

Title	Tn6188 - a novel transposon in <i>Listeria monocytogenes</i> responsible for tolerance to benzalkonium chloride
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Figure S1

<i>L. mono.</i> EGD-e	1	-----MLT	THE	ISE	NEK	P	R	E	K	L	Q	N	Y	G	I	E	A	L	S	S	S	E	L	V	A	L	I	E	T	G	T	K	N	E	S	V	L	T	I	A	N	R	I	I	M	K												
<i>L. mono.</i> F2365	1	-----MLI	HE	ISE	NEK	P	R	E	K	L	Q	N	Y	G	I	E	A	L	S	S	S	E	L	V	A	L	I	E	T	G	T	K	N	E	S	V	L	T	I	A	N	R	I	I	M	K												
<i>L. mar.</i>	1	-----MLI	NE	V	L	E	N	E	K	P	R	E	K	L	Q	N	Y	G	I	E	A	L	S	S	S	E	L	V	A	L	I	E	T	G	T	K	N	E	S	V	L	T	I	A	N	R	I	I	M	K								
<i>L. inn.</i> Clip11262	1	-----MLV	NE	ISE	NEK	P	R	E	K	L	Q	N	Y	G	I	E	A	L	S	T	S	E	L	V	A	L	I	E	T	G	T	K	T	E	S	V	L	T	I	A	N	R	I	M	M	K												
<i>L. wel.</i> SLCC5334	1	-----MLT	SE	ISE	SEK	P	R	E	K	L	Q	N	Y	G	I	E	A	L	S	S	S	E	L	V	A	L	I	E	T	G	T	K	N	E	S	V	L	T	I	A	N	R	I	I	M	K												
<i>L. iv.</i> FSL F6-596	1	-----MLS	NE	IS	G	NEK	P	R	E	K	L	Q	N	Y	G	I	E	A	L	S	T	S	E	L	V	A	I	I	E	T	G	T	K	S	E	S	V	L	T	I	A	N	R	I	I	M	K											
<i>L. seel.</i> SLCC3954	1	-----MLA	NE	IS	G	SEK	P	R	E	K	L	Q	N	Y	G	I	E	A	L	S	T	S	E	L	V	A	I	I	E	T	G	T	K	N	E	S	V	L	T	I	A	N	R	I	I	M	K											
<i>L. gr.</i>	1	-----MQM	K	E	M	Q	I	F	D	K	P	R	E	K	M	Q	T	R	G	A	Q	L	T	I	T	E	L	A	I	L	E	T	G	T	K	E	D	S	V	L	S	L	A	N	K	I	I	L	K									
<i>B. smi.</i> 7_3_47FAA	1	--MSK	E	S	I	R	I	H	N	V	P	R	E	D	R	P	R	E	R	L	I	L	K	G	A	H	S	L	N	H	E	L	A	I	L	L	Q	S	G	T	K	E	S	V	L	Q	L	A	N	R	L	L	N	Q				
<i>B. coag.</i> 36D1	1	----MEK	M	L	I	K	D	F	P	A	E	D	R	P	R	E	R	L	I	R	T	G	A	E	S	L	N	Q	E	L	L	A	I	L	L	R	T	G	T	K	E	S	V	L	E	L	A	N	R	L	I	R	H					
<i>B. subt.</i> 168	1	MVI	H	D	L	P	L	K	L	D	F	P	M	K	E	K	P	R	E	R	L	L	K	V	G	A	E	N	L	A	N	H	E	L	L	A	I	L	L	R	T	G	T	K	H	E	S	V	L	D	L	S	N	R	L	I	R	H
<i>B. weih.</i> KBAB4	1	-----MGI	R	D	M	V	T	R	E	E	Q	P	R	E	R	L	L	E	G	A	G	S	L	N	R	E	L	L	A	V	L	I	R	T	G	T	K	E	E	T	V	L	T	S	D	N	I	L	H									
<i>S. aur.</i> 7B193	1	-----MKI	K	E	M	V	T	S	E	M	P	R	E	R	L	S	H	G	A	K	S	L	N	T	E	L	L	A	I	L	I	N	T	G	R	K	G	F	S	S	I	D	I	S	N	E	L	L	I	K								
<i>S. aur.</i> COL	1	-----MKI	K	E	M	V	T	S	E	M	P	R	E	R	L	S	H	G	A	K	S	L	N	T	E	L	L	A	I	L	I	N	T	G	R	K	G	F	S	S	I	D	I	S	N	E	L	L	I	K								
<i>E. faec.</i> DO	1	----MGK	R	L	I	K	E	V	P	T	S	S	I	P	R	E	R	M	E	I	Y	G	A	E	A	L	S	D	Q	E	L	L	A	I	L	I	R	T	G																			

<i>L. mono.</i>	EGD-e	54	FKNVGE	MQYAS	IEEFQ	LVNGIG	IAKASK	IMAAIE	LGRR	--SIVTEQ	EEVVVR	CPEDAVK
<i>L. mono.</i>	F2365	54	FKNVGE	MQYAS	IEEFQ	LVNGIG	IAKASK	IMAAIE	LGRR	--GIVTEQ	EEVVVR	CPEDAVK
<i>L. mar.</i>		54	FKNVAE	MQYAS	IEEFQ	LVNGIG	IAKASK	IMAAVE	LGRR	--SLVTEQ	EEVVVR	CPEDAVK
<i>L. inn.</i>	Clip11262	54	FKHIAE	MQYAS	IEEFQ	LVNGIG	IAKASK	IMAAVE	LGRI	--SLVTEQ	KEIVIR	CPEDAVK
<i>L. wel.</i>	SLCC5334	54	FKHVAE	MQYAS	IEEFQ	LVNGIG	IAKASK	IMAAIE	LGRR	--SIVTNQ	EEIVIR	CPDDAVK
<i>L. iv.</i>	FSL F6-596	54	FKHVAE	MQYAS	IEEFQ	LINGIG	IAKASK	IMAAIE	LGRI	--SLVTER	EEIVIR	CPGDAVK
<i>L. seel.</i>	SLCC3954	54	FKHVAE	MQYAS	IEELQ	LINGIG	IAKASK	IMAAVE	LGRI	--SLVTER	EEIVIR	CPDDAVK
<i>L. gr.</i>		54	YKSLGD	IKDLT	IEELRS	INGIGL	AKATKI	MAAIEI	IGRI	CLQSESE	EKNNIA	IRSPQDAVS
<i>B. smi.</i>	7_3_47FAA	59	FEGLRML	KDATL	EEITS	IKGIGR	AKAVQI	MAAIE	LGRR	--HSLSLD	ERYVIR	SPEDGAN
<i>B. coag.</i>	36D1	57	FEGLRFL	KDASL	EEMTS	IKGIGT	AKAVQI	LAIE	LGRR	--ANLQHD	TRYVIR	TPODGAN
<i>B. subt.</i>	168	61	FDGLRL	LKEAS	VEELSS	IPGIGM	VKAIQI	LAAVE	LGSR	--HKLANE	EHFVIR	SPEDGAN
<i>B. weih.</i>	KBAB4	55	FDGLRML	KDATL	EEMTS	IHGVI	AKASQI	MAAFEL	GRM	--VRLEYQ	NNRYSI	IRSPEDCAS
<i>S. aur.</i>	71193	54	ASNLNEL	LKSSS	INDLIQ	VKGIGI	LQKAIT	LKAAFE	LGERM	--GRRAE	NNRIKI	TQPSDVAD
<i>S. aur.</i>	COL	54	ASNLNEL	LKSSS	INDLIQ	VKGIGI	LQKAIT	LKAAFE	LGERM	--GRRAE	NNRIKI	TQPSDVAD
<i>E. faec.</i>	DO	57	EGGLAS	LRQAT	LHELEET	IRGIGR	VKAIEI	KALIE	LGRR	--QTDHER	AAPPVR	TSYELAQ
consensus		61	..			..*	*	*	*	*	*	*

<i>L. mono.</i> EGD-e	112	LVMPELAFLFQEHFHCLFLNTKNQVIYRQTIFVGG	LNASIVHPREVFRALRKSAA	IMC
<i>L. mono.</i> F2365	112	LVMPELAFLFQEHFHCLFLNTKNQVIYRQTIFVGG	LNASIVHPREVFRALRKSAA	IMC
<i>L. mar.</i>	112	LVMPELAFLFQEHFHCLFLNTKNQVIYRQTIFVGG	LNASIVHPREVFRALRKSAA	IMC
<i>L. inn.</i> Clip11262	112	LVMPELAFLFQEHFHCI F FLNTKNQVIYRQTIFVGG	LNASIVHPREVFRALRKS S AA	IMC
<i>L. wel.</i> SLCC5334	112	LVMPELAFLFQEHFHCI F FLNTKNQVIYRQTIFVGG	LNASIVHPREVFRALRKS S AA	IMC
<i>L. iv.</i> FSL F6-596	112	LVMPELAFLFQEHFHCI F FLNTKNQVIYRQTIFVGG	LNASIVHPREVFRALRKSAA	IMC
<i>L. seel.</i> SLCC3954	112	LVMPELAFLFQEHFHCI F FLNTKNQVIYRQTIFVGG	LNASIVHPREVFRALRKSAA	IMC
<i>L. gr.</i>	114	IVLPELAFLFQEHFHCVLLNTRNQIVHRQTIFIGS	LNASIVHPREVYGLAVRKSAA	QIMC
<i>B. smi.</i> 7_3_47FAA	117	YVMQEMRFLTQEHFVCLFLNTKNQVLHKQTIFIGS	LNASIVHPREVFK E ALRRSAA	SIIC
<i>B. coag.</i> 36D1	115	YVMNDMRFLSQEHFVCLYLN I KNQVIHRTIFIGS	LNASIVHPREVFK E ALRRSAA	SIIC
<i>B. subt.</i> 168	119	LVMEDMRFLTQEHFVCLYLN T KNQVIHKRTVFIGS	LNSSIVHPREVFK E AFKRSAA	SFIC
<i>B. weih.</i> KBAB4	113	YMM E EMRFLQEHFVCLYLN T KNQVIHRTIFIGS	LNSSIVHPREVFK E AFRRAA	SIIC
<i>S. aur.</i> 71193	112	YMIPTMKDILTQEHFVILLN S KNVVIKETCVFKGTL	NSSIVHPREIFSI A VRENANAI	IIA
<i>S. aur.</i> COL	112	YMIPTMKDILTQEHFVILLN S KNVVIKETCVFKGTL	NSSIVHPREIFSI A VRENANAI	IIA
<i>E. faec.</i> DO	115	QLILEMKDHKQEH L VLCIYLD T KNQVILKKT V FIGS	LNQSV A HPREIFHYAVRYCAARIVL	
consensus	121	***.....*.....*.....*.....*		

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L. mono. EGD-e      172 FHNHPSGDP-TPSSEDLIVTKRLAEAGNIVGITLLDHIIGKNKYISLKEKGYF----
L. mono. F2365     172 FHNHPSGDP-TPSSEDLIVTKRLAEAGNIVGITLLDHIIGKNKYISLKEKGYF----
L. mar.            172 FHNHPSGDP-APSSSEDLIVTKRLAEAGNIVGITLLDHIIGKNKYISLKEKGYF----
L. inn. Clip11262  172 FHNHPSGDP-APSSSEDLIVTKRLAEAGNIVGITLLDHIIGKNKYISLKEKGYF----
L. wel. SLCC5334   172 FHNHPSGDP-TPSSEDLIVTKRLVEAGNIIGITLLDHIIGKNKYISLKEKGYF----
L. iv. FSL F6-596  172 FHNHPSGDP-TPSSEDLIVTKRLVEAGNIIGITLLDHIIGKNKYISLKEKGYF----
L. seel. SLCC3954  172 FHNHPSGDP-SPSSSEDLIVTKRLVEAGNIIGITLLDHIIGKNKYISLKEKGYF----
L. gr.            174 FHNHPSGDP-TPSPEDIQVTKNLAKAGDIIGIPLIDHIIGKGSFTSLKEQGYF----
B. smi. 7_3_47FAA  177 FHNHPSGDP-TPSREDIEVTKRLAECGKIIGIEVLDHLIIGDQKYISLKEKGYL----
B. coag. 36D1      175 FHNHPSGDP-SPSKEDIEVTKRLAECGKIMGIEILDHLIIGEEKKFVSLRQKGYL----
B. subt. 168       179 VHNHPSGDP-TPSREDIEVTRRLFECGNLIGIELLDHLVIGDKKFVSLKEKGYL----
B. weih. KBAB4     173 LHNHPSGDP-APSREDIEVTKRLVECGRIIGIEVLDHIIGDHHKFVSLKEKGYHI----
S. aur. 71193      172 VHNHPSGDV-TPSQEDIITMRLKECGLILGIDLLDHIIGDNRFTSLVEAGYFDEND
S. aur. COL        172 VHNHPSGDV-TPSQEDIITMRLKECGLILGIDLLDHIIGDNRFTSLVEAGYFDEND
E. faec. DO        175 AHNHPSGNV-IPSQQDMNFTKRIQKCGEMMGITVLDHLIIGRKRYFSLREEGMMEEK-
consensus          181 .*****... ** .*...*... ..* ..*...*...*...*...*...*...

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Figure S1: Amino acid based alignment of RadC proteins from various *Firmicutes*.

The alignment was done with MAFFT (Kato H, Toh H (2008), Brief Bioinform 9: 286-298), shading of conserved amino acid residues was performed with Boxshade. The insertion site of Tn6188 and other Tn554-like transposons is highlighted in red. The consensus is displayed at the bottom of each alignment block, asterisks indicate identical positions, dots indicate similar positions.

Abbreviations and accession numbers: *L. mono.* EGD-e (*L. monocytogenes* EGD-e, NP_465074), *L. mono.* F2365 (*L. monocytogenes* F2365, YP_014167), *L. mar.* (*L. marthii*, WP_008947916), *L. inn.* Clip11262 (*L. innocua* Clip11262, NP_470920), *L. wel.* SLCC5334 (*L. welshimeri* SLCC5334, YP_849759), *L. iv.* FSL F6-596 (*L. ivanovii* FSL F6-596, ZP_07873944), *L. seel.* SLCC3954 (*L. seeligeri* SLCC3954, YP_003464701), *L. gr.* (*L. grayi*, WP_003755617), *B. smi.* 7_3_47FAA (*Bacillus smithii* 7_3_47FAA, ZP_09354272), *B. coag.* 36D1 (*Bacillus coagulans* 36D1, YP_004860597), *B. subt.* 168 (*Bacillus subtilis* 168, NP_390682), *B. weih.* KBAB4 (*Bacillus weihenstephanensis* KBAB4, YP_001647086), *S. aur.* 71193 (*Staphylococcus aureus* 71193, AFH69892), *S. aur.* COL (*Staphylococcus aureus* COL, YP_186546), *E. faec.* DO (*Enterococcus faecium* DO, AFK59806)