

Supplemental material

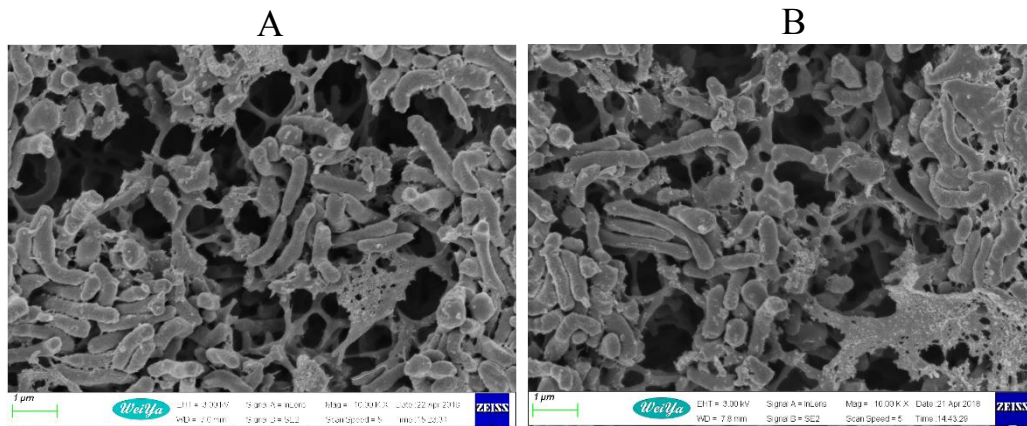


Fig. S1: Representative scanning electron microscopy (SEM) images of $\Delta gluP$ strain biofilms cultured on NC membranes with 1 g/L(A) and 4 g/L(B) glucose in an agar plate.

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HP0115 : CAAAGAGTTGGAA CACCC TTTGCTT GACTAAAATCAA -22
HP0295 : GCTTATTTTGGAA TACTTTT AGCTTGT TTTGTAAAAAA -14
HP0367 : GTGTTTTTAGGAA TAGAGTTT GCTTATCTTATCTTTAA -25
HP0870 : AGCTATTTAGGAA CAACTTTT GCTTTATTTTGCATAGA -28
HP1032 : ACGCTTGGGGGTA CTTGATTGCGT TGTGTTTGTGCGTC -148
HP1076 : TCATAAAAAGGAA CGAAAAATGCTTGTGAATGATCAAT -19
HP1120 : TAAAAAATGGC TAGTATTTGCTTGAATACGGCTGAA -21
HP1154 : GTTGGATTTGGAA CGCCTTTT GCTTTTACGCTTTTAA -56
HP1233 : TCTCATTAGGAA TGGATTTT GCTTAACATTAGCGTAA -22
HP1174 : TCTTTTTAAGGGGC ---- TTTGCATTTTTTACTC--AT -88
          GG a      tttGcTt      a
    
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Fig. S2 Alignment of promoter sequences of four known σ^{54} -dependent genes [HP0115 (flaB), HP0295 (flgL), HP0870 (flgE1) and HP1120], six genes and operons in *H. pylori* that belong to the RpoN regulon (Niehus et al., 2004), and *Hp1174* (*gluP*). Numbers to the right of the sequences indicate the distance from the putative ATG start codon of the ORFs. The bottom lane shows the derived consensus sequence. The shading was done using the GENEDOC software (<http://iubio.bio.indiana.edu/soft/molbio/ibmpc/genedoc-readme.html>). Black boxes indicate 100% conserved residues in all sequences; grey boxes indicate nucleotides conserved in more than half the promoters.

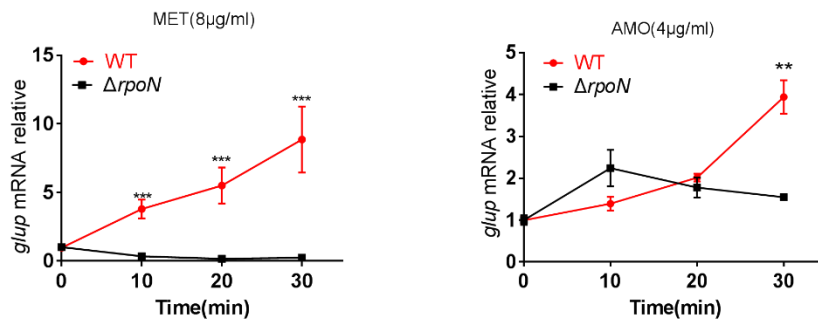


Fig. S3 qRT-PCR analysis of the mRNA levels of *gluP* in WT and $\Delta rpoN$ ($\Delta\sigma^{54}$) strains exposed to metronidazole(MET) and amoxicillin(AMO) for different time periods. The results were compared to WT without drugs treatment (CTL). The signal was normalized to the 16S rRNA levels. Data are means \pm SEM from three independent experiments. Significance by paired *t* test: **, $P < 0.01$; ***, $P < 0.001$.

Table S1: The names of C-MDR and C-DSS strains used in this study. R:resistance, S:sensitive.

Bacteria names	Antibiotics				
	Clarithromycin	Amoxicillin	Levofloxacin	Tetracycline	Metronidazole
G295	R	S	R	S	R
G236	R	S	R	S	R
G141	R	S	R	S	R
G28	R	S	S	S	R
C-MDR G124	R	S	R	S	S
G450	R	S	R	S	R
E660	S	R	S	R	S
E325	R	S	R	R	R
E412					
E702					
G405					
E313			Sensitive		
C-DSS E204					
E222					
G303					
G352					

References

Niehus E, Gressmann H, Ye F, Schlapbach R, Dehio M, Dehio C, Stack A, Meyer TF, Suerbaum S, Josenhans C. 2004. Genome-wide analysis of transcriptional hierarchy and feedback regulation in the flagellar system of *Helicobacter pylori*. *Mol Microbiol* 52:947–961.

