Supplementary Information

Identification and characterization of the novel colonization factor CS30 based on whole genome sequencing in enterotoxigenic *Escherichia coli* (ETEC)

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Supplementary Information

FIGURES

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Putative major subunit APADNDASKATLNFSGRVTSSLCOVKTDDLTKDISLGEVSKSALAASGKGPAOSFOVNLI
                                                                            60
FasA 987P
                    APAENNTSOANLDFTGKVTASLCOVDTSNLSOTIDLGELSTSALKATGKGPAKSFAVNLI
                                                                            60
                     Putative major subunit NCDTTTNDISYVLADANGNGAGASTYLVPKSGDTAAEGVGVFVETSNGTKVNIGTAQ
                                                                            120
FasA 987P
                    NCDTTLNSIKYTIAGNNNTG----SDTKYLVPASNDTSASGVGVYIQDNNAQAVEIGTEK
                                                                            116
                     **** * * * * * *
                                         * * * * * :
                                                                            180
Putative major subunit TLNVVSNGATALSEQVIPLRAYIGTQNGTGGTIGTNGLKAGTVDATGVLTIRANYKANTP
FasA 987P
                    TVPVVSNGGLALSDQSIPLQAYIGTTTGNPDT--NGGVTAGTVTASAVMTIRSAGTP*--
                                                                            171
                     *: *****. ***:* ***:**** .*. * . *:.**** *:.*:***:
Putative major subunit *
                        180
FasA 987P
                       171
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Figure S1. Amino acid sequence comparison between the putative major subunit and the major subunit FasA (987P). The major subunits share 58.3% of the amino acid sequence. Isolate E873 was used as a representative for all isolates harboring the novel CF. Deduced amino acid sequences were aligned using ClustalO. Amino acids that are identical (*), strongly similar (:), weakly similar (.) or different () are indicated.



Figure S2. Expression of the *csmA* **gene in E873.** Dotted curve shows the growth curve $(OD_{600} = 0.9)$ of isolate E873 cultured at 37°C and the solid line the gene expression of *csmA* measured by qRT-PCR during seven hours. The highest expression was seen after three hours. Fold change is calculated relative to the expression levels at 2 hours at 37°C. Expressions at 20°C was virtually undetectable (not shown).



E873 $\Delta csmA$

Figure S3. A schematic figure over the construction of the E873 Δ csmA mutant. Amplification of the left and the right fragment was performed to fuse together with pMT-suicide-SacB (pSS) in a primerless PCR. Incorporation of the csmA::Kan fragment was integrated into the pSS followed by integration by homologous recombination with the plasmid carrying CS30.



Figure S4. Gene expression of *csmA-G*. Specific primers were used to amplify fragments within the genes encoding CsmA-G by regular PCR. The major subunit (*csmA*) is not expressed in the mutant (m), E873 Δ csmA, where a Kanamycin cassette was inserted. The wildtype strain (wt), E873, and the complemented mutant (cm), E873 Δ csmA pMT-csmA, express all genes (*csmA-csmG*). PCR products: *csmA* = 218 bp; *csmB* = 230 bp; *csmC* = 208 bp; *csmD* = 879 bp; *csmE* = 142 bp; *csmF* = 348 bp; *csmG* = 232 bp.

TABLES

CF	Mor	phology ^{a,1}	Size (kD) ^{b,1}	Accession number	Refs
CFA/-like					
group					
CFA/I	F	7 nm	25.0	M55661.1	2,3
CS1	F	7 nm	15.2	AY536429 1	4-7
CS2	F	7 nm	15.4	Z47800	5,7,8
CS4	F	6 nm	15.0	AF296132.1	9
CS14	F	7 nm	15.0/15.5	AY283611	10
CS17	F	7 nm	15.5	AY515609.1	11
CS19	F	7 nm	15.0	AY288101.1	11
PCFO71*	n.d.	n.d.	n.d.	AY513487.1	12
CS5-like group					
CS5	Н	5 nm	18.6	AJ224079	13
CS7	Н	3-6 nm	18.7	AY009095.1	14
Class Ib-					
group ^c					
CS12	F	7 nm	17.9	AY009096.1	15
CS18	F	7 nm	18.5	AF335469.1	16
CS20	F	7 nm	17.5	AF438155	17
CS26*	n.d.	n.d.	n.d.	HQ203050	18
CS27A*	n.d.	n.d.	n.d.	HQ203047	18
CS27B*	n.d.	n.d.	n.d.	HQ203048	18
CS28A*	n.d.	n.d.	n.d.	HQ203049	18
CS28B*	n.d.	n.d.	n.d.	HQ203046	18
Additional					
CS3	f	2-3 nm	15.0	FN822745.1	5,7,19
CS6	nF		15.1/15.9	U04844	9,20,21
CS8	F	7 nm	25.3	AB059751	22
CS21	F	7 nm	25.2	EF59570.1	23
CS15	nF		18.2	X65623	24
CS22	f	n.d.	15.0	AF145205.1	25
CS10	nF		16.0	n.a.	26
CS11	f	3 nm	n.d.	n.a.	27
CS13 ^d	f	n.d.	24.8	X71971	28
CS23 ^d	f/nF		16.9	JQ434477	29

Table S1. Characteristics of human ETEC CFs.

^a F = fimbrial; f = fibrillar; nF = non-fimbrial; H = helical.

^b The size of the major subunit was predicted using the published amino acid sequences.

^c All CFs in Class 1b are related to the porcine CF 987P (F6)¹⁸.

^dCS13 and CS23 are related to the porcine CF K88 $(F4)^{29}$.

n.d. = not determined.

n.a. = not available.

* Putative ETEC CFs

Protein Peptide Sequences **ETEC** isolates E873 E1101 E1523 E1586 37°C/20°C 37°C/20°C 37°C/20°C 37°C/20°C CsmF NTVLNFTENSSVK 1.6* 2.2 3.1 2.9 CsmA VTSSLCQVK SALAASGK AGTVDATGVLTIR ATLNFSGR 2.3 2.0 2.9 2.9

Table S2. Peptides identified by quantitative mass spectrometric (QMS) analyses in bacterial cultures grown at 37°C or 20°C.

*Numbers indicate the ratio of peptides identified in the samples cultured at 37°C and 20°C.

Table S3. Adhesion of strains E873 (CS30), E873 ΔcsmA and E873 ΔcsmA pMT-csmA to Caco-2 cells

Studing	Caco-2 cells	
	% cells with adherent bacteria ^b	
E873 CS30 37°C ^a	92.9%±1.9	
E873 CS30 20°C ^a	4.2%±2.6	
E873 ΔcsmA	2.9%±0.65	
E873 ΔcsmA pMT-csmA +IPTG	28.3%±12.5	
E873 ΔcsmA pMT-csmA –IPTG	4.5%±2.8	

^a Strain E873 was used as a representative strain for all four identified CS30 positive strains. Similar adhesion indexes were seen for all CS30 positive strains.

^b Percent mean \pm of cells with at least one adhering bacterium.

Strains	Relevant characteristics	Reference				
<i>E. coli</i> S17-1	λpir, auxotrophic to Proline	Supplied by M. Lebens				
E. coli S17-1- (csmA::Kan)	λpir, auxotrophic to Proline, harboring pJT-SacB-Cm-(csmA::Kan)	This study				
ETEC E873	LT, STp, CS30	icddr,b, Dhaka, Bangladesh				
ETEC E873 (ΔcsmA)	LT, STp, CS30 (csmA::Kan)	This study				
ETEC E873 (ΔcsmA pMT-	LT, STp, CS30 (csmA::Kan), pMT-	This study				
csmA)	csmA					
Plasmids						
pMT-SacB-Cm	Cm, suicide plasmid	Supplied by M. Lebens ³⁰				
pMT-SacB-Cm-(csmA::Kan)	Cm, Kan, LT::Kan	This study				
pMT-ctxA	Cm	Supplied by M. Lebens				
Primers*	Sequence (5'-3')	Product (bp)				
CS30 detection						
For-csmA	AGTCAGCTCTTGCAGCCAGT	219				
Rev-csmA	CCTTGGTACCATTGCTGGTT					
For-csmB	ATCCGTGTTCTCTGTTCGGG	220				
Rev-csmB	ACCATTCAAGGCTTTCGGGT	230				
For-csmC	GTGCAAGAGTTAGGTGTTGCTG	208				
Rev-csmC	GCGCTCGGCTTCTTTTCTTT	208				
For-csmD	TATTCGAGAGGCTGACGGGA	879				
Rev-csmD	TTATCGTTCCCCCAACTGCC					
For-csmE	ACCCAGGAAGTTTGGTTTGGT	142				
Rev-csmE	TCAGGAGTGCTTTTCGGGTA					
For-csmF	AGTTAGCGAACGGGGATCAA	348				
Rev-csmF	TATCTGTCGGGACGACTTGC					
For-csmG	TGCTAATGACGGCACAGGAG	232				
Rev-csmG	CATGCGATAATACGCCCCCT					
Kanamycin insertion						
For-csmA	CCACTTTCTTCCAGCAACCA					
For-csmA-Litmus3	CTGGCGTAGCTTGGCGTAATCATGGGTCACACGCCCTGAAAAGTT					
Rev-csmA	TGAGGGCTCTACCCTGAAAA					
Rev-csmA-Litmus2	CTGGCGTAATAGCGAAGAGGCCCTGCGTGCCTACATTGGTACT					
For-upstream-csmA	TGCAACGCAGTGCTTAAATC					
Rev-Downstream-csmA	CATCACCCGAACAGAGAACA					
Litmus 3	GGGCCTCTTCGCTATTACGCCAG					
Litmus 2	CCATGATTACGCCAAGCTACGCCAG					

Table S4. Strains, plasmids and primers used in the study.

*All primers have been designed in this study.

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