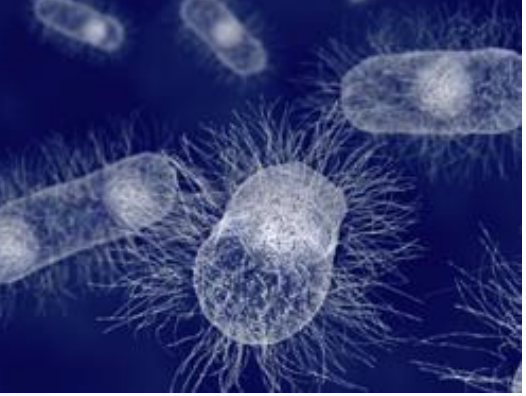

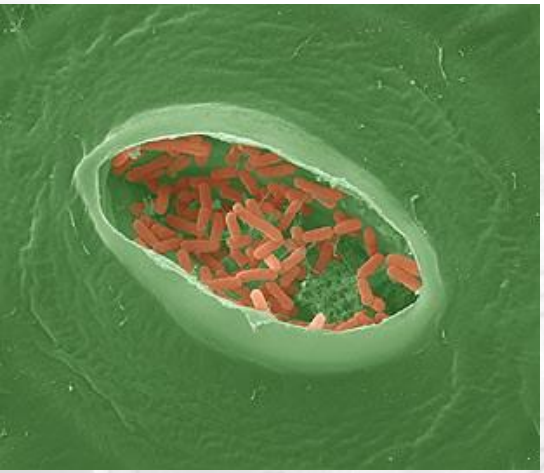

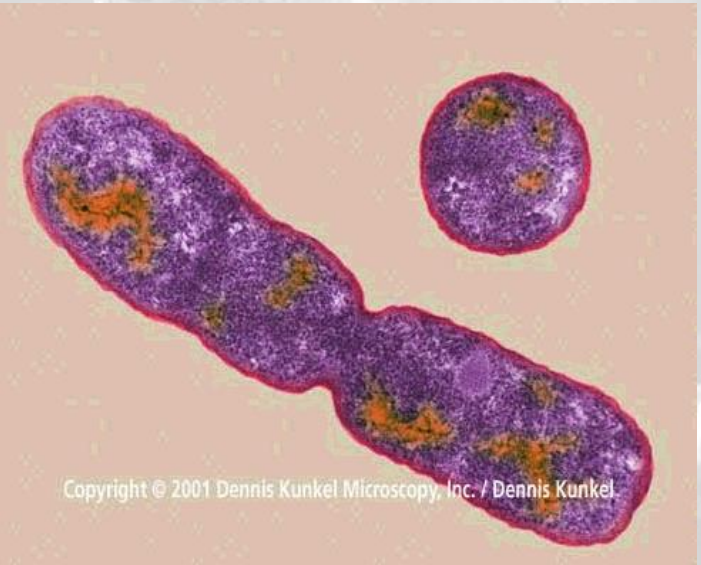

Hybridstammer blandt diarre-fremkaldende *E. coli*

Flemming Scheutz

The International Centre for Reference and Research on *Escherichia* and *Klebsiella*

Fødevarebårne Infektioner (FBI)

Bakterier, parasitter & svampe

STATENS SERUM INSTITUT

Definition of *hybrid*

1: an offspring of two animals or plants of different races, breeds, varieties, species, or genera a *hybrid* of two roses
2: a person whose background is a blend of two diverse cultures or traditions
3a: something heterogeneous in origin or composition **:** COMPOSITE
hybrids of complementary DNA and RNA strands
a *hybrid* of medieval and Renaissance styles
3b: something (such as a power plant, vehicle, or electronic circuit) that has two different types of components performing essentially the same function
drives a *hybrid* that gets really good mileage

Enterohemorrhagic *Escherichia coli* Hybrid Pathotype O80:H2 as a New Therapeutic Challenge

Nurcan Soysal, Patricia Mariani-Kurkdjian, Yasmine Smail, Sandrine Liguori, Malika Gouali, Estelle Loukiadis, Patrick Fach, Mathias Bruyand, Jorge Blanco, Philippe Bidet, Stéphane Bonacorsi

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 22, No. 9, September 2016

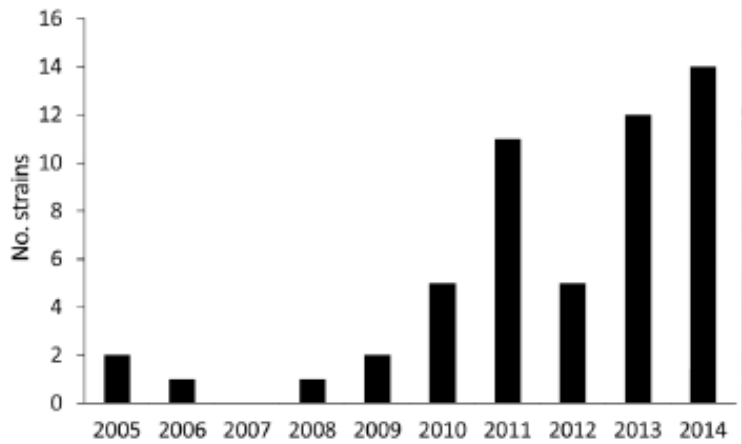

Figure 1. Number of enterohemorrhagic *Escherichia coli* O80:H2 strains detected annually, France, January 2005–October 2014.

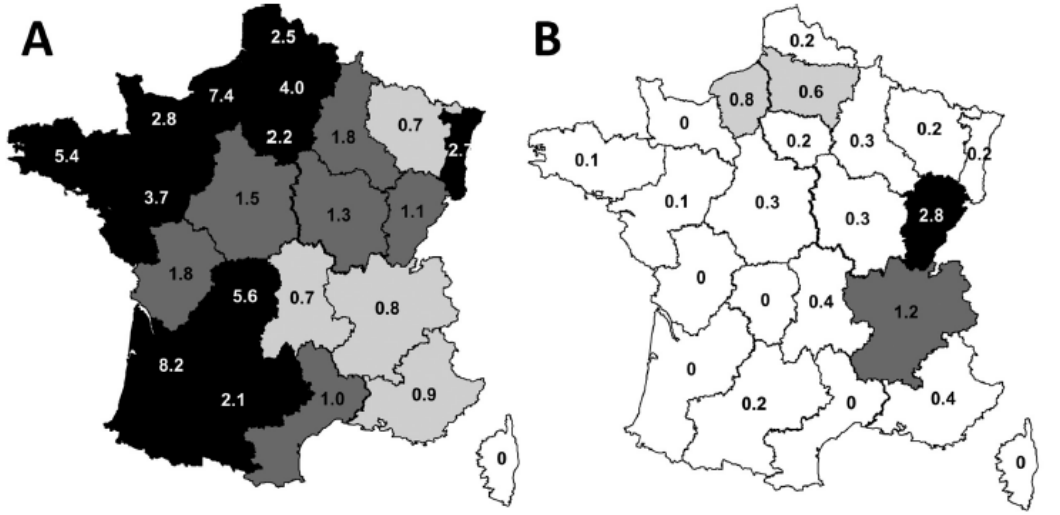

Figure 2. Regional 10-year cumulative incidence rates of hemolytic uremic syndrome cases caused by enterohemorrhagic *Escherichia coli* serotypes O157:H7 and O80:H2, France, January 2005–October 2014. A) Serotype O157:H7. B) Serotype O80:H2. White, <0.5 cases/100,000 children; light gray shading, 0.5–0.7 cases/100,000 children; medium gray shading, 0.8–0.9 cases/100,000 children; dark gray shading, 1–2 cases/100,000 children; black, >2 cases/100,000 children.

48/53 (91%) had HUS; Median age for these 48 patients was 1.2 years

Karakteristik af 57 STEC-ExPEC O80:H2

69% combination af *stx2* subtyper:
***stx2c/2d* (62%)**
***stx2a/2d* (7%)**
31% kun en subtype:
***stx2a* (22%)**
***stx2d* (9%)**
Alle *eae*-ξ
87% enterohemolysin *ehxA*
Alle 57 isolater: ≥4 gener fra pS88 plasmidet: *sitA*, *cia*, *hlyF*, *ompT*
98% *iss* og *iroN* genes
96% *cvaA* gene
61% *iucC* og *etsC*

pS88 plasmidet

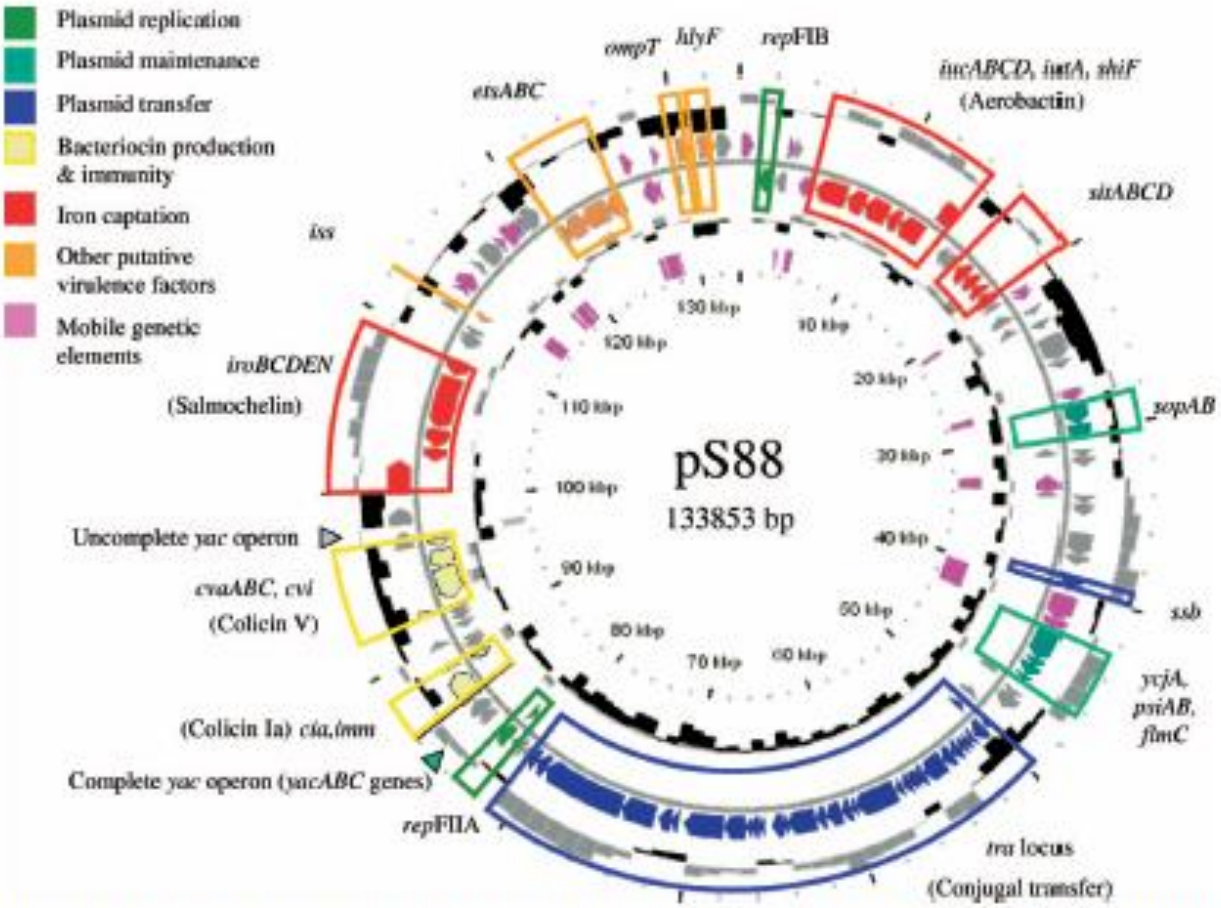

FIG. 1. Circular representation of the *Escherichia coli* strain S88 plasmid (pS88). Circles display (from the outside) (i) GC percent deviation (GC window − mean GC) in a 1,000-bp window, (ii) predicted ORFs transcribed in the clockwise direction, (iii) predicted ORFs transcribed in the counterclockwise direction, (iv) GC skew (G + C/G − C) in a 1,000-bp window, (v) transposable elements (pink), and (vi) coordinates in kilobase pairs (kbp) from the origin of replication. Genes displayed in circles ii and iii are categorized by color as follows: red, iron uptake systems; orange, other putative virulence factors; yellow, bacteriocin production and immunity; pink, mobile genetic elements; dark blue, plasmid transfer; green, plasmid replication; teal, plasmid maintenance; gray, unknown.

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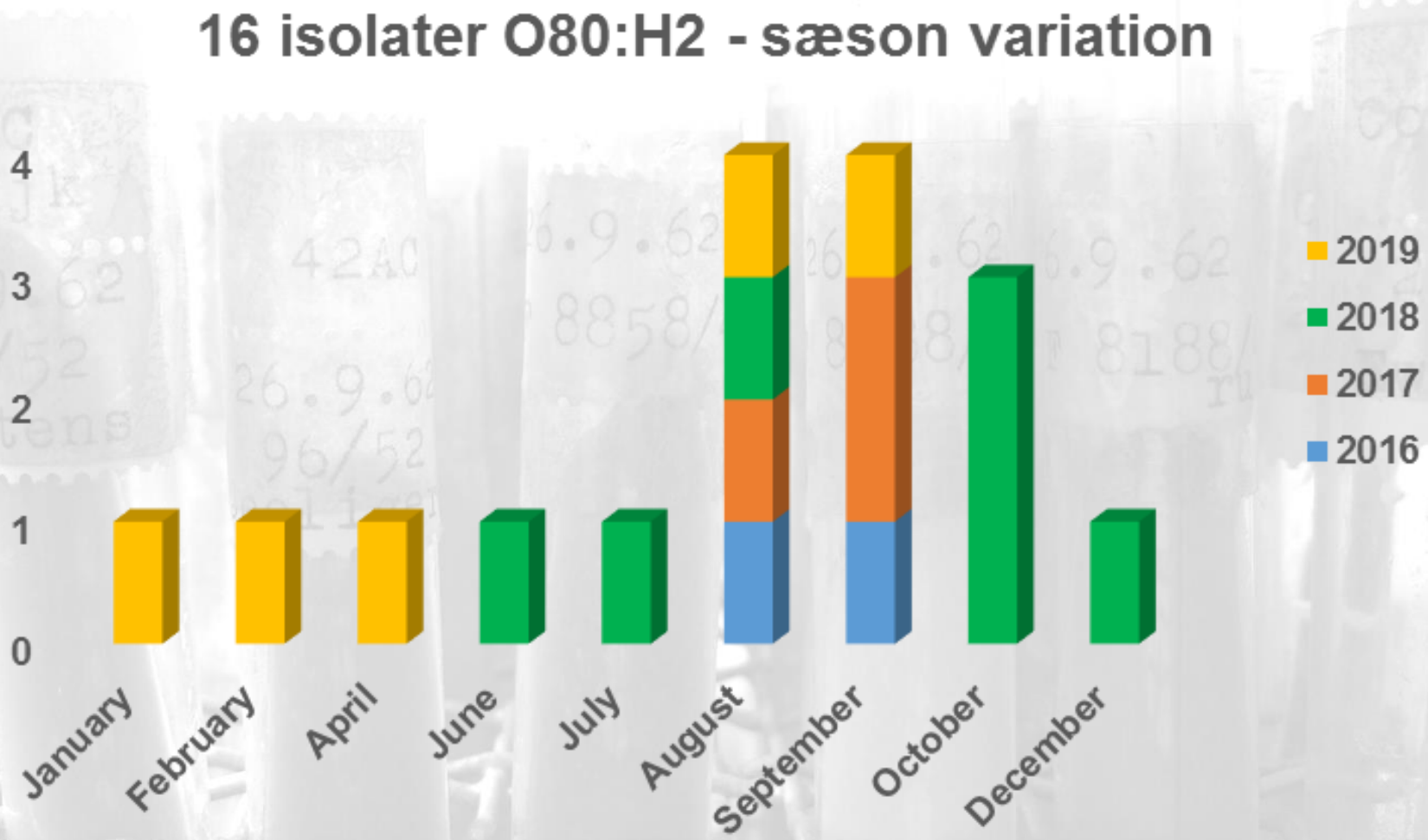
Research note

Table 1
Characteristics, conventional virulence genes, extraintestinal pathogenic *Escherichia coli* plasmid pS88-related genes and extended-spectrum β-lactamase production of the studied Belgian *E. coli* O80:H2

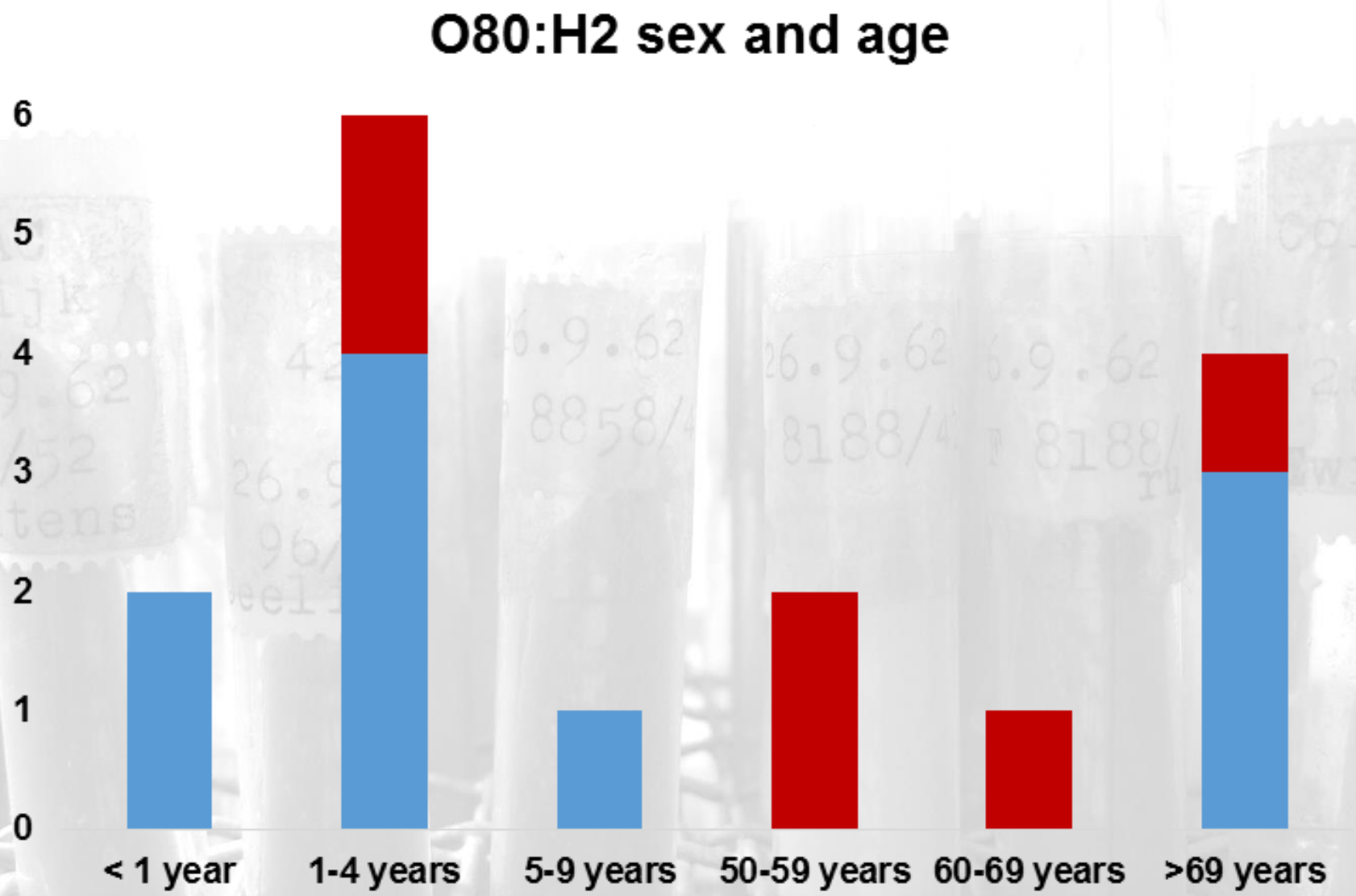
Strain	Source	Year	Patient characteristics[b]					Virulence genes			pS88 related genes										ESBL[c]
			Sex	Age	Prov.	HUS	GI	*stx*	*eae*	*ehxA*	*cia*	*cvaA*	*eitB*	*etsC*	*hlyF*	*iroN*	*iss*	*iucC*	*ompTp*	*sitA*	
EH1752	Human	2008	F	1 y	FB	N	D	*stx2d*	*eaeξ*	+	+	+	−	+	+	+	+	+	+	+	−
EH1764		2008	F	72 y	UNK	N	D	*stx2d*	*eaeξ*	+	+	+	−	+	+	+	+	+	−	+	−
EH2262		2013	F	49 y	FB	N	D	*stx2a*	*eaeξ*	+	+	+	−	+	+	+	+	+	+	+	−
EH2400		2014	F	61 y	WF	N	D	*stx2d*	*eaeξ*	+	+	+	−	+	+	+	+	+	+	+	−
EH2436		2014	F	78 y	WB	UNK	UNK	*stx2d*	*eaeξ*	−	+	+	−	+	+	+	+	+	+	+	−
EH2549		2015	F	60 y	A	N	BD	*stx1a*	*eaeξ*	+	+	+	−	−	−	−	+	−	−	−	+
EH2644		2015	F	11 m	WB	Y	D	*stx2d*	*eaeξ*	+	+	+	−	+	+	+	+	+	+	+	−
EH2786		2016	F	2 y	BCR	UNK	UNK	*stx2a*	*eaeξ*	+	+	+	−	−	+	+	+	−	+	+	−
EH2808		2016	F	61 y	N	Y	UNK	*stx2d*	*eaeξ*	+	+	+	−	+	+	+	+	+	+	+	−
FMV 36819_3[a]	Calf	1987	UNK	2.5 m	WB	NR	D	*stx1a*	*eaeξ*	+	+	+	−	−	+	+	+	−	+	+	−
FMV 36819_5[a]		1987	UNK	2.5 m	WB		D	*stx1a*	*eaeξ*	−	−	+	−	−	−	−	−	−	−	−	−
ARSIA 22		2009	UNK	UNK	L		D	/	*eaeξ*	+	+	+	−	−	+	+	+	−	+	+	−
ARSIA 23		2009	UNK	UNK	N		D	/	*eaeξ*	+	−	+	−	−	+	+	+	−	+	+	−
ARSIA 94		2010	M	1 m	Lu		D	/	*eaeξ*	+	+	+	−	+	+	+	+	+	+	+	−
ARSIA 150		2012	M	6.5 m	L		D	/	*eaeξ*	+	+	+	−	−	+	+	+	−	+	+	−
ARSIA 212		2013	F	4.5 m	L		D	/	*eaeξ*	+	+	+	−	−	+	+	+	−	−	+	−
ARSIA 3042		2014	M	16 d	L		D	/	*eaeξ*	+	+	+	−	−	+	+	+	−	+	+	−
ARSIA 3088		2015	M	17 d	Lu		D	/	*eaeξ*	+	+	+	−	−	+	+	+	−	−	+	+

[a] Strains FMV 36849_3 and FMV 36819_5 originate from the same calf.
[b] F, female; M, male; UNK, unknown; yr, years; m, months; d, days; Prov., Province of residence; FB, Flemish Brabant; WF, West Flanders; WB, Walloon Brabant; A, Antwerp; BCR, Brussels Capital Region; N, Namur; L, Liège; Lu, Luxembourg; HUS, haemolytic uraemic syndrome; N, no; UNK, unknown; Y, yes; NR, not relevant; GI, gastrointestinal symptoms; D, diarrhoea; UNK, unknown; BD, bloody diarrhoea.
[c] ESBL, extended spectrum β-lactamase production.

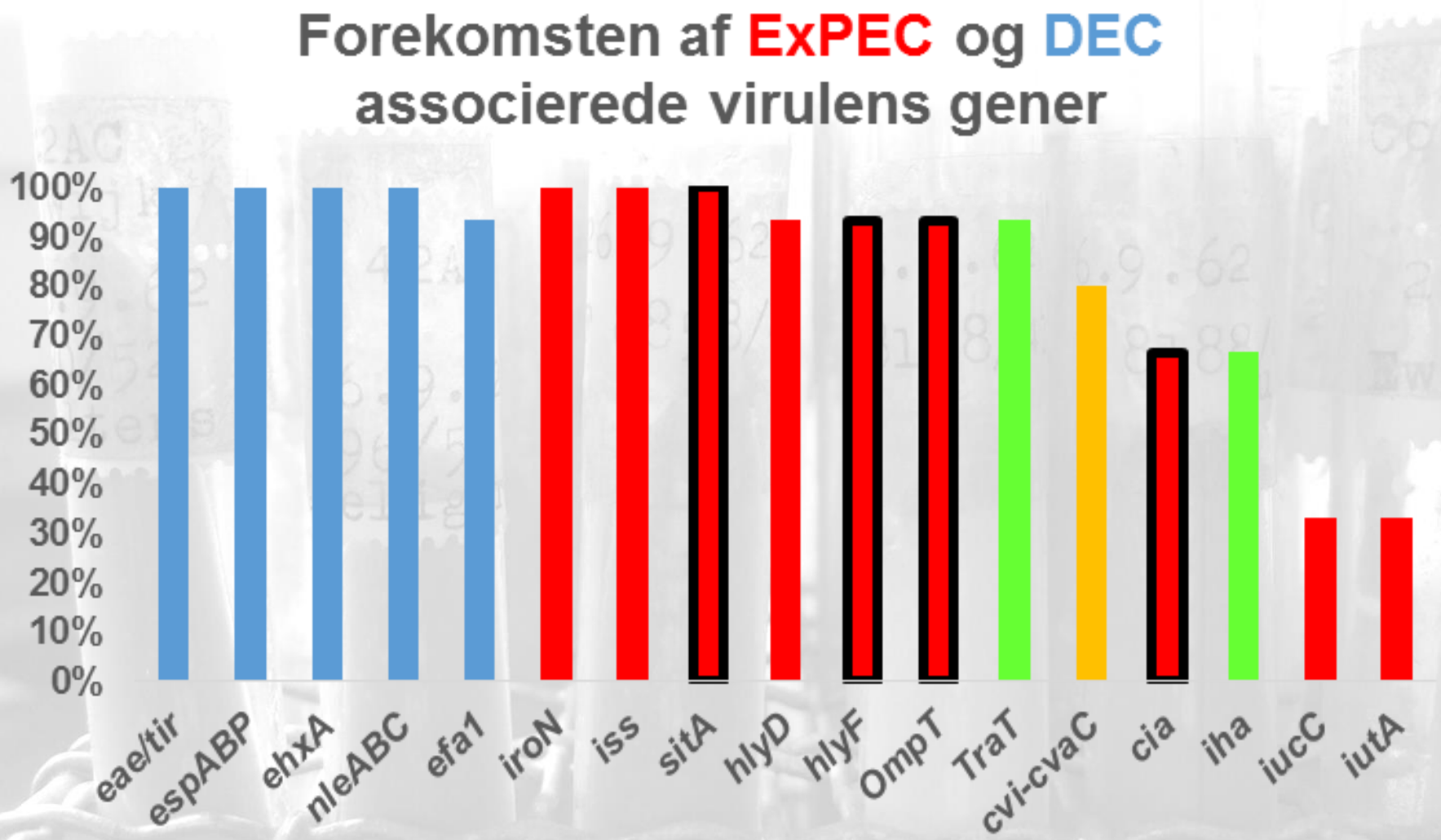
Har vi STEC-ExPEC O80:H2 i Danmark?



STEC-ExPEC O80:H2 i Danmark



STEC-ExPEC O80:H2 i Danmark



Whole-Genome Characterization and Strain Comparison of VT2f-Producing *Escherichia coli* Causing Hemolytic Uremic Syndrome

Laura Grande, Valeria Michelacci, Roslen Bondi, Federica Gigliucci, Eelco Franz, Mahdi Askari Badouei, Sabine Schlager, Fabio Minelli, Rosangela Tozzoli, Alfredo Caprioli, Stefano Morabito

Table 2. Characteristics of VT2f-producing *Escherichia coli* investigated in a comparative analysis of the virulence profile of strains isolated from humans with mild and severe disease and from the animal reservoir*

Source and strain	Year isolated	Serotype	Phylotype	MLST	LEE	*adfO*	*efa1*	*cif*	*nleA*	*nleB*	*nleC*	*Hly*	*katP*	*espP*	Intimin type
Human diarrhea															
M856	2008	ONT:H6	B2	ST583	+	+	–	+	–	+	+	–	–	–	α-2
M858	2008	O125:H6	B2	ST583	+	+	–	+	–	+	–	–	–	–	α-2
M859	2009	O113:H6	B2	ST121	+	+	–	+	–	–	–	–	–	–	α-2
M884	2011	O96:H7	B2	ST28	+	+	–	+	+	+	–	–	–	–	β-2
M885	2011	O132:H34	B2	ST582	+	+	–	–	–	+	+	–	–	–	β-2
M900	2012	O145:H34	B2	ST722	+	+	–	–	–	+	–	–	–	–	ι
BCW5711	2012	O63:H6	B2	ST583	+	+	–	+	+	–	+	–	–	–	α-2
BCW5746	2012	O63:H6	B2	ST583	+	+	–	+	–	–	+	–	–	–	α-2
BCW5743	2012	O63:H6	B2	ST583	+	+	–	+	–	–	+	–	–	–	α-2
BCW5739	2012	O63:H6	B2	ST583	+	+	–	+	–	–	+	–	–	–	α-2
BCW5717	2012	O63:H6	B2	ST583	+	+	–	+	–	–	+	–	–	–	α-2
Pigeon															
ED360	1997	O45:H2	B1	ST20	+	+	–	+	+	+	+	–	–	–	β
ED361	1997	O75:H2	B1	ST20	+	+	–	+	+	+	+	–	–	–	β
ED363	1997	O4:H2	B1	UNK	+	+	–	+	+	+	+	–	–	–	β
ED366	1997	ONT:H2	B1	ST2685	+	+	–	+	+	+	+	–	–	–	β
ED369	1997	O45:H2	B1	ST20	+	+	–	+	+	+	+	–	–	–	β
ED377	1997	O4:H2	B1	UNK	+	+	–	+	+	+	+	–	–	–	β
ED430	2000	O45:H2	B1	ST20	+	+	–	+	+	+	+	–	–	–	β
ED444	2000	O128:H2	B1	ST20	+	+	–	+	+	+	+	–	–	–	β
HUS															
EF453	2013	O80:H2	B1	ST301	+	+	+	–	+	+	+	+	–	+	ξ
EF467	2013	O26:H11	B1	ST21	+	+	+	+	+	+	+	+	+	+	β
EF476	2014	O55:H9	B1	ST301	+	+	+	–	+	+	+	+	–	+	ξ

*Human samples were diarrheal or fecal samples from HUS cases and pigeon samples were feces from asymptomatic birds. LEE, locus of enterocyte effacement; MLST, multilocus sequence type; UNK, unknown; +, positive; –, negative.

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Molecular Characterization and Comparative Genomics of Clinical Hybrid Shiga Toxin-Producing and Enterotoxigenic *Escherichia coli* (STEC/ETEC) Strains in Sweden

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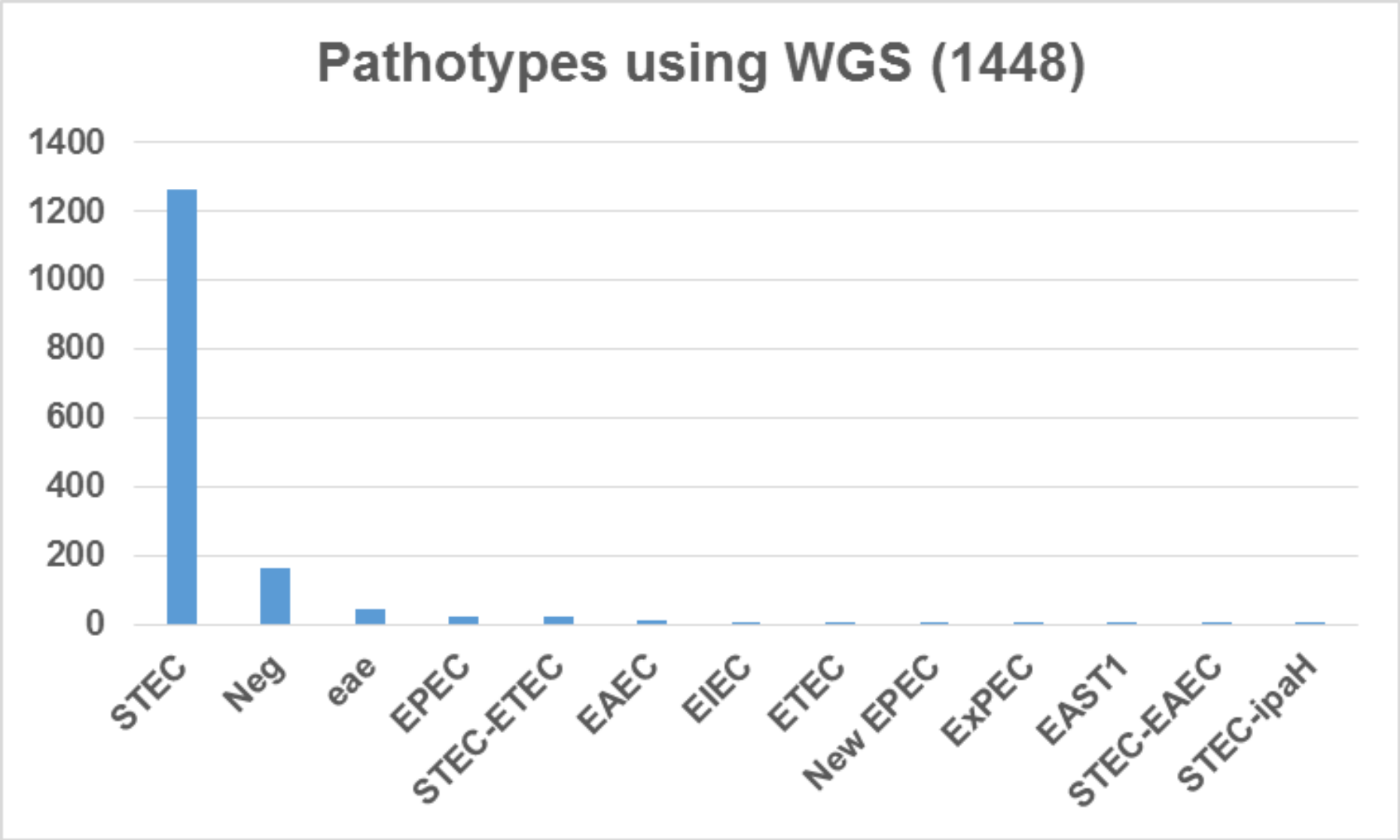
Strain	Serotype	*stx* subtype	*sta* subtype	ST	Sampling year	Clinical symptom	Duration of *stx* shedding (day)	Age of patients (year)
SE572	O187:H28	*stx2g*	*sta4*, *sta5*	200	2005	D	11	1
SE573	O15:H16	*stx2g*	*sta4*	325	2009	D, AP, F	16	56
SE574	O136:H12	*stx2a*	*sta4*, *sta4*, *sta5*	329	2014	N	18	10
SE575	O100:H30	*stx2e*	*sta1*	993	2017	D	—	82

Table 1. Characteristics of STEC/ETEC hybrid strains in this study. D: Diarrhea. AP: Abdominal pain. F: Fever. N: No symptoms, individual was sampled due to contact tracing around an index case. -: Unavailable.

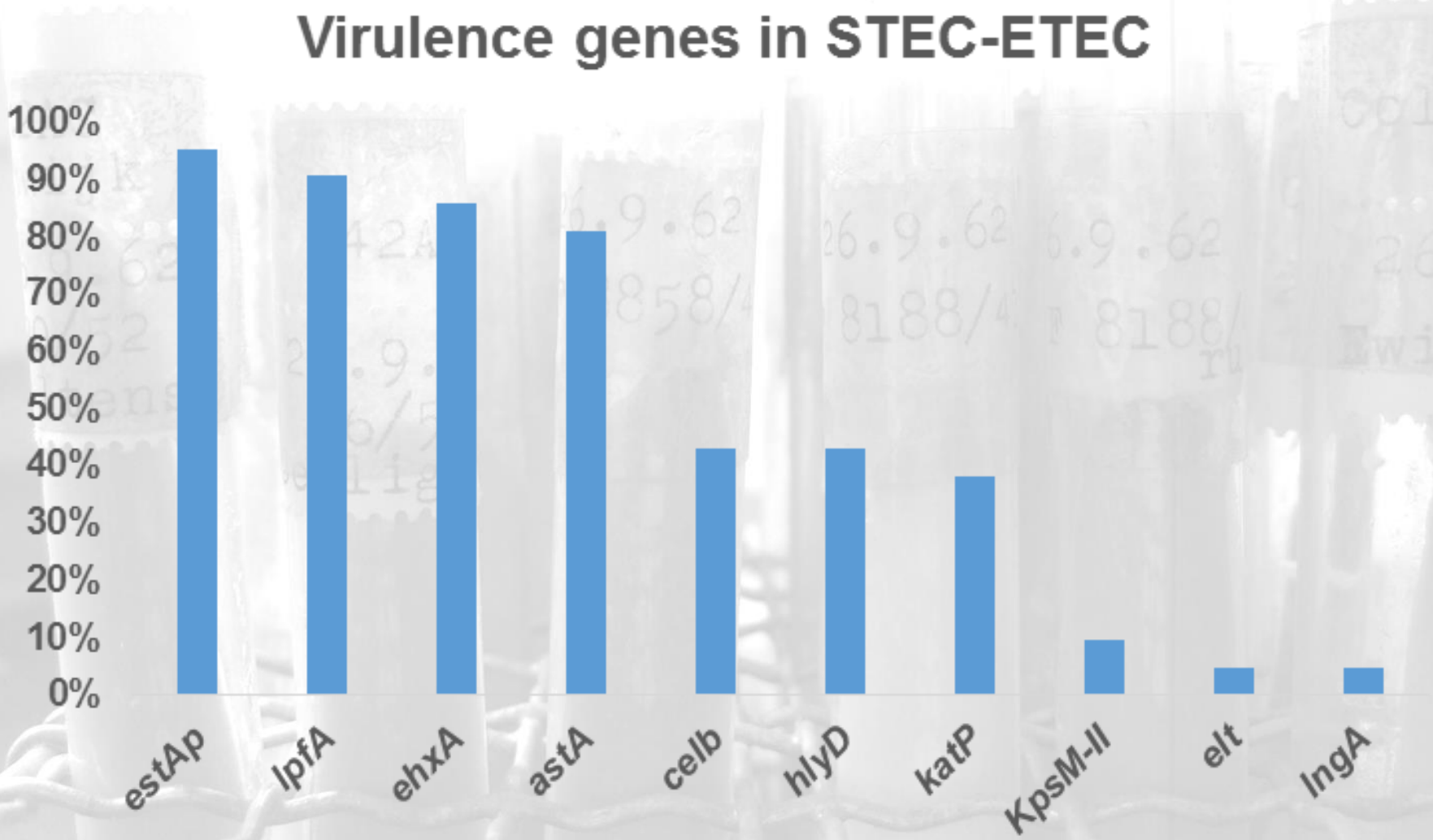
Har vi STEC-ETEC i Danmark?



21 STEC-ETEC i Danmark

GRUPPE	MLST ST	SEROTYPE	*stx*_sub	Enterotoxin	Total
STEC-ETEC	58	O 8:H 9	*stx2e*	*estA*p	1
STEC-ETEC	200	O187:H28	*stx2g*	*estA*p	12
STEC-ETEC	325	O 15:H16	*stx2g*	*estA*p	1
STEC-ETEC	2353	O 6:H16	*stx1a*	*elt*	1
STEC-ETEC	5822	H 7	*stx2g*	*estA*p	2
STEC-ETEC	5822	O?:H 7	*stx2g*	*estA*p	1
STEC-ETEC	5822	Oru:H 7	*stx2g*	*estA*p	2
STEC-ETEC	8880	O 13:H23	*stx2d*	*estA*p	1
Hovedtotal					21

21 STEC-ETEC i Danmark



Hybrids of Shigatoxigenic and Enterotoxigenic *Escherichia coli* (STEC/ETEC) Among Human and Animal Isolates in Finland

O. Nyholm[1], S. Heinikainen[2], S. Pelkonen[2], S. Hallanvuo[3], K. Haukka[1,4] and A. Siitonen[1]

Table 1. STEC/ETEC hybrid strains in Finland

Strain number	Origin	Isolation year	Serotype	stx_1 subtype	stx_2 subtype(s)	*eae*	*escV*	EHEC-*hlyA*	*estIa*	*astA*	Anti-microbial susceptibility[a]	Sorbitol	PGUA[b]
IH57218	THL/diarrhoea, age 7.3 years	2001	O2:H27	–	stx_{2a}	–	–	+	+	+	S	+	–
FE96344	THL/asymptomatic, age 46.1 years	2010	O2:H27	–	stx_{2a}	–	–	+	+	+	S	+	–
IH53473	THL/HUS, age 1.9 years	1997	O101:H-	–	stx_{2a}	+	+	+	+	–	S	+	+
FE102798	Evira/bovine faeces	2002	O2:H27	–	stx_{2a}	–	–	+	+	+	R (Str)	+	–
FE102800	Evira/bovine faeces	2002	O2:H27	–	stx_{2a}, stx_{2d}	–	–	+	+	+	R (Str)	+	–
FE102810	Evira/bovine faeces	1999	O2:H27	–	stx_{2a}, stx_{2d}	–	–	+	+	+	S	+	–
FE102829	Evira/bovine faeces	2000	O2:H27	–	stx_{2a}, stx_{2d}	–	–	+	+	+	S	+	–
FE102837	Evira/bovine faeces	2003	O2:H27	–	stx_{2a}, stx_{2d}	–	–	+	+	+	S	+	–
FE102839	Evira/bovine faeces	2003	O2:H27	–	stx_{2a}, stx_{2d}	–	–	+	+	+	S	+	–
FE102867	Evira/bovine faeces	2003	O2:H27	–	stx_{2a}, stx_{2d}	–	–	+	+	+	S	+	–
FE103622	Evira/bovine faeces	2003	O2:H27	–	stx_{2a}	–	–	+	+	+	S	+	–
FE102804	Evira/bovine faeces	1999	O2:H27	–	stx_{2a}, stx_{2d}	–	–	+	+	+	S	+	–
FE103145	Evira/bovine faeces	1999	O2:H27	–	stx_{2a}	–	–	+	+	+	S	+	–
FE102865	Evira/bovine faeces	2003	O15:H16	–	stx_{2g}	–	–	+	+	+	S	+	+
FE102873	Evira/bovine faeces	1998	O15:H16	–	stx_{2g}	–	–	+	+	+	S	+	+
FE102868	Evira/bovine faeces	2003	O74:H28	–	stx_{2g}	–	–	+	+	+	S	+	+
FE102891	Evira/bovine faeces	1998	O116:H28	–	stx_{2a}, stx_{2g}	–	–	–	+	+	S	+	+
FE102863	Evira/bovine faeces	2003	O128:H8	–	stx_{2g}	–	–	+	+	+	S	+	+
FE102841	Evira/bovine faeces	2003	O136:H12	stx_{1c}	stx_{2a}	–	–	+	+	+	I (Sul)	+	+
FE102838	Evira/bovine faeces	2003	O136:H12	stx_{1c}	stx_{2a}	–	–	+	+	+	S	+	+
FE103613	Evira/bovine faeces	1998	O136:H12	stx_{1a}	–	–	–	+	+	+	S	+	+
FE102813	Evira/moose faeces	2000	O141:H8	–	stx_{2g}	–	–	+	+	+	S	+	+
FE103623	Evira/bovine faeces	2003	O168:H8	–	stx_{2g}	–	–	+	+	+	S	+	+
FE103612	Evira/bovine faeces	2000	OX182:H16	–	stx_{2g}	–	–	–	+	+	S	+	+
FE103621	Evira/bovine faeces	2003	OX182:H-	stx_{1a}	–	–	–	+	+	+	S	+	+

[a]S = Susceptible to tested 12 anti-microbials: ampicillin, chloramphenicol, streptomycin, sulphonamide, tetracycline, trimethoprim, ciprofloxacin, gentamicin, nalidixic acid, cefotaxime, mecillinam and imipenem. R (Str) = Resistance to streptomycin and susceptible to the other 11 anti-microbials. I (Sul) = Intermediate susceptibility to sulphonamide and susceptible to the other 11 anti-microbials.
[b]Production of β-glucuronidase.

Hybrid Shiga Toxin-Producing and Enterotoxigenic *Escherichia* sp. Cryptic Lineage 1 Strain 7v Harbors a Hybrid Plasmid

Susan R. Leonard,[a] Mark K. Mammel,[a] David A. Rasko,[b] David W. Lacher[a]

Division of Molecular Biology, Center for Food Safety and Applied Nutrition, U.S. Food and Drug Administration, Laurel, Maryland, USA[a]; Department of Microbiology and Immunology, Institute for Genome Sciences, School of Medicine, University of Maryland, Baltimore, Maryland, USA[b]

TABLE 1 Characteristics of the STEC/ETEC hybrid strains included in this study

Strain[a]	Serotype	Phylogroup	Location/year	Source	Shiga toxin(s)	Heat-stable enterotoxin(s)	Colonization factor	Plasmid replicon(s)	Accession no. (reference)[b]
7v	O2:H25	CL1	Hong Kong	Feces of healthy cattle	Stx2g	STa4[c]	K88	FIB(AP001918), FII(pSE11)	AEXD02000000 (50)
628591-2	O2:H25	CL1	USA/2010	Coriander	Stx2g[c]	STa4	K88	FIB(AP001918), FII(pSE11)	IZDN01000000 (this study)
1.2741	O2:H25	CL1	Unknown	Bovine	Stx1a, Stx2g	STa4, STa5	K88	FIB(AP001918), FII(pSE11)	AEZI02000000
FE95160	O2:H25	CL1	Burkina Faso/2008	Bovine intestine	Stx1a	STa5		FIB(AP001918), FII(pSE11)	LFZI01000000 (15)
E807	O2:H45	CL1	Australia	Freshwater sediment	Stx1a, Stx2a	STa5	K88	FIB(AP001918), FII(pSE11), Col156	AEJX01000000 (24)
IH53473	O101:H33	A	Finland/2001	Infant with HUS	Stx2a	STa4		FII(29), X1	LFZH01000000 (16)
CFSAN026836	O109:H48	A	USA/1999	Pond water	Stx1a	STa4	K88	FIB(AP001918), FII(pSE11), FIC	LDCY01000000
CFSAN026835	O109:H48	A	USA/1999	Bovine	Stx1a	STa4	K88	FIB(AP001918), FII(pSE11), FIC	LDCZ01000000
CVMN33742PS	O136:H16	A	USA/2011	Farm environment	Stx2g	STa4	K88	FIB(AP001918), FII(pSE11), Col156, Col(MG828), ColRNAI, Col(MGD2)	IUDF01000000
CVMN33429PS	O136:H16	A	USA/2011	Farm environment	Stx1a	STa4, STa5	K88	FIB(AP001918), FII(pSE11), FIC, ColRNAI	IWZR01000000
CFSAN026844	O136:H16	A	USA/1999	Bovine	Stx1a	STa4, STa5	K88	FIB(AP001918), FII(pSE11), A/C2, ColRNAI	LDCW01000000
CFSAN026843	O136:H16	A	USA/1999	Deer	Stx1a	STa4, STa5	K88	FIB(AP001918), FII(pSE11), A/C2, ColRNAI	LGZN01000000
S1191	O141:H4	A	Unknown	Pig with edema disease	Stx2e	STb1	F18	FII(pCoo), FII, X1, X4, I1, Y	AFEA02000000 (51)
K88	O141:H4	A	China	Pig	Stx2e	STb1	K88	FIB(AP001918), FII(pSE11), FII(pCoo), FIC, X4, I1, pO111, ColRNAI	LBBN01000000
UMNF18	O147:H4	A	Iowa/2007	Pig with diarrhea	Stx2e	STa1	F18	FII(pCoo), X1, X4, I1, ColRNAI	AGTD01000000 (7)
2.3916	O147:H4	A	Unknown	Pig	Stx2e	STa1, STb1	F18	FII(pCoo), X1, I1, P, Y	AFAB02000000
IH57218	O2:H27	A	Finland/1997	Child with diarrhea	Stx2a	STa4		FII	LFZJ01000000 (16)
E149	O138:H14	D	England	Pig	Stx2e	STa1, STb1	F18	FII(pCoo), X1, I1, P, ColRNAI	IZXA01000000 (12)
C165-02	O73:H18	D	Denmark	Patient with bloody diarrhea	Stx2d	STb2	Tcf[d]	FIB(AP001918), FII(29), FIA, I1, pO111	AFDR02000000 (52)
3020-98	O187:H52	B1	Virginia/1998	Infant with diarrhea	Stx1c	STa4		FIB(AP001918), FII	AVRH01000000 (12)
MDP04-01392	O187:H52	B1	Maryland/2004	Cantaloupe	Stx1c	STa4		FIB(AP001918), FII	IZDI01000000 (12)
MDP04-02111	O187:H52	B1	Michigan/2004	Cilantro	Stx1c	STa4		FIB(AP001918), FII	IZDK01000000 (12)
MI02-35	O187:H52	B1	Michigan/2002	Patient with bloody diarrhea	Stx1c	STa4		FIB(AP001918), FII, L/M(pMU407)	IZDL01000000 (12)
857226	O187:H52	B1	Unknown	Raw milk Havarti cheese	Stx1c	STa4		FIB(AP001918), FII	IZDM01000000 (this study)

Jpn. J. Infect. Dis., 70, 347-348, 2017

Laboratory and Epidemiology Communications

First Isolation of a Hybrid Shigatoxigenic and Enterotoxigenic *Escherichia coli* Strain Harboring the *stx2* and *elt* Genes in Korea

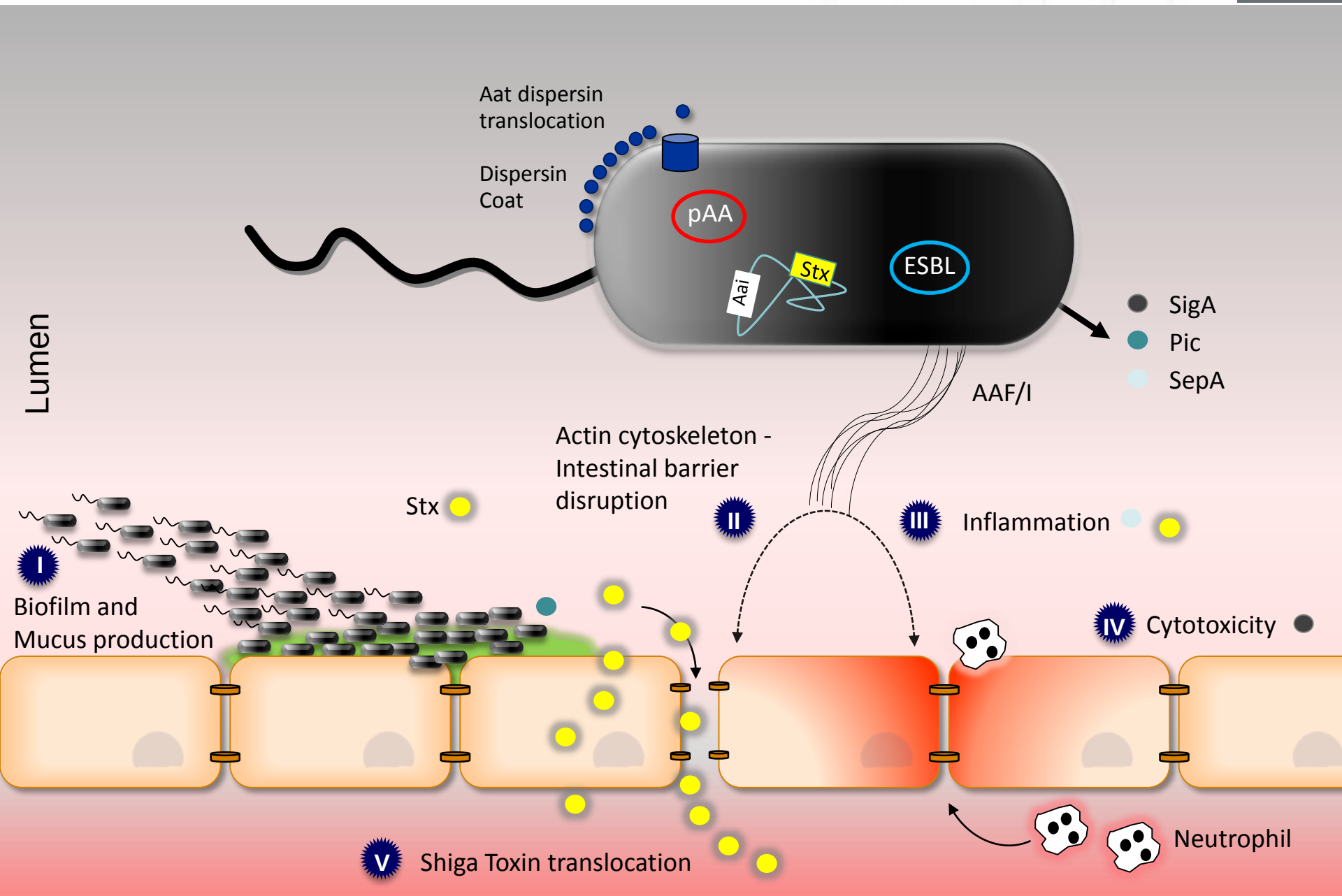
Kyung-Hwan Oh[1], Eunkyung Shin[1], Su-Mi Jung[1], Jinsuk Im[2], Seung-Hak Cho[1], Sahyun Hong[1], Cheon-Kwon Yoo[3], and Gyung Tae Chung[1]*

Table 1. Identification and characterization of new pathotype *E. coli* isolated in Korea

Category	Identification/characterization
Toxin type	*stx2a*, *elt*
Serotype	O159:HUT
EHEC virulence factor	–
Colonization factor	*CS12*
Sequence type	ST171
Motillity	+
Antimicrobial resistance	tetracycline

Andre crossovers i Danmark?

GRUPPE	ST	SEROTYPE	*stx*_sub
STEC-*ipaH*	ND	*Shigella flexneri 2a*	*stx1a*
STEC-EAEC	ND	O104:H 4	*stx2a*

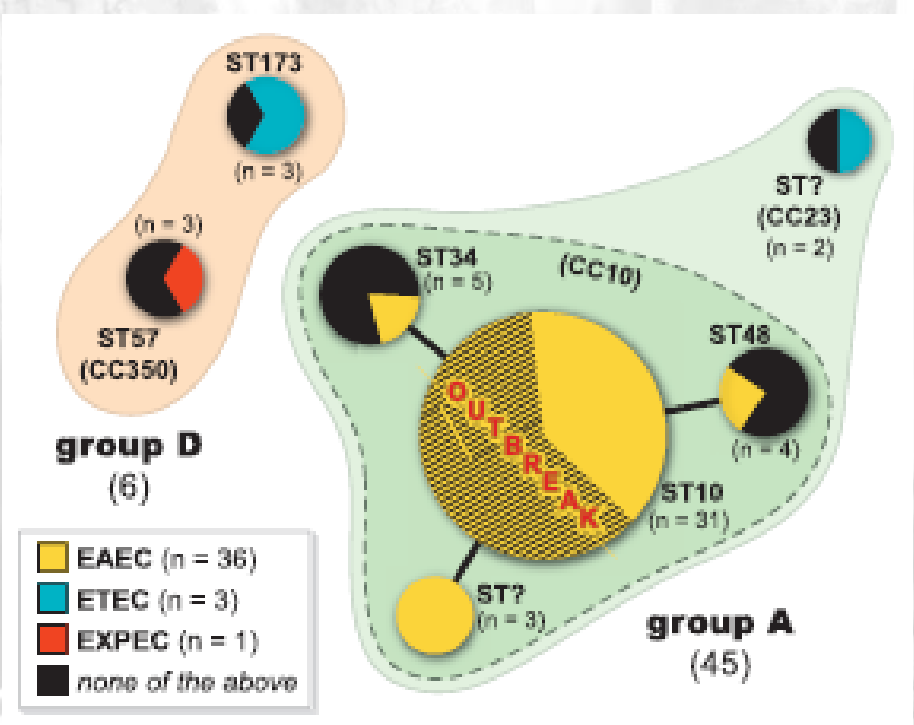

Aat dispersin translocation
Dispersin Coat
pAA
Aai
Stx
ESBL
Lumen
SigA
Pic
SepA
AAF/I
Actin cytoskeleton - Intestinal barrier disruption
Stx
II
III
Inflammation
I
Biofilm and Mucus production
IV
Cytotoxicity
Neutrophil
V
Shiga Toxin translocation

Crossovers

JCM
JournalsASM.org

Enteroaggregative *Escherichia coli* O78:H10, the Cause of an Outbreak of Urinary Tract Infection

Bente Olesen,[a,b] Flemming Scheutz,[b] Rebecca L. Andersen,[a] Megan Menard,[c] Nadia Boisen,[d] Brian Johnston,[c] Dennis S. Hansen,[a] Karen A. Krogfelt,[e] James P. Nataro,[d] and James R. Johnson[c]



Genes present in>90% of outbreak isolates included *fimH* (type 1 fimbriae); *fyuA*, *traT*, and *iutA* (associated with ExPEC);

***sat*, *pic*, *aatA*, *aggR*, *aggA*, *aar*, *aaiC*, *aap*, and *ORF3* (associated with EAEC)**

[cited 2011 Apr].
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Evidence of Evolving Extraintestinal Enteroaggregative *Escherichia coli* ST38 Clone

To the Editor: Several clones of extended-spectrum β-lactamase (ESBL)–producing extraintestinal pathogenic *Escherichia coli* (ExPEC) have globally expanded their distribution, including multilocus sequence types (MLSTs) ST38, ST131, ST405, and ST648 (*1*). ExPEC infections often originate from the patient's own intestinal flora, although the degree of overlap between diarrheagenic *E. coli* and ExPEC pathotypes is unclear. Relatively little is known about antimicrobial drug resistance in the most common diarrheagenic *E. coli* groups, including enteroaggregative *E. coli* (EAEC), and bacterial gastroenteritis is generally managed without use of antimicrobial drugs.

The ability of diarrheagenic *E. coli* to cause extraintestinal infections

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GCCTAAAGGA
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TRANSPARENT PROCESS OPEN ACCESS

EMBO Molecular Medicine

Crossovers

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Heteropathogenic virulence and phylogeny reveal phased pathogenic metamorphosis in *Escherichia coli* O2:H6

Martina Bielaszewska[1,†], Roswitha Schiller[1,2,†], Lydia Lammers[1], Andreas Bauwens[1], Angelika Fruth[3], Barbara Middendorf[1], M Alexander Schmidt[4], Phillip I Tarr[5], Ulrich Dobrindt[1,2], Helge Karch[1] & Alexander Mellmann[1,*]

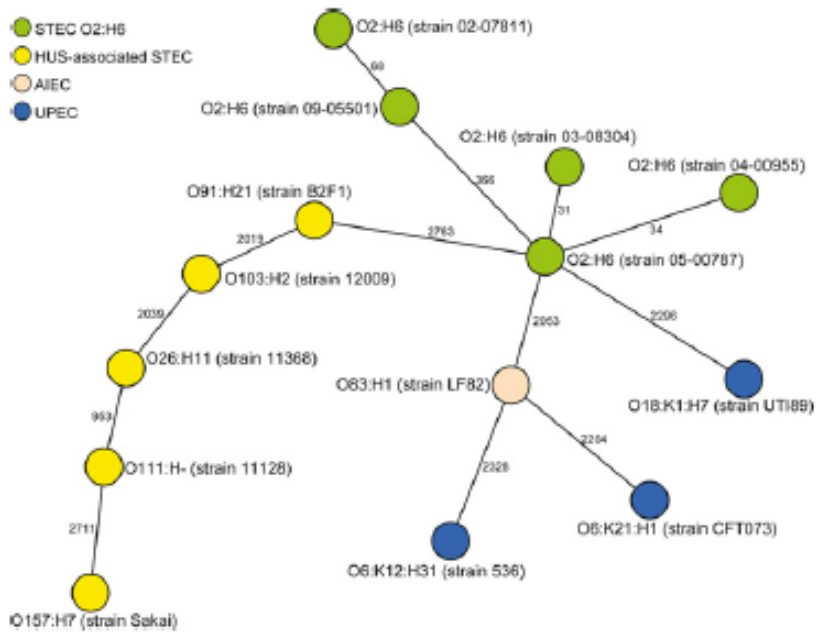
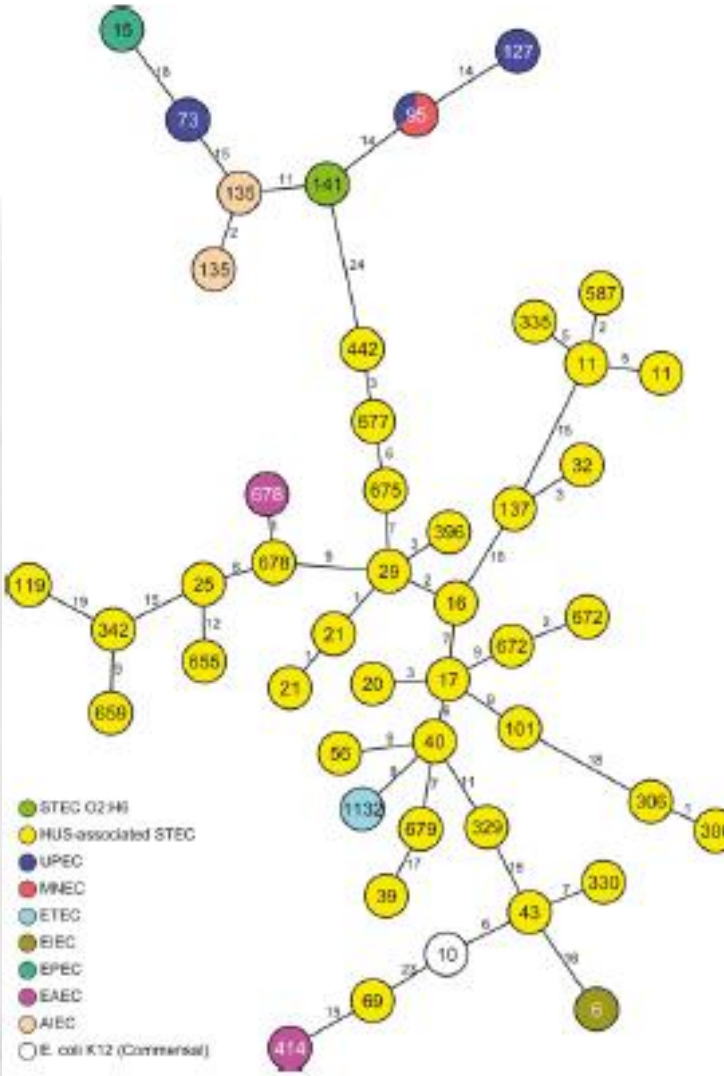


Figure 2. Phylogenetic relationships of STEC O2:H6 to prototypic UPEC, AIEC and most closely related and prototypic HUS-associated STEC based on whole genome sequencing. Minimum spanning tree is based on allelic profiles of 2827 genes present in all strains investigated (see supplementary Table S1). The different pathotypes are distinguished by colors of the circles and the serotypes and strain numbers (in parentheses) are given.



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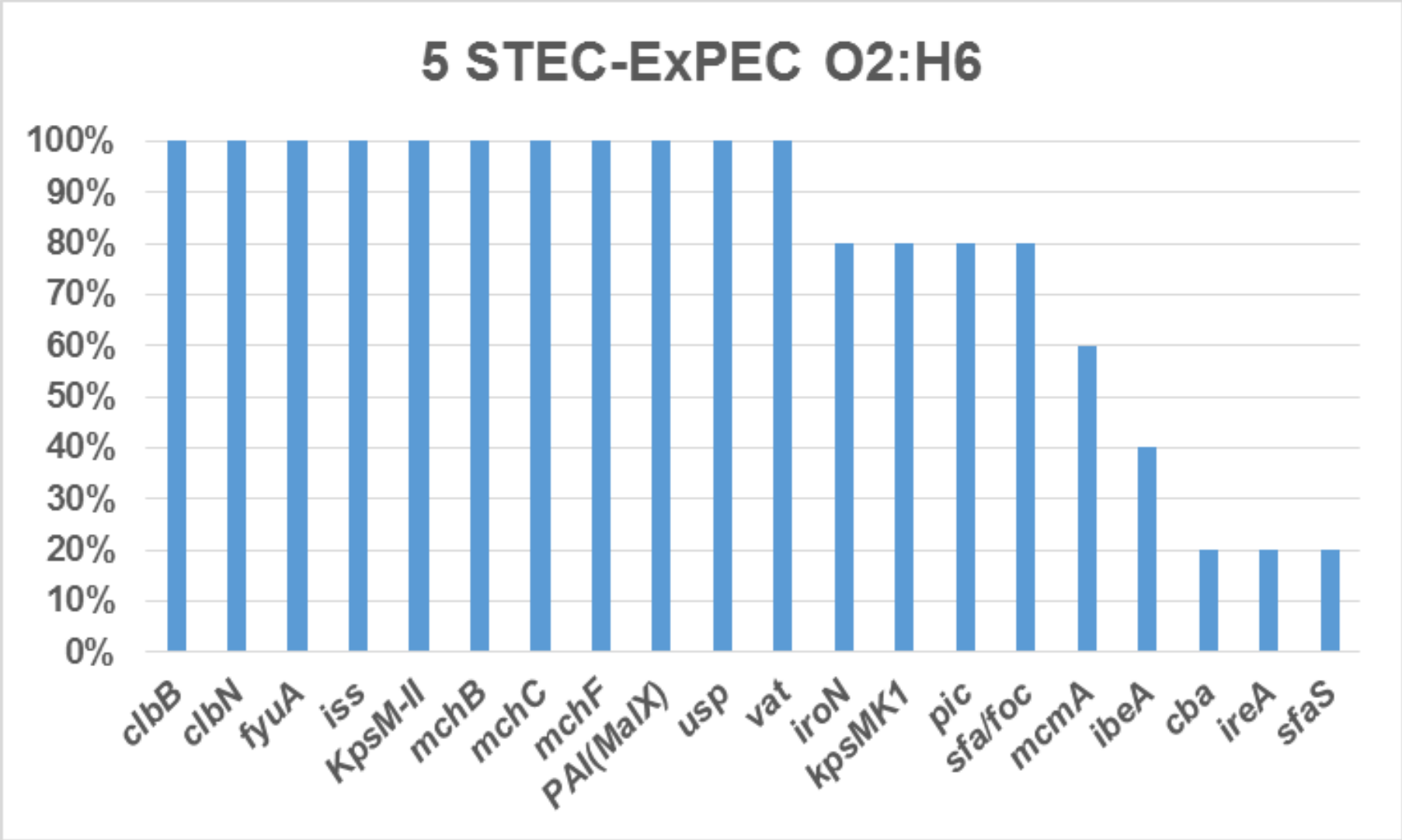
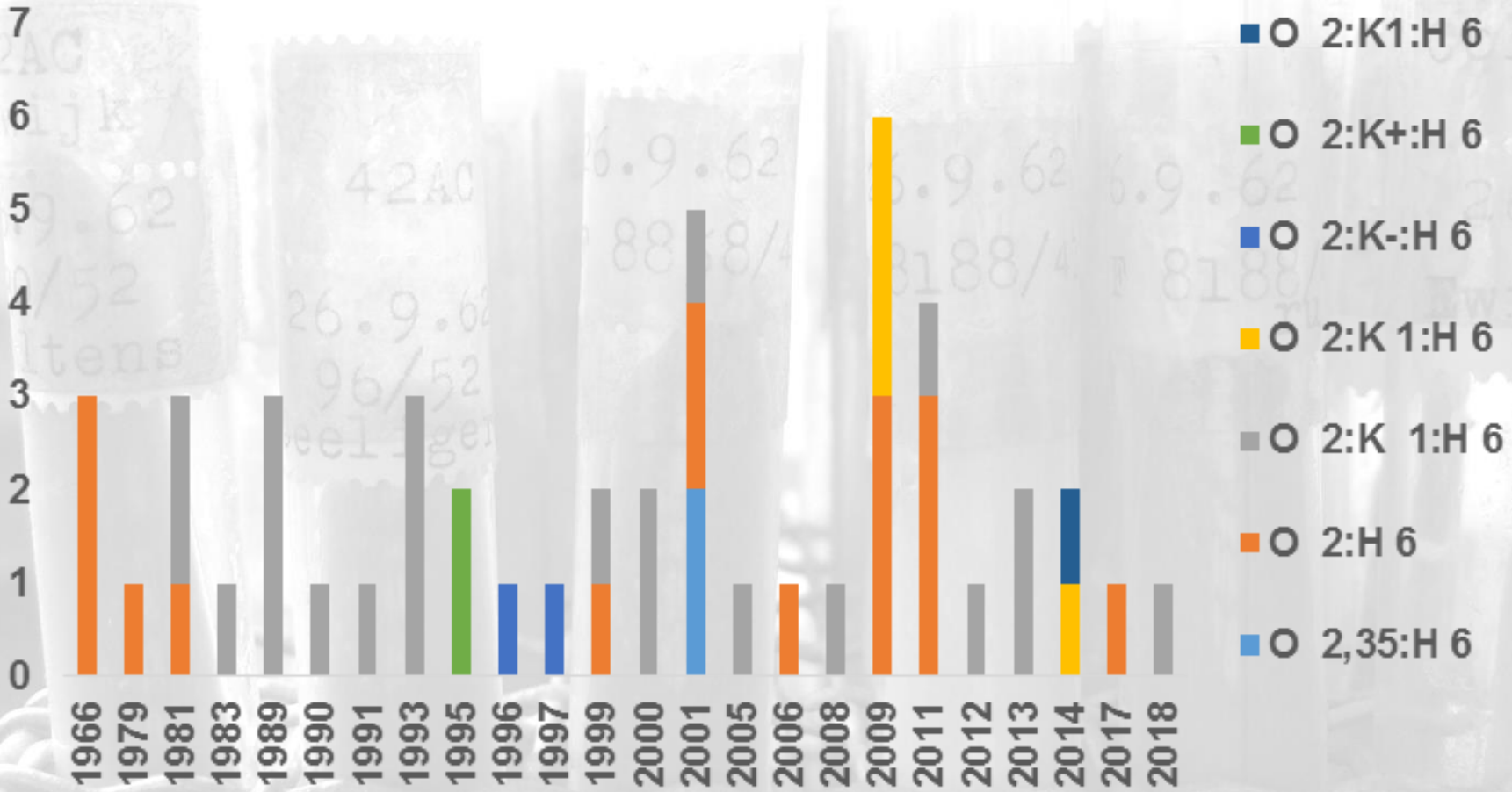


49 patienter med O2:(K1:)H6



49 patienter med O2:(K1:)H6

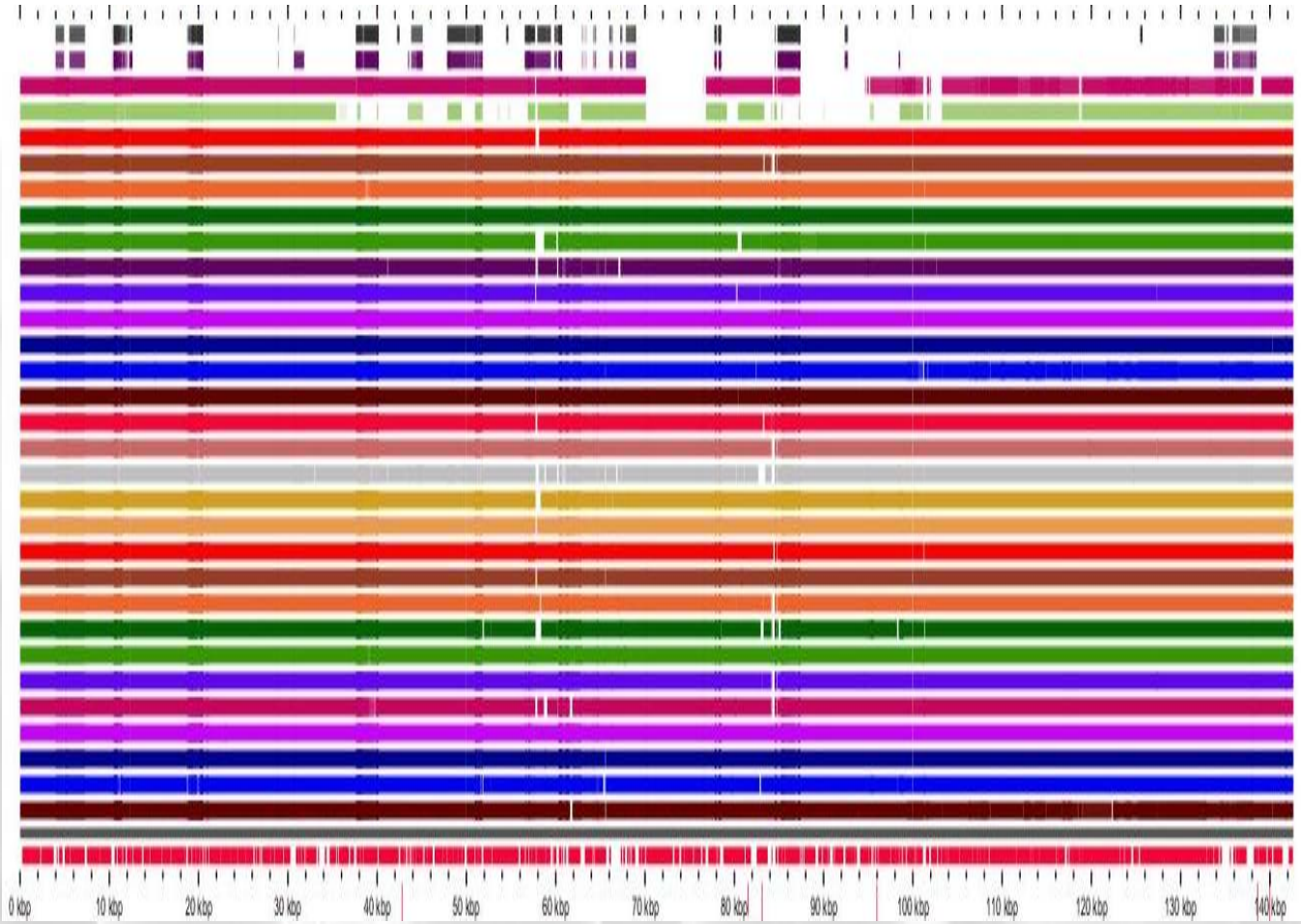
NA	15
D	13
Bacteraemia	9
UTI	3
BD	3
Meningitis	1
Bacteraemia, recurrent; second	1
PD	1
Bacteraemia, recurrent; index	1
Endocardit	1
BD; Long term carrier	1

ST131 *fimH27* clones, harbouring *aggR* and AAF/V fimbriae, causes bacteraemia in Mozambique children: emergence of new variants

- **17.5% (57/325) analyzed isolates were EAEC.**
  - **Incidence rate of 45.3 episodes/10^5 children-years-at-risk among infants**
  - **Case fatality ratio of 14.6% (6/41)**
  - **44 EAEC strains were sequenced**
- **72.7% (32/44) harboured the ExPEC genes, *iutA, fyuA* and *traT***
- **88.6% (39/44) harbored the aggregative adherence fimbriae type V variant (AAF/V)**
- **ST-131 O25:H4 accounted for 84.1% (37/44)**
- **ExPEC ST131 that picked up the EAEC virulence pAA plasmid**
  - **This pAA-ExPEC ST131 strain is highly similar to a Danish ESBL outbreak strain (DANMAP)**
- **Conclusion: emergence of a new subclone of O25:H4 ST-131 *E. coli* harboring both ExPEC and EAEC virulence genes, associated with poor outcome in bacteraemic Mozambican children.**

Mandomando et al unpublished

Virulence pAA5 Plasmid in EAEC ST131



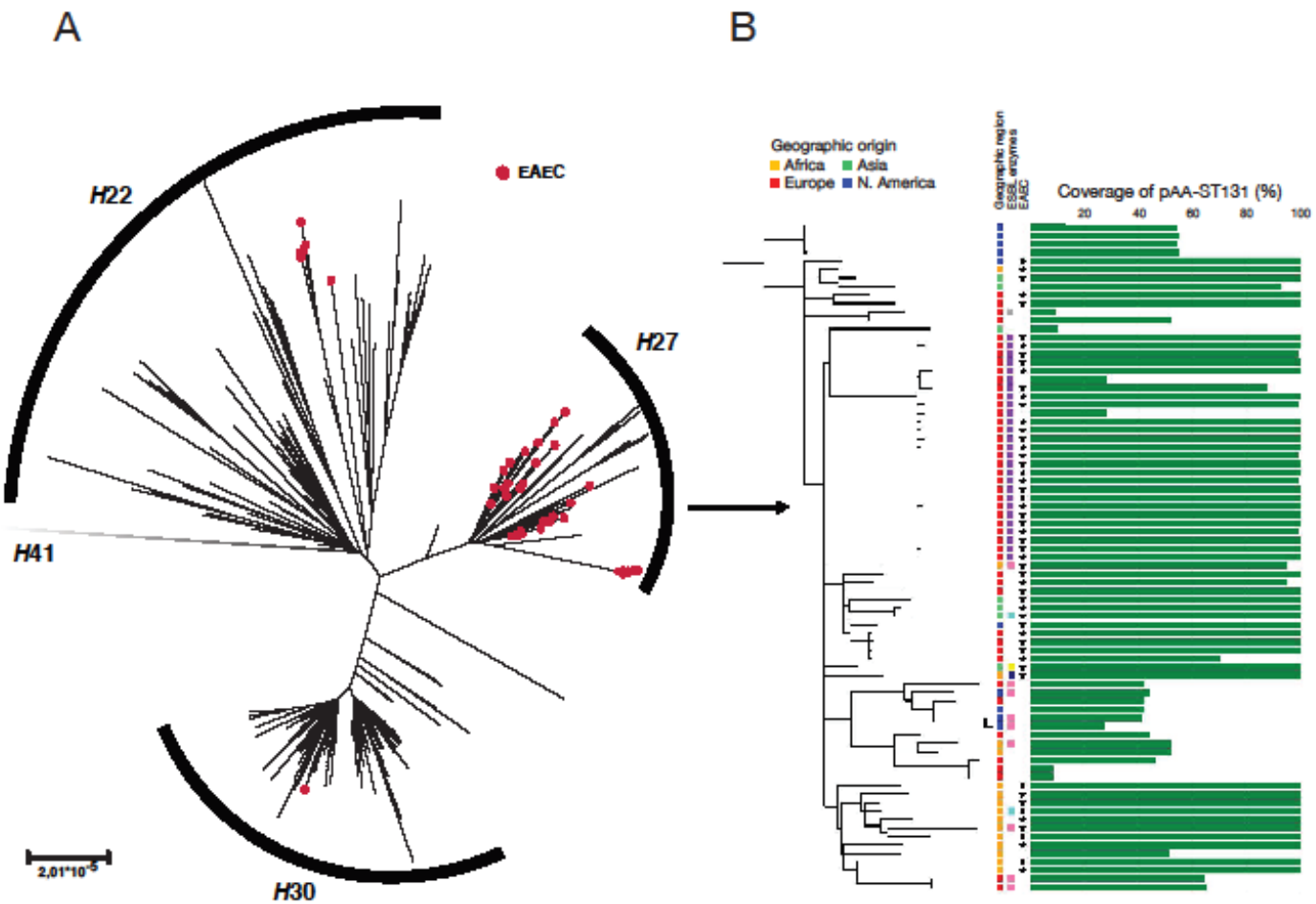
	Serotype	MLST	AAF
C194-15	O125ab:H-	ST-10	
C169-15	O125ab:H-	ST-10	
C205-15	O166:H15	ST-349	AAF/V
C188-15	O153:H30	ST-38	AAF/I
C218-15	Oru:H 4	ST-131	AAF/V
C213-15	O 25:H 4	ST-131	AAF/V
C212-15	O 25:H 4	ST-131	AAF/V
C211-15	O 25:H 4	ST-131	AAF/V
C209-15	O 86:H 4	ST-131	AAF/V
C207-15	O 25:H 4	ST-131	AAF/V
C206-15	Oru:H 4	ST-131	AAF/V
C204-15	O 86:H 4	ST-131	AAF/V
C202-15	O 25:H 4	ST-131	AAF/V
C200-15	O 69:H 4	ST-131	AAF/V
C199-15	O 25:H 4	ST-131	AAF/V
C198-15	O 25:H 4	ST-131	AAF/V
C197-15	O 25:H-	ST-131	AAF/V
C193-15	O 25:H 4	ST-131	AAF/V
C185-15	O 25:H 4	ST-131	AAF/V
C184-15	O 25:H 4	ST-131	AAF/V
C179-15	O127:H 4	ST-131	AAF/V
C178-15	O 25:H 4	ST-131	AAF/V
C177-15	O 25:H 4	ST-131	AAF/V
C171-15	O 25:H 4	ST-131	AAF/V
C170-15	O 25:H 4	ST-131	AAF/V
C168-15	O?:H 4	ST-131	AAF/V
C167-15	O 25:H 4	ST-131	AAF/V
C166-15	Oru:H 4	ST-131	AAF/V
C165-15	O 25:H 4	ST-131	AAF/V
C164-15	O 25:H 4	ST-131	AAF/V
C159-15	O 25:H 4	ST-131	AAF/V

ST131

Reference pAA

DK EAEC ESBL strain

Boisen et al unpublshed



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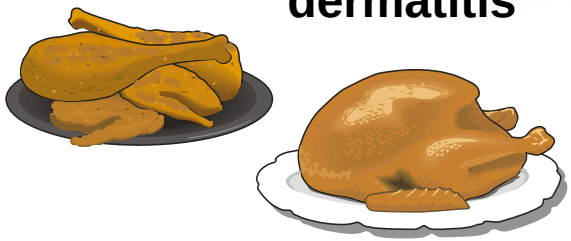
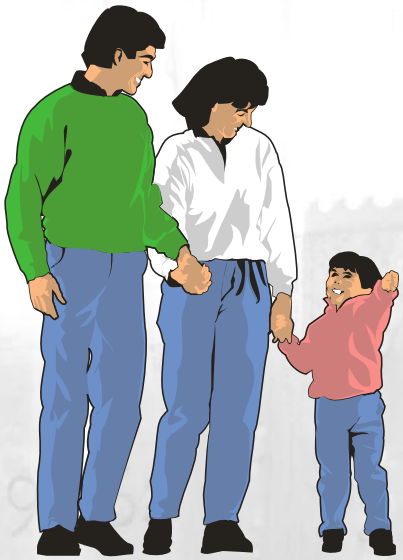
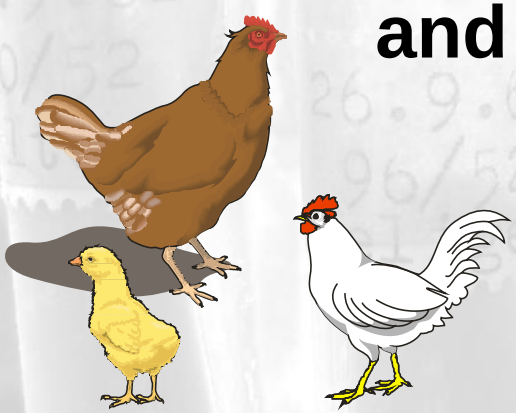
E. coli O45:K1:H7 causing an outbreak of neonatal meningitis and sepsis in Germany



dermatitis

colonisation





septicaemia

colonisation
septicaemia
meningitis

Non-publiched data by Rita Prager, Helmut Tschäpe *et al.*

Veterinary Microbiology 167 (2013) 506–512

Contents lists available at ScienceDirect

Veterinary Microbiology

journal homepage: www.elsevier.com/locate/vetmic

Poultry as reservoir for extraintestinal pathogenic *Escherichia coli* O45:K1:H7-B2-ST95 in humans

Azucena Mora [a,*], Susana Viso [a], Cecilia López [a], María Pilar Alonso [b], Fernando García-Garrote [b], Ghizlane Dabhi [a], Rosalía Mamani [a], Alexandra Herrera [a], Juan Marzoa [a], Miguel Blanco [a], Jesús E. Blanco [a], Maryvonne Moulin-Schouleur [c,d], Catherine Schouler [c,d], Jorge Blanco [a]

[a] Department of Microbiology and Parasitology, Faculty of Veterinary Sciences, University of Santiago de Compostela, 27002 Lugo, Spain
[b] Unit of Microbiology, Hospital Universitario Lucus Augusti, 27003 Lugo, Spain
[c] Laboratoire de Pathogénie Bactérienne, INRA, UMR 1282 Infectiologie et Santé Publique, F-37380 Nouzilly, France

…The most prevalent and highly pathogenic O45:K1:H7-B2-ST95 shows a successful persistence since the 90s to the present, with parallel evolution both in human and poultry …

… In conclusion, poultry could be acting as a reservoir of O45:K1:H7-B2-ST95 and other pathogenic ST95 serotypes in humans

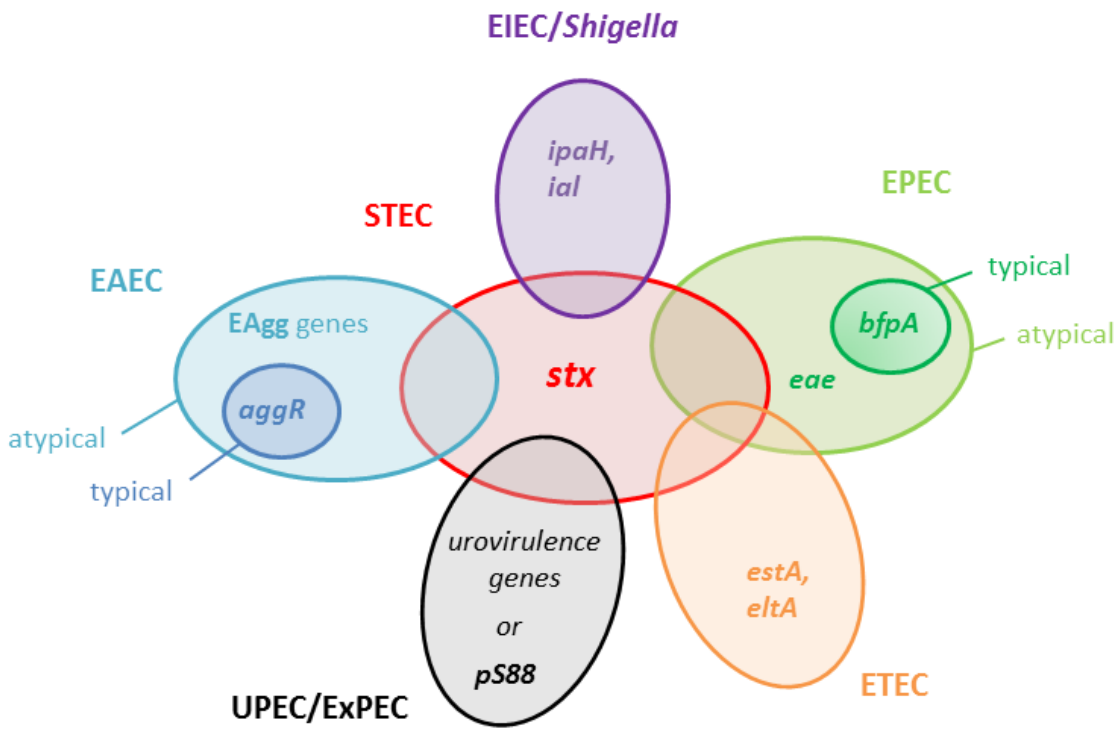
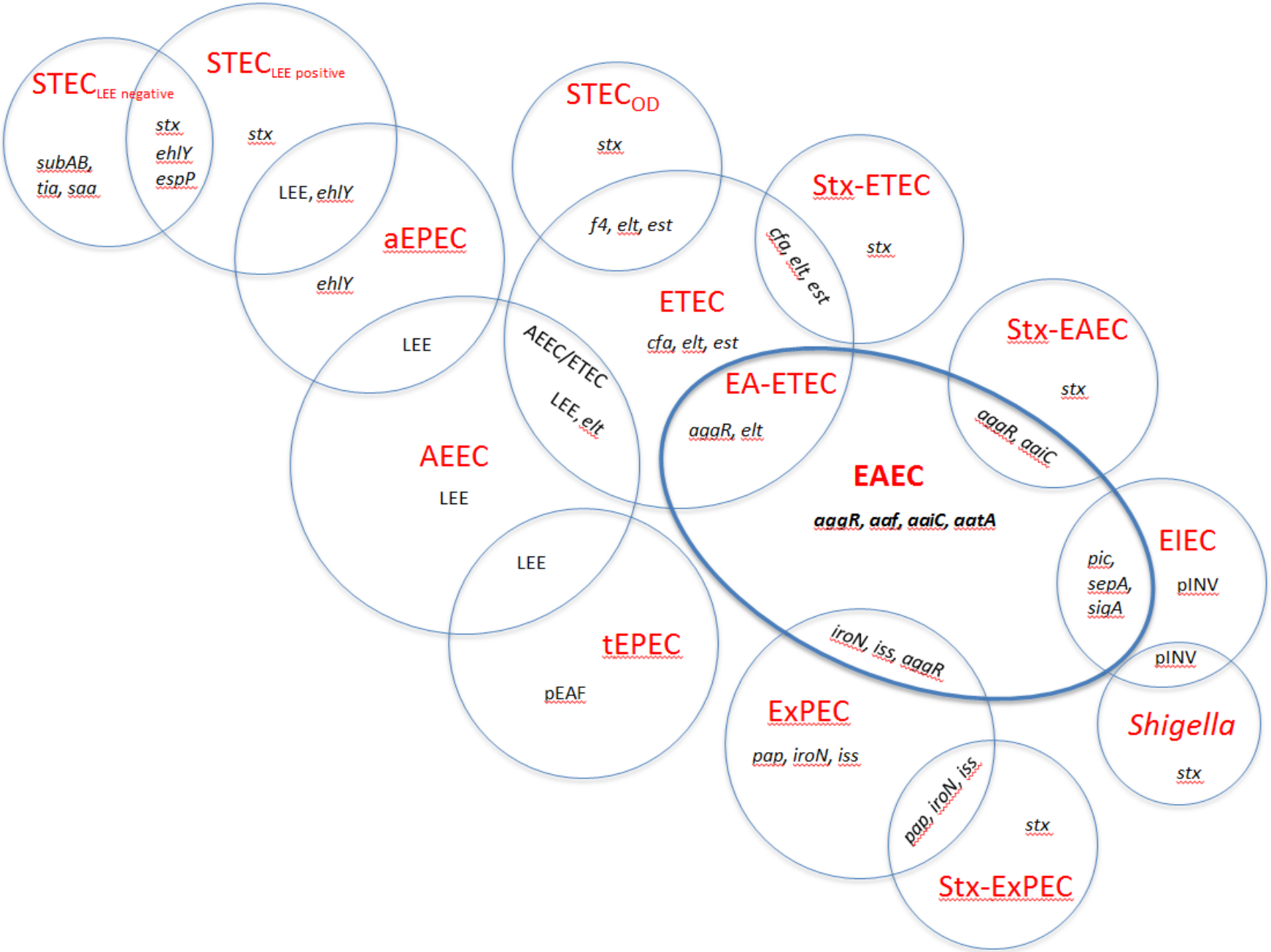


Figure 3: Schematic representation of hybrid *Escherichia coli* pathotypes

STEC: Shiga toxin-producing *E. coli*, *stx*: Shiga toxin encoding gene; EIEC: enteroinvasive *E. coli*, *ial* and *ipaH*: virulence genes necessary for invasion of the intestinal epithelial cells; EPEC: enteropathogenic *E. coli*, *eae*: intimin encoding gene, *bfpA*: bundle-forming pili encoding gene; ETEC: enterotoxinogenic *E. coli*, *estA*: heat-stable enterotoxin encoding gene, *eltA*: heat-labile enterotoxin encoding gene; UPEC: uropathogenic *E. coli*, ExPEC: extraintestinal pathogenic *E. coli*, pS88: ExPEC-like virulence plasmid; EAEC: enteroaggregative *E. coli*, EAgg: enteroaggregative, *aggR*: transcriptional activator encoding gene.


STEC LEE negative
subAB, tia, saa
STEC LEE positive
stx
ehlY
espP
stx
LEE, ehlY
aEPEC
ehlY
LEE
AEEC
LEE
STEC OD
stx
f4, elt, est
ETEC
cfa, elt, est
AEEC/ETEC
LEE, elt
Stx-ETEC
stx
cfa, elt, est
EA-ETEC
aagR, elt
EAEC
aagR, aaf, aaiC, aatA
Stx-EAEC
stx
aagR, aaiC
EIEC
pINV
pic, sepA, sigA
pINV
Shigella
stx
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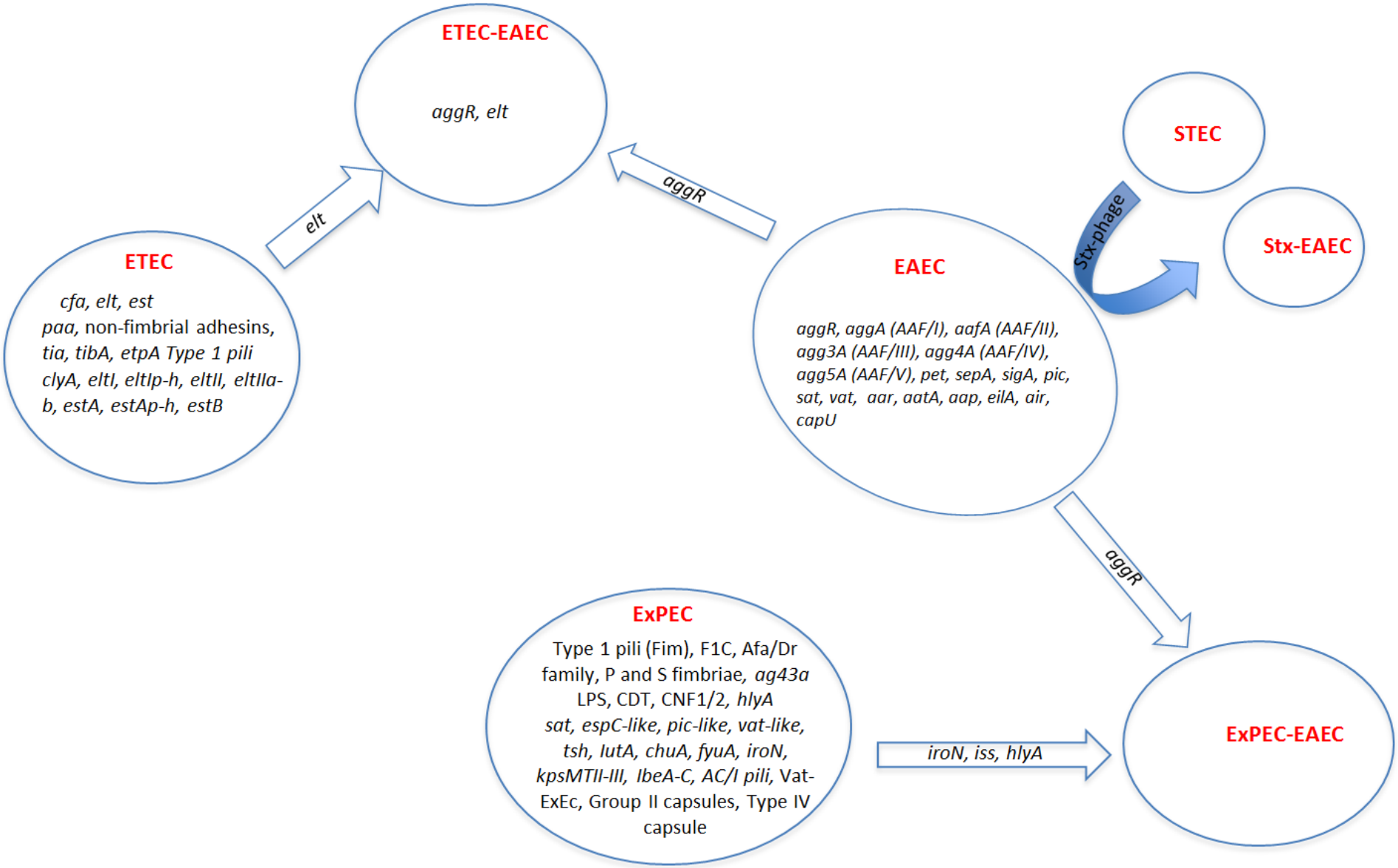
stx
Stx-ExPEC



The white arrows indicate the transfer of genetic determinants between EAEC and other pathogenic *E. coli*. The solid arrow indicates the acquisition of a Stx-converting bacteriophage. The *E. coli* pathotype represented by each bubble is indicated in red, while the genes identifying the single pathogenic groups or exchanged between groups of *E. coli* are shown in black

Gene alleles (159) for ETEC

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Camilla Hald Nielsen
Offline
Ulønnet studerende, Mikrobiologi & Infektionskontrol
Tilføj

cfaA: Colonisation factor antigen a, CFA/1:
cfaB: Colonisation factor antigen b, CFA/1:
cfaC: Colonisation factor antigen c, CFA/1:
cfaE: Colonisation factor antigen e, CFA/1:
cfaD: Colonisation factor antigen d, CFA/1:
cooB: CS1:
cooD: Fimbrial subunit B, CS1:
cooC: Fimbrial subunit B, CS1:
csoB: CS1:
csoA: CS1:
cotB: CS2:
cotA: CS2:
cotC: CS2:
cotD: CS2:
CS3_put_chaperone:
CS3_lpfC: putative outer membrane usher protein
CS3_put_major_subunit:
csaA: Periplasmic chaperone-like protein, CS4:
csaB: CS4 major fimbriae subunit, CS4:
csaC: Usher protein, CS4:
csaE: Minor pilin protein, CS4:
csaD: Truncated, CS4:
csfC: Outer membrane usher protein, CS5:
csfD: Minor fimbrial subunit, CS5:
csfE: CS5:
csfF: CS5:

tia: Invasion determinant:
tibC: Glycosyltransferase
tibA:
estap: Heat-stable enterotoxin STa porcine variant:
estb: Heat-stable enterotoxin STb
estah: Heat-stable enterotoxin STa Human variant:
eltIAh_1: Heat-labile enterotoxin A subunit, LT1: A1
eltIAh_2: Heat-labile enterotoxin A subunit, LT2: A2
eltIAh_3: Heat-labile enterotoxin A subunit, LT3: A3
eltIAh_4: Heat-labile enterotoxin A subunit, LT4 and LT6: A4
eltIAh_5: Heat-labile enterotoxin A subunit, LT5: A5
eltIAh_7: Heat-labile enterotoxin A subunit, LT7: A7
eltIAh_8: Heat-labile enterotoxin A subunit, LT8: A8
eltIAh_9: Heat-labile enterotoxin A subunit, LT9: A9
eltIAh_10: Heat-labile enterotoxin A subunit, LT10: A10
eltIAh_11: Heat-labile enterotoxin A subunit, LT11: A11
eltIAh_12: Heat-labile enterotoxin A subunit, LT12: A12
eltIAh_13: Heat-labile enterotoxin A subunit, LT13: A13
eltIAh_14: Heat-labile enterotoxin A subunit, LT14: A14
eltIAh_15: Heat-labile enterotoxin A subunit, LT15: A15
eltIAh_16: Heat-labile enterotoxin A subunit, LT16: A16
eltIBh_1: Heat-labile enterotoxin B subunit, LT1: B1
eltIBh_2: Heat-labile enterotoxin B subunit, LT2: B2
eltIBh_3: Heat-labile enterotoxin B subunit, LT3: B3
eltIBh_4: Heat-labile enterotoxin B subunit, LT4: B4
eltIBh_5: Heat-labile enterotoxin B subunit, LT5: B5

Gene content of the ExPEC database downloaded from NCBI and added to the VirulenceFinder database.

38 ExPEC specific genes

Gene	Description	No. from NCBI	No. in db
afaA	Transcriptional regulator	14	4
afaB	Periplasmic chaperone	12	6
afaC	Outer membrane usher protein	13	11
afaD	Afimbrial adhesin	62	37
afaE	Adhesin protein	42	30
cea	colicin E1	132	23
chuA	Outer membrane hemin receptor	423	79
cia	colicin ia	259	37
cib	colicin ib	24	6
clbB	Hybrid nonribosomal peptide / polyketide megasynthase	270	77
cvaC	microcin C	166	10
etsC	Putative type I secretion outer membrane protein	169	18
focC	S fimbrial/F1C minor subunit	710	2*
focG	F1C adhesin	9	2
focI	S fimbrial/F1C minor subunit	5	1
fyuA	Siderophore receptor	465	98
hlyF	Hemolysin F	287	21
hra	Heat-resistant agglutinin	1	1
ibeA	Invasin of brain endothelial cells;	369	66
irp2	High molecular weight protein 2 non ribosomal peptide synthetase	1033	346
iucC	Aerobactin synthetase	335	47
iutA	Ferric aerobactin receptor	350	71
kpsE	Capsule polysaccharide export inner-membrane protein	54	21
kpsM	Polysialic acid transport protein	94	82
mcbA	Bacteriocin microcin B17	949	2
neuC	Polysialic acid capsule biosynthesis protein	961	68
ompT	Outer membrane protease (protein protease 7)	3564	314
papA	Major pilin subunit	116	29
papC	Outer membrane usher P fimbriae	786	40
sfaD	S fimbrial/F1C minor subunit	18	10
sfaE	S fimbrial/F1C minor subunit	3	3*
sfaS	sialic acid-binding adhesin	54	2
sitA	Iron transport protein	369	56
tcpC	Tir domain-containing protein	24	3
terC	Tellurium ion resistance protein	126	25
traT	Outer membrane protein complement resistance	1386	200
usp	Uropathogenic specific protein	19	6
yfcV	Fimbrial protein	768	82
Total		14441	1929

*Two sfaE and focC alleles were 100% identical, and are called focCsfaE in the database

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"WE FINISHED THE GENOME MAP, NOW WE CAN'T FIGURE OUT HOW TO FOLD IT!"