

Table S1. Phenotypic differences displayed by Biolog GEN III plates of *E. coli* strains used in the present study. Only differences between the strains are shown.

Compound/Condition ^a	<i>E. coli</i> Strains				
	ATCC 25922	O157H7	O104:H4 (Ec 01) (2011C-3493) ^b	O104:H4 (Ec 02) (2009EL-2050) ^b	O104:H4 (Ec 03) (2009EL-2071) ^b
Sucrose	—	+	+	+	+
D-Raffinose	—	+	+	+	+
8% NaCl	+	—	+	+	+
D-Sorbitol	+	—	+	+	+
D-Aspartic Acid	—	—	+	+	+
D-Serine	+	—	—	—	—
Gelatin	—	—	—	—	±
L-Arginine	—	—	—	—	±
D-Saccharic	+	—	—	—	—
Naladixic Acid	—	—	+	+	+
K Tellurite	—	+	+	+	+
β-Hydroxy-DL-Butyric	+	—	—	—	—
Propionic Acid	—	+	+	+	+
Na Bromate	—	±	+	—	—

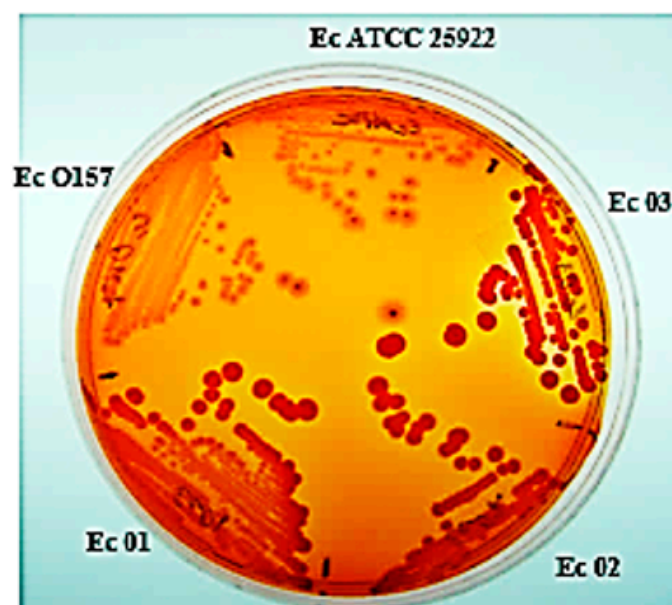
^a Symbols represent: +, positive; ±, weak; —, negative.

^b CDC designation for *E. coli* O104:H4 strains. Ec 01, Ec 02, and Ec 03 are designations of the respective Ec strains in this study.

Table S2. Comparison of antibiotic susceptibilities between *E. coli* O104:H4 strains and *E. coli* O157:H7.

Antibiotic	Ec O157:H7	Ec 01 (2011C-3493)	Ec 02 (2009EL-2050)	Ec 03 (2009EL-2071)
Minimum inhibitory concentration (MIC), µg/ml				
Trimethoprim	0.060	64.000	64.000	64.000
Co-Trimoxazole	0.500	64.000	64.000	64.000
Sulfamethoxazole	64.000	64.000	64.000	64.000
Azithromycin	4.000	1.000	0.125	0.125
Doxycycline	0.500	8.000	8.000	0.250
Tigecycline	0.060	0.060	0.060	0.060
Cefepime	0.030	64.000	0.030	0.250
Faropenem	0.125	0.125	0.125	0.030
Ertapenem	0.030	0.030	0.030	0.030
Piperacillin	1.000	64.000	64.000	32.000
Penicillin G	64.000	32.000	64.000	64.000
Amoxicillin	2.000	64.000	64.000	64.000
Ceftazidime	0.250	32.000	0.030	0.125
Imipenem	0.125	0.125	0.125	0.125
Cefazolin	2.000	64.000	2.000	4.000
Ampicillin	0.125	32.000	32.000	32.000
Aztreonam	0.250	32.000	0.125	0.250
Chloramphenicol	2.000	0.500	2.000	2.000
Arbekacin	8.000	2.000	1.000	4.000
Amikacin	2.000	0.250	0.500	1.000
Gentamicin	1.000	0.125	0.250	0.250
Netilmicin	1.000	0.250	0.060	0.125
Streptomycin	8.000	64.000	64.000	64.000
Ofloxacin	0.030	0.125	0.125	0.250
Sparfloxacin	0.030	0.030	0.030	0.030
Moxifloxacin	0.060	0.125	0.030	0.125
Gemifloxacin	0.060	0.030	0.030	0.030
Ciprofloxacin	0.015	0.030	0.125	0.125
Novobiocin	32.000	4.000	32.000	32.000

A. Binding of Congo Red by *E. coli* strains.



B. Pellets of *E. coli* strains.

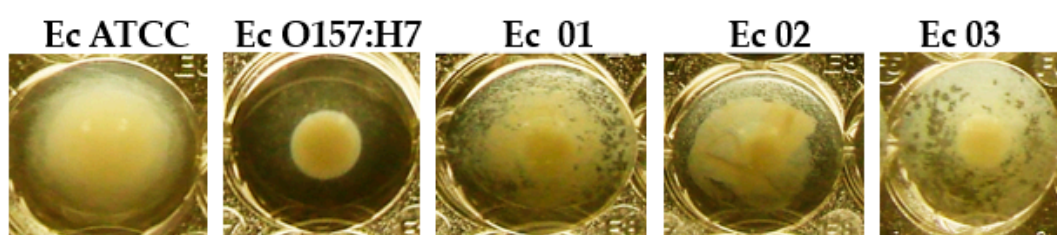


Figure S1. Characteristics of *E. coli* strains used in the present study.

AggA Major pilin

	10	20	30	40	50
Ec01	MKTLKNMRRK	NLYITLGLVS	LLSGGANAAS	QOTTQTIRLT	VTNDCPVTIT
Ec02	MKTLKNMRRK	NLYITLGLVS	LLSGGANAAS	QOTTQTIRLT	VTNDCPVTIT
Ec03	MKTLKNMRRK	NLYITLGLVS	LLSGGANAAS	QOTTQTIRLT	VTNDCPVTIT
	60	70	80	90	100
Ec01	TTPPQTVGVS	STTPIGFSAK	VTTSDQCIKA	GAKVWLWGTG	PANKWVLQHA
Ec02	TTPPQTVGVS	STTPIGFSAK	VTTSDQCIKA	GAKVWLWGTG	PANKWVLQHA
Ec03	TTPPQTVGVS	STTPIGFSAK	VTTSDQCIKA	GAKVWLWGTG	PANKWVLQHA
	110	120	130	140	150
Ec01	KVAKQKYTLN	PSIDGGADFV	NQGTDAKIYK	KLTSGNKFLN	ASVSVNPKTQ
Ec02	KVAKQKYTLN	PSIDGGADFV	NQGTDAKIYK	KLTSGNKFLN	ASVSVNPKTQ
Ec03	KVAKQKYTLN	PSIDGGADFV	NQGTDAKIYK	KLTSGNKFLN	ASVSVNPKTQ
	160	167			
Ec01	VLIPGEYTM	LHAAVDF			
Ec02	VLIPGEYTM	LHAAVDF			
Ec03	VLIPGEYTM	LHAAVDF			

AggB Minor pilin

	10	20	30	40	50
Ec01	MLKKSILPMS	CGVLVMVMSG	LLDAAEITLI	SHKTLESQLR	DGMKLATGRI
Ec02	MLKKSILPMS	CGVLVMVMSG	LLDAAEITLI	SHKTLESQLR	DGMKLATGRI
Ec03	MLKKSILPMS	CGVLVMVMSG	LLDAAEITLI	SHKTLESQLR	DGMKLATGRI
	60	70	80	90	100
Ec01	ACREPHNGFY	IWINASQNGK	VGHYIVQNNR	ETKHELKVKI	GGGGWSSSLR
Ec02	ACREPHNGFY	IWINASQNGK	VGHYIVQNNR	ETKHELKVKI	GGGGWSSSLR
Ec03	ACREPHNGFY	IWINASQNGK	VGHYIVQNNR	ETKHELKVKI	GGGGWSSSLR
	110	120	130	140	145
Ec01	EGQRGVYRQG	EEKQAIFDIM	SDGNQYSAPG	EYIFSVSGEC	ITSRG
Ec02	EGQRGVYRQG	EEKQAIFDIM	SDGNQYSAPG	EYIFSVSGEC	ITSRG
Ec03	EGQRGVYRQG	EEKQAIFDIM	SDGNQYSAPG	EYIFSVSGEC	ITSRG

AggC Usher protein

	10	20	30	40	50
Ec01	MKTSSFIIVI	LLCFRIENVI	AHTFSFDASL	LNHGSGGIDL	TLLEKGGQLP
Ec02	MKTSSFIIVI	LLCFRIENVI	AHTFSFDASL	LNHGSGGIDL	TLLEKGGQLP
Ec03	MKTSSFIIVI	LLCFRIENVI	AHTFSFDASL	LNHGSGGIDL	TLLEKGGQLP
	60	70	80	90	100
Ec01	GIYPVDIILN	GSRIDSRDIF	FYTKKNRHGE	YYLKPCLTRD	ILINYGVKIE
Ec02	GIYPVDIILN	GSRIDSRDIF	FYTKKNRHGE	YYLKPCLTRD	ILINYGVKIE
Ec03	GIYPVDIILN	GSRIDSRDIF	FYTKKNRHGE	YYLKPCLTRD	ILINYGVKIE
	110	120	130	140	150
Ec01	EYPNLFRQNS	EKNRDSSDCA	DLSVIPQATE	DYHFIKQQLI	LGIPQVAIHP
Ec02	EYPNLFRQNS	EKNRDSSDCA	DLSVIPQATE	DYHFIKQQLI	LGIPQVAIHP
Ec03	EYPNLFRQNS	EKNRDSSDCA	DLSVIPQATE	DYHFIKQQLI	LGIPQVAIHP
	160	170	180	190	200
Ec01	PLTGIAHETM	WDDGISAFLL	NWQVEGGHWE	YRSNTRNSSD	NFWASLEPGI
Ec02	PLTGIAHETM	WDDGISAFLL	NWQVEGGHWE	YRSNTRNSSD	NFWASLEPGI
Ec03	PLTGIAHETM	WDDGISAFLL	NWQVEGGHWE	YRSNTRNSSD	NFWASLEPGI
	210	220	230	240	250
Ec01	NLGSWRIRNL	TTWNKSSGQS	GKWESSYIRV	ERGLNNIKSR	LTFGDDYTPS
Ec02	NLGSWRIRNL	TTWNKSSGQS	GKWESSYIRV	ERGLNNIKSR	LTFGDDYTPS
Ec03	NLGSWRIRNL	TTWNKSSGQS	GKWESSYIRV	ERGLNNIKSR	LTFGDDYTPS
	260	270	280	290	300
Ec01	DIFDSVPFRG	GMLGSDENMV	PYNQREFAPV	VRGIARTQAR	IEVRQNGYLI
Ec02	DIFDSVPFRG	GMLGSDENMV	PYNQREFAPV	VRGIARTQAR	IEVRQNGYLI
Ec03	DIFDSVPFRG	GMLGSDENMV	PYNQREFAPV	VRGIARTQAR	IEVRQNGYLI
	310	320	330	340	350
Ec01	QSRIVSPGAF	ALTDLPVTGN	GGDLQVWVLE	SDGTIQTFNV	PFTTPAIALR
Ec02	QSRIVSPGAF	ALTDLPVTGN	GGDLQVWVLE	SDGTIQTFNV	PFTTPAIALR
Ec03	QSRIVSPGAF	ALTDLPVTGN	GGDLQVWVLE	SDGTIQTFNV	PFTTPAIALR
	360	370	380	390	400
Ec01	EGYLKYNVTV	GEYRPSDDSI	EGAYLGQLTA	MYGLPWSLTA	FGGIQVSEHY
Ec02	EGYLKYNVTV	GEYRPSDDSI	EGAYLGQLTA	MYGLPWSLTA	FGGIQVSEHY
Ec03	EGYLKYNVTV	GEYRPSDDSI	EGAYLGQLTA	MYGLPWSLTA	FGGIQVSEHY
	410	420	430	440	450
Ec01	QGNAALGLGLS	LGGFGSISLD	TIYSRGQQKG	YSNEIGKTWR	VRYDKSFELT
Ec02	QGNAALGLGLS	LGGFGSISLD	TIYSRGQQKG	YSNEIGKTWR	VRYDKSFELT
Ec03	QGNAALGLGLS	LGGFGSISLD	TIYSRGQQKG	YSNEIGKTWR	VRYDKSFELT
	460	470	480	490	500
Ec01	GTSFAAGYQD	SSAGYHSLAD	VLDTYRNGTA	YRSYDNRIRR	TTINISQALG
Ec02	GTSFAAGYQD	SSAGYHSLAD	VLDTYRNGTA	YRSYDNRIRR	TTINISQALG
Ec03	GTSFAAGYQD	SSAGYHSLAD	VLDTYRNGTA	YRSYDNRIRR	TTINISQALG

	510	520	530	540	550
Ec01	EWGSVALNGG	RDEYRDKVKQ	DYIGASYSNS	WKGITFAVNW	SRNNNIGDYY
Ec02	EWGSVALNGG	RDEYRDKVKQ	DYIGASYSNS	WKGITFAVNW	SRNNNIGDYY
Ec03	EWGSVALNGG	RDEYRDKVKQ	DYIGASYSNS	WKGITFAVNW	SRNNNIGDYY
	560	570	580	590	600
Ec01	SNSLRTENNL	NLWMSIPMKR	WLGDDDKGVT	ATAQIQRITG	QNTLYETGLN
Ec02	SNSLRTENNL	NLWMSIPMKR	WLGDDDKGVT	ATAQIQRITG	QNTLYETGLN
Ec03	SNSLRTENNL	NLWMSIPMKR	WLGDDDKGVT	ATAQIQRITG	QNTLYETGLN
	610	620	630	640	650
Ec01	GRAFGQKLYW	DIREQIVPGS	KYDADTSLN	LRWSGGYGEL	TGMYSYNRNT
Ec02	GRAFGQKLYW	DIREQIVPGS	KYDADTSLN	LRWSGGYGEL	TGMYSYNRNT
Ec03	GRAFGQKLYW	DIREQIVPGS	KYDADTSLN	LRWSGGYGEL	TGMYSYNRNT
	660	670	680	690	700
Ec01	RQMNVTSGS	MAIHSGGIAF	GQKTDDTMAL	IAAPGIAGAS	VGGWPGVSTD
Ec02	RQMNVTSGS	MAIHSGGIAF	GQKTDDTMAL	IAAPGIAGAS	VGGWPGVSTD
Ec03	RQMNVTSGS	MAIHSGGIAF	GQKTDDTMAL	IAAPGIAGAS	VGGWPGVSTD
	710	720	730	740	750
Ec01	FRGYTLVGHV	SPYQENIITL	DPTTFPDNTE	VSQTDRRVIP	TKGALVQAEF
Ec02	FRGYTLVGHV	SPYQENIITL	DPTTFPDNTE	VSQTDRRVIP	TKGALVQAEF
Ec03	FRGYTLVGHV	SPYQENIITL	DPTTFPDNTE	VSQTDRRVIP	TKGALVQAEF
	760	770	780	790	800
Ec01	KTRVGNRALV	TLTRKDGTL	PFGTVVTLE	KTGEAFESAG	VVDDKGKVYL
Ec02	KTRVGNRALV	TLTRKDGTL	PFGTVVTLE	KTGEAFESAG	VVDDKGKVYL
Ec03	KTRVGNRALV	TLTRKDGTL	PFGTVVTLE	KTGEAFESAG	VVDDKGKVYL
	810	820	830	840	842
Ec01	SGLSEAGKLK	AQWGTNSQCY	ADYKLPLKKG	MSGIFLTRAV	CM
Ec02	SGLSEAGKLK	AQWGTNSQCY	ADYKLPLKKG	MSGIFLTRAV	CM
Ec03	SGLSEAGKLK	AQWGTNSQCY	ADYKLPLKKG	MSGIFLTRAV	CM

AggD Chaperone protein

	10	20	30	40	50
Ec01	MKIRRIVSTI	AIALSVFTFA	HAQSFENVEN	NAKVFSLHLG	ATRMLYKPNS
Ec02	MKIRRIVSTI	AIALSVFTFA	HAQSFENVEN	NAKVFSLHLG	ATRMLYKPNS
Ec03	MKIRRIVSTI	AIALSVFTFA	HAQSFENVEN	NAKVFSLHLG	ATRMLYKPNS
	60	70	80	90	100
Ec01	SGETLAVINE	HNYPILVQAN	VLSEDQKNIA	PFIITPPLFR	LDALQSSRLR
Ec02	SGETLAVINE	HNYPILVQAN	VLSEDQKNIA	PFIITPPLFR	LDALQSSRLR
Ec03	SGETLAVINE	HNYPILVQAN	VLSEDQKNIA	PFIITPPLFR	LDALQSSRLR
	110	120	130	140	150
Ec01	IVKTEGAFPI	DRESLQWICV	KAIPPKYEDK	WAKEEVSGKK	SDEATMNIQV
Ec02	IVKTEGAFPI	DRESLQWICV	KAIPPKYEDK	WAKEEVSGKK	SDEATMNIQV
Ec03	IVKTEGAFPI	DRESLQWICV	KAIPPKYEDK	WAKEEVSGKK	SDEATMNIQV
	160	170	180	190	200
Ec01	SVSSCIKLFV	RPADVKGQPD	DVAGKIKWQK	VGNKLKGVNP	TPFYMDIAEL
Ec02	SVSSCIKLFV	RPADVKGQPD	DVAGKIKWQK	VGNKLKGVNP	TPFYMDIAEL
Ec03	SVSSCIKLFV	RPADVKGQPD	DVAGKIKWQK	VGNKLKGVNP	TPFYMDIAEL
	210	220	230	240	250
Ec01	RVGEKEITET	HYIAPFSSYE	YPMPVNGGGD	VRWKVVTDYG	GISKTFETGL
Ec02	RVGEKEITET	HYIAPFSSYE	YPMPVNGGGD	VRWKVVTDYG	GISKTFETGL
Ec03	RVGEKEITET	HYIAPFSSYE	YPMPVNGGGD	VRWKVVTDYG	GISKTFETGL
	252				
Ec01	NI				
Ec02	NI				
Ec03	NI				

Figure S2. Comparison of the amino acid sequences of the AggA, AggB, AggC, and AggD AAF/I proteins from *E. coli* O104:H4 2011C-3493, 2009E-2050, and 2009E-2071 strains.