SUPPLEMENTARY DATA

High molecular / low acetylated chitosans reduce adhesion of *Campylobacter jejuni* to host cells by blocking JlpA

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Table S1: Primers for amplification of the *C. jejuni* genes *flpA* and *jlpA*, for the cold shock expression plasmid pCOLD I, and for multiplex PCR for identification of *Campylobacter*.

Table 2: Primers for amplification of the *C. jejuni* genes *flpA* and *jlpA*, for the cold shock expression plasmid pCOLD I, and for multiplex PCR for identification of *Campylobacter*.

	Sequence (5´- 3´)
Amplicon: *flpA* in pCOLD I	
flpA_NdeI-FOR	TATATCATATGAGCTTGCCAAAGGTTGAAAG
flpA_XbaI-Rev	ATATATCTAGAGACTGAGCCGCCTTAACTTTG
Amplicon: pCOLD I (sequencing primers)	
pCOLDI FOR	ACGCCATATCGCCGAAAGG
pCOLDI REV	GGCAGGGATCTTAGATTCTG
Amplicon: *jlpA* in pCOLD I	
jlpA_NdeI-FOR	CCCGGGCATATGTGCGGAAATTCCATAG
jlpA_PstI-REV	ATATATCTGCAGAAATGACGCTCCGCCCA
16S rDNA	GGGAGGCAGCAGTRRGGAAT
	TGACGGGCGGTGRGTACAAG
asp Aspartokinase	GGTATGATTTCTACAAGCGAG
	ATAAAAGACTATCGTCGCGTG
hipO Hippuricase	GACTTCGTGCAGATATGGATGCTT
	GCTATAACTATCCGAAGAAGCCATCA

Table S2: Relative proliferation [%] of *C. jejuni* after 48 h ($t_{1/48h}$) under chitosan influence and 48 h ($t_{2/96h}$) after changing to test compound-free, unsupplemented media relative to the untreated control UC ($t_{1/48h}$ value = 100 %). The UC after 96 h ($t_{2/96h}$ value) had a relative proliferation of 181 ± 17 % (related to the ($t_{1/48h}$ value = 100 %). Relative values represent the mean ± SD from n = 3 independent experiments with n = 4 technical replicates.

Chitosan		**Concentration [mg/mL]**		
	***t* [h]**	**5**	**2.5**	**1.25**
		Relative proliferation [%] UC $t_{1/48h}$= 100%; UC $t_{2/96h}$ = 181 %		
134	$t_{1/48h}$	0 ± 0	54 ± 63	74 ± 40
	$t_{2/96h}$	190 ± 75	176 ± 68	176 ± 10
114	$t_{1/48h}$	26 ± 36	10 ± 10	89 ± 55
	$t_{2/96h}$	194 ± 14	100 ± 28	161 ± 48
652	$t_{1/48h}$	24 ± 18	33 ± 25	87 ± 59
	$t_{2/96h}$	123 ± 24	137 ± 27	161 ± 18
651	$t_{1/48h}$	6 ± 5	6 ± 8	177 ± 123
	$t_{2/96h}$	157 ± 54	119 ± 27	172 ± 70
661	$t_{1/48h}$	33 ± 25	137 ± 106	156 ± 91
	$t_{2/96h}$	284 ± 242	273 ± 209	175 ± 136
90/20	$t_{1/48h}$	10 ± 13	10 ± 15	181 ± 128
	$t_{2/96h}$	174 ± 45	145 ± 40	197 ± 107
80/20	$t_{1/48h}$	10 ± 3	7 ± 5	111 ± 76
	$t_{2/96h}$	177 ± 58	129 ± 42	207 ± 112
70/20	$t_{1/48h}$	7 ± 6	1 ± 1	123 ± 92
	$t_{2/96h}$	115 ± 20	120 ± 15	141 ± 50


Ser Asp Met Ser Asn Ile Ala Phe Glu Trp Glu Pro Leu Tyr Asn Glu Asn Ile Lys Gly Phe Tyr Leu Tyr Arg Ser Ser Asp Glu Asn Pro Asp Phe Lys Leu Val Gly Thr Ile Lys Asp Lys Phe Gln Thr His Tyr Val Asp Thr Lys Leu Glu Pro Gly Thr Lys
(in frame with Factor Xa site)
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2
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10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170
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(in frame with Factor Xa site)
Fn3
Fn3
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2
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(in frame with Factor Xa site)
Fn3
Fn3
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350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510
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(in frame with Factor Xa site)
Fn3
Fn3
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2
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520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680
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(in frame with Factor Xa site)
Fn3
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2
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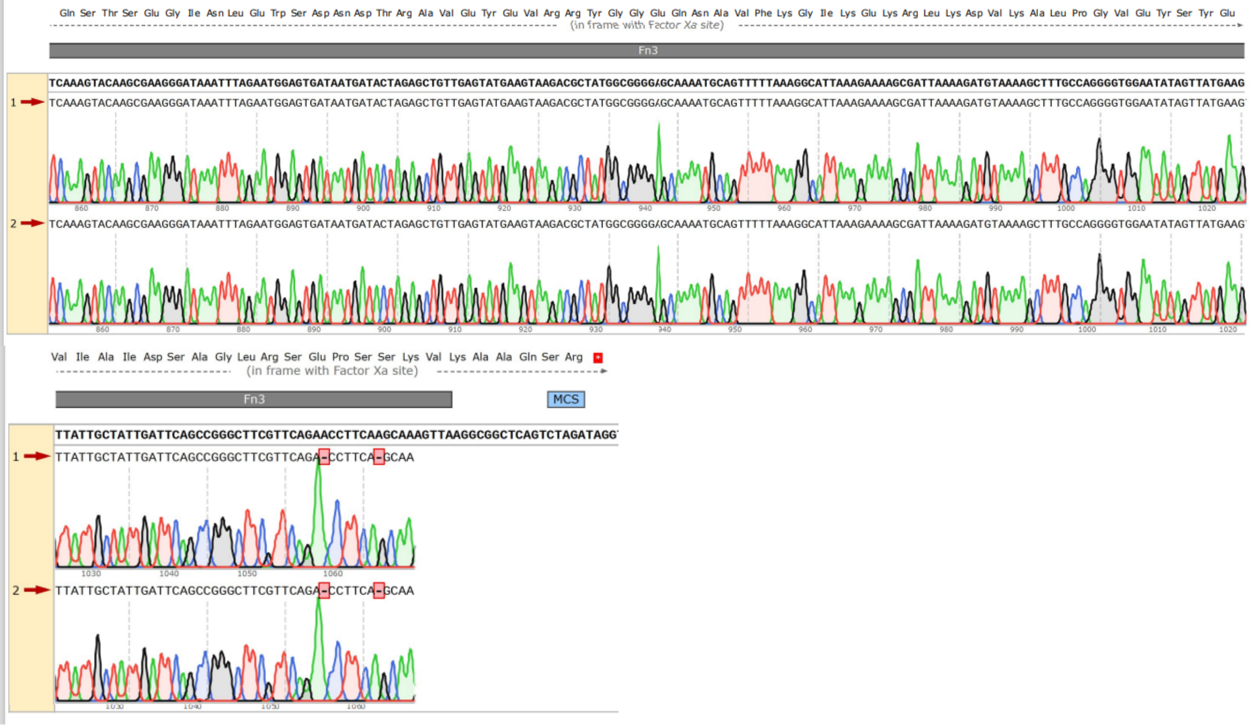

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1 TTATTGCTATTGATTCAGCCGGGCTTCGTTCAGA-CCTTCA-GCAA
2 TTATTGCTATTGATTCAGCCGGGCTTCGTTCAGA-CCTTCA-GCAA
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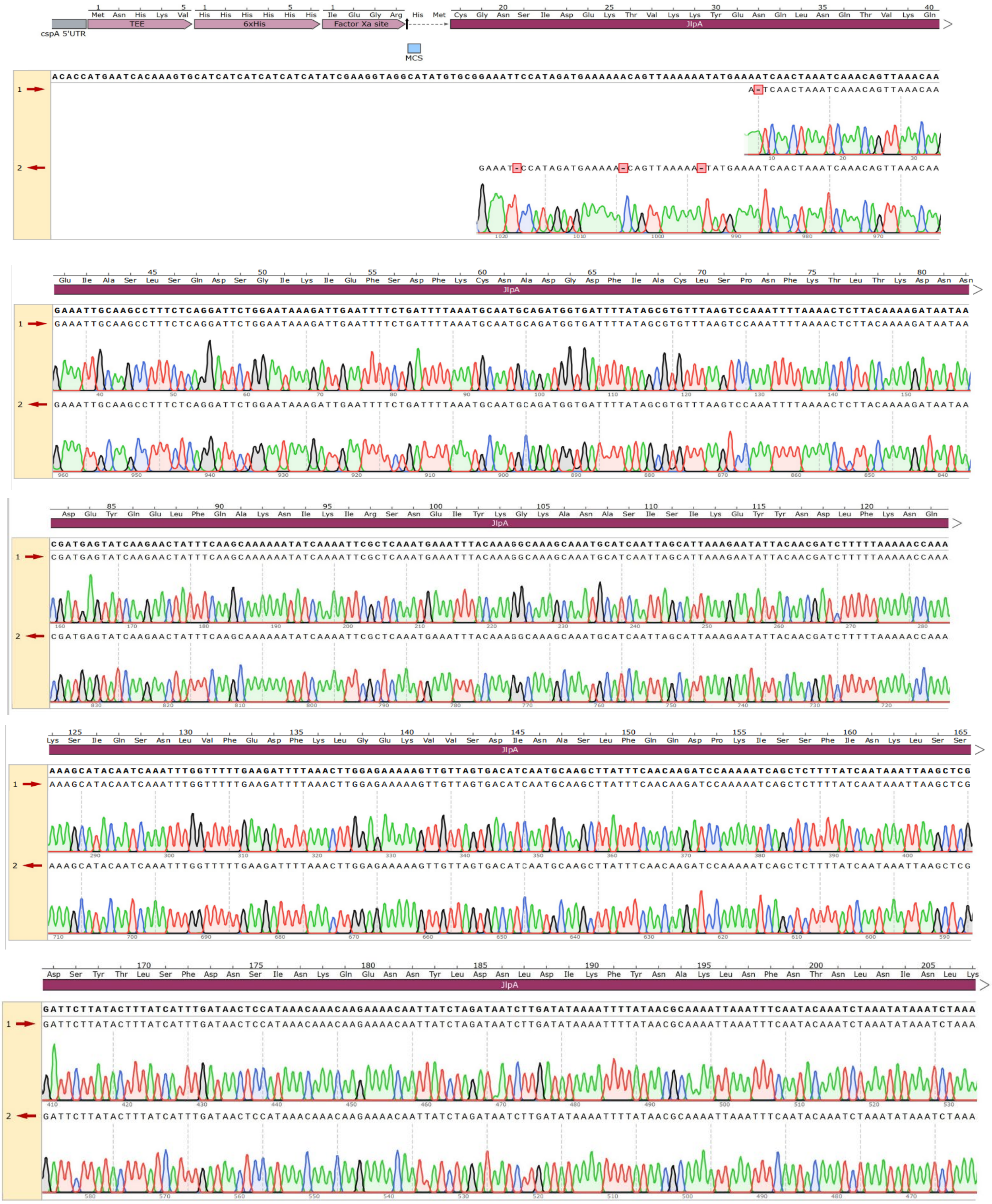
Figure S1: Sequence alignment of the *flpA* gene products of the forward and reverse primers with the theoretical *flpA* sequence for cloning into pCOLD using SnapGene. The reference sequence is shown above in bold letters. (1): Sequence of the PCR product with the forward primer. (2) Sequence of the PCR product with the reverse primer. In the figure, the sequenced bases are indicated by the letter code as well as by color: RED/T: thymine; BLUE/C: cytosine; GREEN/A: Adenine; GREY/G: Guanine. In addition, the coded amino acids are listed in this representation.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TEE
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JlpA
1
2

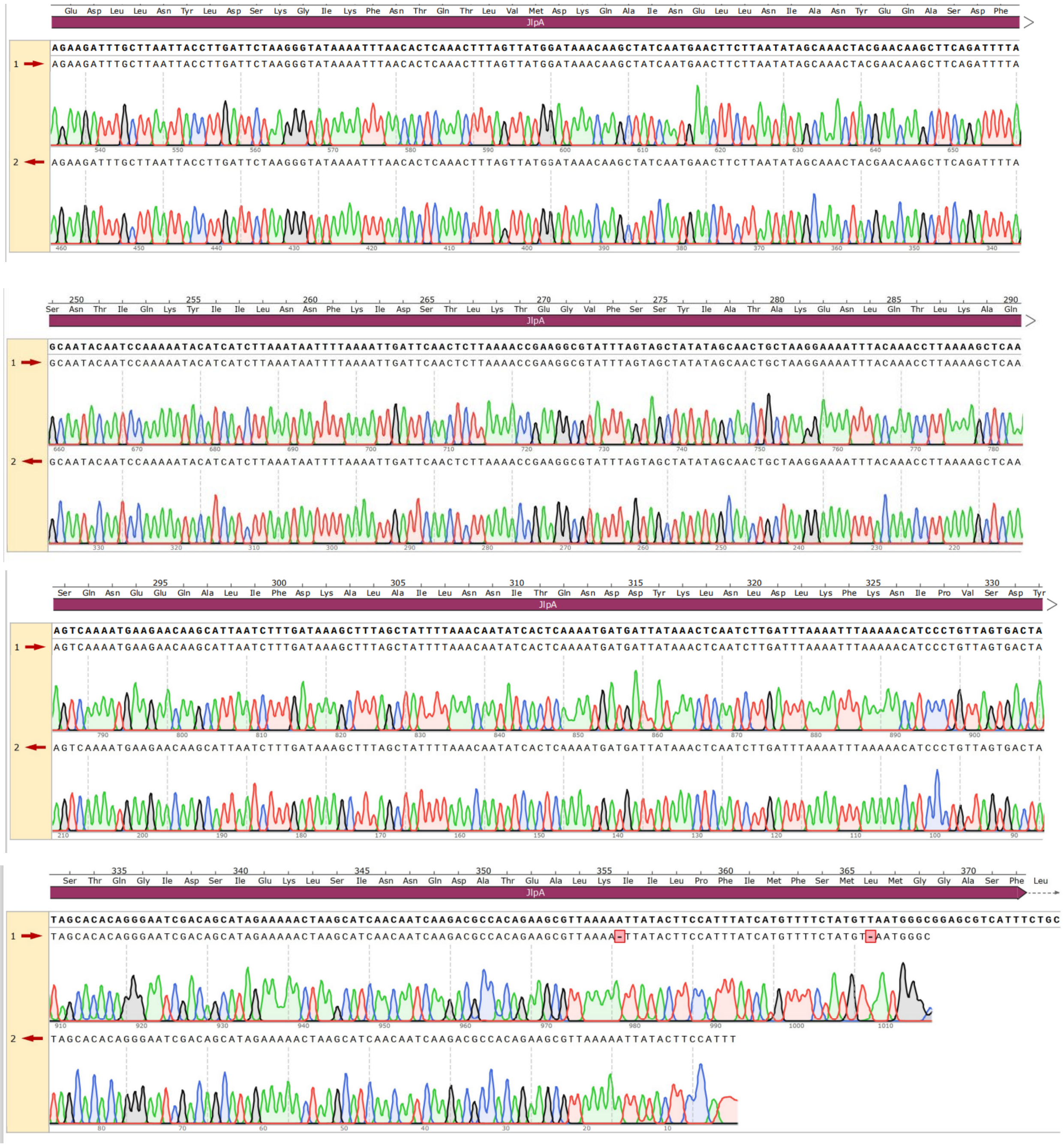

Figure S2: Sequence alignment of the jlpA gene product of the forward and reverse primers with the theoretical jlpA sequence for cloning into pCOLD using SnapGene. Reference sequence is shown above each in thick letters. (1): Sequence of the PCR product with the forward primer. (2) Sequence of the PCR product with the reverse primer. Nucleotides are indicated by the letter code and by color: RED/T: thymine; BLUE/C: cytosine; GREEN/A: adenine; GREY/G: guanine.

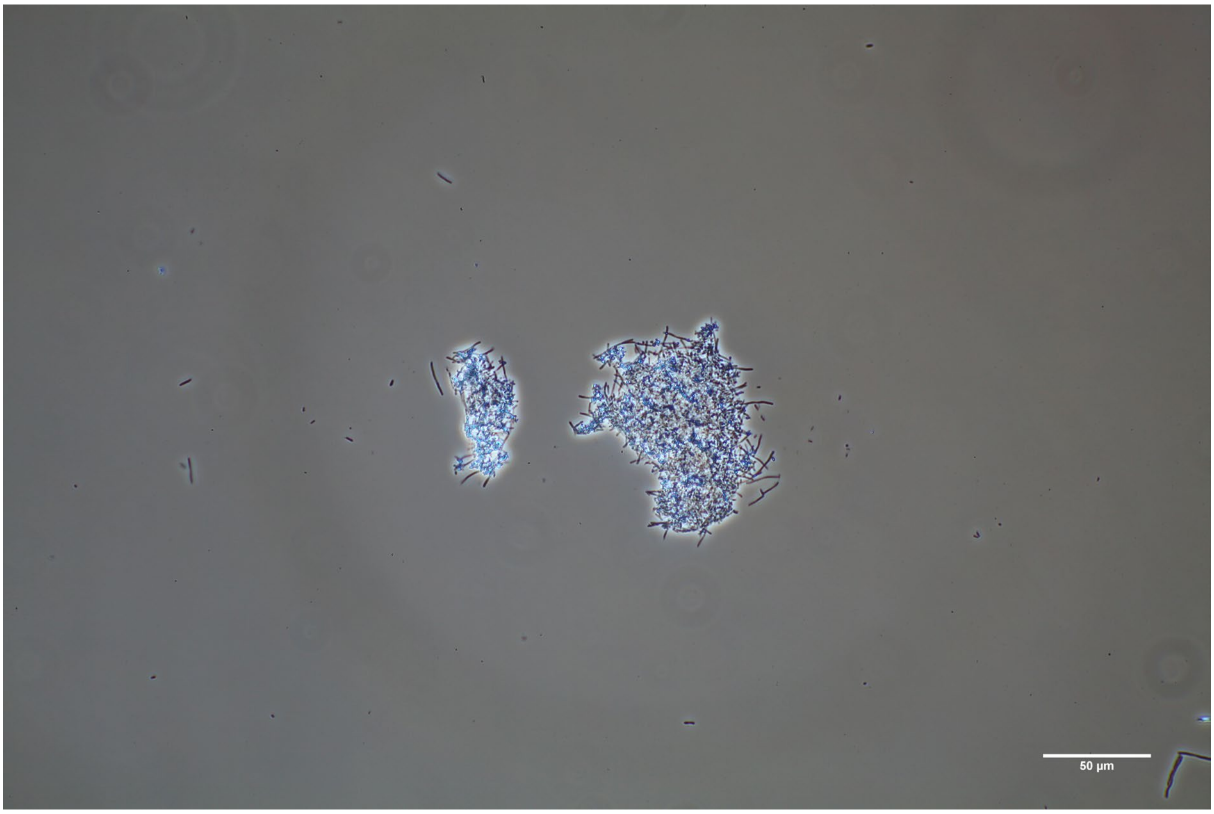

Figure S3: Chitosan 134 treated *Campylobacter jejuni* after 72 h of incubation leads to strong bacterial agglomeration and elongation of bacteria.