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

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L. mono. EGD-e      1 -----MLTHEISENEKPREKLQNYGIEALSSSELVALIIETGTKNESVLTIANRIIMK
L. mono. F2365     1 -----MLIHEISENEKPREKLQNYGIEALSSSELVALIIETGTKNESVLTIANRIIMK
L. mar.            1 -----MLINEVLENEKPREKLQNYGIEALSSSELVALIIETGTKNESVLTIANRIIMK
L. inn. Clip11262  1 -----MLVNEISENEKPREKLQNYGIEALSTSELVALIIETGKTESVLTIANRIMMK
L. wel. SLCC5334   1 -----MLTSEIISESEKPREKLQNYGIEALSSSELVALIIETGTKNESVLTIANRIIMK
L. iv. FSL F6-596  1 -----MLSNETSGNEKPREKLQNYGIEALSTSELVAIIIIETGTKSESVLTIANRIIMK
L. seel. SLCC3954  1 -----MLANEISGSEKPREKLQNYGIEALSTSELVAIIIIETGTKNESVLTIANRIIMK
L. gr.            1 -----MOMKEMQIFDKPREKMOTRGOAQLTITELLAAILLETGTKEDSVLSLANKIILK
B. smi. 7_3_47FAA  1 --MSKESLRTHNVPREDRPRERLILKGAHSLSNHELIAILLQSGTKESVQLANRLLNQ
B. coag. 36D1     1 ----MEKMLIKDFPAEDRPRERLIRTGAESLSNQELLAILLRTGTKEESVLELANRLIRH
B. subt. 168      1 MVIHDLPLKDKDFPMKEKPRERLLKVGAEENLANHELLAILLRTGTKEESVLDLSNRLRS
B. weih. KBAB4    1 -----MNGIRDVREEQPRERLLLEGAGSLSNRELLAVLIRTGSKEETVLTLSDNILHH
S. aur. 71193     1 -----MKIKEMVTSEMPRERLLSHGAKSLSNTELLAILINTGRKGFSSIDISNELLKS
S. aur. COL       1 -----MKIKEMVTSEMPRERLLSHGAKSLSNTELLAILINTGRKGFSSIDISNELLKS
E. faec. DO       1 ----MGKRLIKEVPTSSLPRERMEIYGAEALSQDELLAILLIRTQHYPYSVMSIAGNLLKT
consensus         1 ..... ..***...*...*...***.....*.....

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L. mono. EGD-e      54 FKNVGEQYASIEEFQLVNGIGIYAKASKIMAAIELGRRI--SIVTEQEEVVVRCPEDAVK
L. mono. F2365     54 FKNVGEQYASIEEFQLVNGIGIYAKASKIMAAIELGRRI--GIVTEQEEVVVRCPEDAVK
L. mar.            54 FKNVAEQYASIEEFQLVNGIGIYAKASKIMAAVELGRRI--SLVTEQEEVVVRCPEDAVK
L. inn. Clip11262  54 FKHIAEQYASIEEFQLVNGIGIYAKASKIMAAVELGKRI--SLVTEQKEIVIRCPEDA VK
L. wel. SLCC5334   54 FKHVAEQYASIEEFQLVNGIGIYAKASKIMAAIELGRRI--SIVTNQEEIVIRCPDDAVK
L. iv. FSL F6-596  54 FKHVAEQYASIEEFQLVNGIGIYAKASKIMAAIELGKRI--SLVTEREEIVIRCPGDAAK
L. seel. SLCC3954  54 FKHVAEQYASIEEFQLVNGIGIYAKASKIMAAVELGKRI--SLVTEREEIVIRCPDDAVK
L. gr.            54 YKSLGDIKDLTIEELRSINGIGLAKATKIMAAIEIGKRICLOSESEKNNIAIRSPQDAVS
B. smi. 7_3_47FAA  59 FEGLRMLKDATIEEITSIKGIGRAKAVQIMAAIELGRRI--HSLSLDERYVIRSPEDGAN
B. coag. 36D1     57 FEGLRFLK DASLEEMTSSIKGIGTAKAVQILAAATELGRRI--ANLQHDTRYVIRTPQDAN
B. subt. 168      61 FDGLRLLKEASVEELSSIPGIGMVKAIQILAAVELGSR I--HKLANEQHFVIRSPEDGAN
B. weih. KBAB4    55 FDGLRMLKDATIEEEMSIHGIVGIYAKASQILMAAFELGRRI--VRLEYQNRYSIRSPEDCAS
S. aur. 71193     54 ASNLNELKKSINDLIQVKGIGIQKAITLKA AFELGERM--GRR AENNRKIKITQPSDVAD
S. aur. COL       54 ASNLNELKKSINDLIKVKGIGIQKAITLKA AFELGERM--GRR AENNRKIKITQPSDVAD
E. faec. DO       57 FGGLASLRQATHELEELRGIGRVKAIETKALIELGRRI--QTDHERAAPVVRTSYELAQ
consensus         61 .. ..... ..*.*.*.*.*.*.*.*.....

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L. mono. EGD-e      112 LVMPELAFLEFQEHFHCFLNLTKNQVIYRQTIFVGGNLNASIVHPREVFRLALRKSAA S I M C
L. mono. F2365     112 LVMPELAFLEFQEHFHCFLNLTKNQVIYRQTIFVGGNLNASIVHPREVFRLALRKSAA S I M C
L. mar.            112 LVMPELAFLEFQEHFHCFLNLTKNQVIYRQTIFVGGNLNASIVHPREVFRLALRKSAA S I M C
L. inn. Clip11262  112 LVMPELAFLEFQEHFHCIFLNLTKNQVIYRQTIFVGGNLNASIVHPREVFRLALRKSAA S I M C
L. wel. SLCC5334   112 LVMPELAFLEFQEHFHCIFLNLTKNQVIYRQTIFVGGNLNASIVHPREVFRLALRKSAA S I M C
L. iv. FSL F6-596  112 LVMPELAFLEFQEHFHCIFLNLTKNQVIYRQTIFVGGNLNASIVHPREVFRLALRKSAA S I M C
L. seel. SLCC3954  112 LVMPELAFLEFQEHFHCIFLNLTKNQVIYRQTIFVGGNLNASIVHPREVFRLALRKSAA S I M C
L. gr.            114 IVLPPELAFLEFQEHFHCVLNLTNRNQVIYRQTIFIGSLNASIVHPREVFYGLAVRKSAAQ I M C
B. smi. 7_3_47FAA  117 YVMQEMRFLTQEHFVCLFLNLTKNQVIYRQTIFIGSLNASIVHPREVFKEALRRSAAS I I C
B. coag. 36D1     115 YVMNDRFLSQEHFVCLYLN IKNQVIYRQTIFIGSLNASIVHPREVFKEALRRSAAS I I C
B. subt. 168      119 LVMEDMRFLTQEHFVCLYLN IKNQVIYRQTIFIGSLN S S I V H P R E V F K E A F K R S A A S I I C
B. weih. KBAB4    113 YMMEMRFLQEQEHFVCLYLN IKNQVIYRQTIFIGSLN T S I V H P R E V F K E A F R R A A S I I C
S. aur. 71193     112 YMIPTMKDLTQEHFVILLN S K N V I K E T C V F K G T L N S S I V H P R E I F S I A V R E N A N A I I A
S. aur. COL       112 YMIPTMKDLTQEHFVILLN S K N V I K E T C V F K G T L N S S I V H P R E I F S I A V R E N A N A I I A
E. faec. DO       115 QLTLEMKDHKQEHFLVCIYLD TKNQVILKKTIVF I G S L N Q S V A H P R E I F H Y A V R Y C A A R I V L
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-TPSSEDLIVTKRLVEAGSIIGITLLDHIIGKNKYISLKEKGYF----
L. seel. SLCC3954  172 FHNHPSGDP-SPSSSEDLIVTKRLVEAGNIIGITLLDHIIGKNKYISLKEKGYF----
L. gr.           174 FHNHPSGDP-TPSPEDIQVTKNLAKAGDIIGIPLIDHIIGKGSFTSLKEQGYF----
B. smi. 7_3_47FAA 177 FHNHPSGDP-TPSREDIEVTKRLAECGKIIGIEVLDHLIIGDQKYISLKEKGYL----
B. coag. 36D1     175 FHNHPSGDP-SPSKEDIEVTKRLAECGKIMGIEILDHLIIGEKKFVSLRQKGYL----
B. subt. 168     179 VHNHPSGDP-TPSREDIEVTRRLFECGNLIGIELLDHLVIGDKKFVSLKEKGYL----
B. weih. KBAB4   173 LHNHPSGDP-APSREDIEVTKRLVECGRIIGIEVLDHIIGDHFVSLKEKCHI----
S. aur. 71193    172 VHNHPSGDV-TPSQEDIITMRLKECGLILGIDLLDHIIGDNRFTSLVEAGYFDEND
S. aur. COL      172 VHNHPSGDV-TPSQEDIITMRLKECGLILGIDLLDHIIGDNRFTSLVEAGYFDEND
E. faec. DO      175 AHNHPSGNV-IPSQODMNFVKRIQKCGEMMGITVLDHLIIGRKRYFSLREEGMMEEK-
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)