

Supplemental Table S3. Characteristics of *aggR*-positive EAEC strains/clusters and the number of strains possessing the virulence genes and the *bla*_{CTX-M} gene.

cluster/strain	ST or CG	No. of strains			EAEC virulence													UPEC virulence					ESBL CTX-M (subtype)	serotype (% No./Total)	biofilm index	
					plasmid										chromosome			<i>sfa</i>	<i>pap</i>	<i>afa</i>	<i>aer</i>	<i>cnf1</i>				
					<i>aggR</i>	<i>aatA</i>	<i>aap</i>	AAF1	AAF2	AAF3	AAF4	AAF5	<i>pet</i>	<i>astA</i>	<i>sepA</i>	<i>sat</i>	<i>pic</i>									<i>aaiC</i>
C1 K7484 K7668 K7701 K7164 K7225	CG200	2	2		2	2	2	0	2	0	0	0	2	2	0	0	2	2	0	0	0	0	0	0	O126:H27 (45%,13/29) O126:HND (24%, 7/29)	0.89 ± 0.80
C2		2	2		2	2	2	0	2	0	0	0	2	0	0	0	2	2	0	0	0	0	0	0		
C3		19	18	1	19	14	16	0	17	0	0	0	14	18	0	0	16	18	0	0	1	0	0	0		
K2626		1	1		1	1	1	0	1	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0		
C4		3	3		3	3	3	0	0	0	0	2	0	1	1	1	2	3	0	0	0	0	0	0		
C5		41	29	12	41	41	39	0	0	0	0	39	3	15	18	28	33	40	0	0	0	18	0	0		
K761	1	1		1	1	1	0	0	0	0	1	0	1	1	0	1	1	0	0	0	1	0	0			
K3536	1	1		1	1	1	0	0	0	0	1	0	0	1	0	1	1	0	0	0	0	0	0			
K3538	1	1		1	1	1	0	0	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0			
K8028	1	1		1	1	1	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0			
K665	1	1		1	1	1	0	0	0	0	1	0	1	1	0	1	1	0	0	0	0	0	0			
K692	1	1		1	1	1	0	0	0	0	1	0	1	0	1	1	1	0	0	0	0	0	0			
K2518	CG295	1	1		1	0	1	0	0	0	1	0	0	1	1	0	1	1	0	0	0	0	0	0	O126:HND	0.55 ± 0.13
C6		2		2	2	2	2	0	0	0	1	1	0	0	1	2	2	2	0	0	0	1	0	0	O126:H12	
K4586	CG3570	1	1		1	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	0	1	0	0	O86a:H27 (61%, 11/18)	0.57 ± 0.25
C7		16	8	8	16	14	15	0	0	0	14	1	0	3	16	10	16	16	1	0	0	13	0	0	O86a:HND (22%, 4/18)	
K9517		1	1		1	1	1	0	0	0	1	0	0	0	1	1	1	1	0	0	0	1	0	0		
K4513	ST162 clx*	1	1		1	0	1	0	0	0	0	1	0	1	0	0	0	0	1	1	0	0	0	0	OUT:H19	0
K8077	ST3750 clx	1	1		1	1	1	1	0	0	0	0	0	1	0	1	1	1	0	0	0	1	0	0	O164:H10	0.84
K5200	ST540 clx	1	1		1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	OUT:H30	0
C8	ST10	3		3	3	3	3	0	0	0	0	2	0	0	0	0	2	2	0	0	0	3	0	1(55)	O86a:H2	0.45 ± 0.26
C9 C10 K2361	CG34	2	2		2	1	2	0	0	0	0	0	0	1	1	2	2	0	0	0	0	0	0	OUT:H33 (90%, 9/10)	1.31 ± 0.52	
		7	7		7	7	7	0	0	0	0	1	1	1	5	2	7	5	0	0	0	4	0			0
		1	1		1	1	1	0	0	0	0	1	0	0	1	0	1	1	0	0	0	0	0			0
K7672	CG131	1	1		1	1	1	0	0	0	0	1	0	0	0	1	0	0	0	0	1	1	0	1(14)	O25:H4 (83%, 29/35) O25:H10 (6%, 2/35)	0.31 ± 0.22
C11		30	30		30	30	22	0	0	0	0	30	2	2	4	21	0	0	0	0	29	28	0	23(14)		
K7459		1	1		1	1	1	0	0	0	0	1	0	0	0	1	0	0	0	0	1	1	0	1(14)		
C12		2	2		2	1	1	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	2(14)		
K4966		1	1		1	1	1	0	0	0	0	1	0	1	0	1	0	0	1	1	1	1	0	0		
K2605	ST538 clx	1	1		1	0	1	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	OUT:H4	0.53
K5922	ST1873	1	1		1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	OUT:H4	0
K3606	ST127	1	1		1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	1(14)	O6:H31	NT
K7495	ST643 clx	1	1		1	1	1	0	1	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	O114:H7	0
K7691	CG95	1	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	O91:HND	0.22
K4840		1	1		1	1	1	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	O111:H7	0.18
K5185		1	1		1	1	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	O111:H7	0.02
C13	ST501	2	1	1	2	2	2	0	0	0	0	0	1	0	0	1	2	0	2	0	2	0	1(14)	O86a:H4, O86a:H1	0.23 ± 0.03	
K6863	ST714	1	1		1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	1(14)	O20:H11	0.21
K9542	ST3032	1		1	1	1	1	1	0	0	0	0	0	0	0	0	1	1	0	1	1	1	0	0	O126:H31	1.23
C14	CG38	2	1	1	2	1	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1(15)	O86a:H30, OUT:HND	0.19 ± 0.03
K6756		1	1		1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	O86a:H18	0
K4619	ST31 clx	1	1		1	1	1	1	0	0	0	0	0	1	1	0	1	1	0	0	1	0	0	0	OUT:H18	0.04
K5105	ST69 clx	1	1		1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	OUT:H18	0

A clonal group (CG) was defined as a group of closely related sequence type and named in accordance with the dominant ST. A cluster was defined as a group of strains showing the same MLS. Major clonal groups are in bold black column. Dark gray and light gray boxes represent ≥50% and <50% positivity, respectively. The CTX-M subtype is shown in parenthesis in the ESBL column. Incidences of serotype in each group are shown in parentheses in the serotype column. The biofilm index of each group is shown as the average ± standard deviation. Abbreviations: T, total; K, Kagoshima; O, Osaka; EAEC, enteroaggregative *Escherichia coli*; UPEC, uropathogenic *E. coli*; ESBL, extended-spectrum β-lactamase: clx, complex.