>
Transport and binding protein	2.770	HP0300	JHP0285	Dipeptide ABC transporter, permease protein, <i>dppC</i>
Energy metabolism	2.762	HP0590	JHP0538	OorB subunit of the 2-oxoglutarate oxidoreductase involved in the TCA cycle, <i>oorB</i>
Transport and binding proteins	2.717	HP0693	JHP0635	Short-chain fatty acids transporter, <i>atoE</i>
Fatty acid and phospholipid metabolism	2.710	HP0891	JHP0824	Acyl coenzyme A thioesterase, <i>vdID</i>
Conserved hypothetical	2.646	HP0920	JHP0854	Integral membrane protein

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