

Title	Tn6188 - a novel transposon in Listeria monocytogenes responsible for tolerance to benzalkonium chloride
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Publication date	2013
Original Citation	Müller A, Rychli K, Muhterem-Uyar M, Zaiser A, Stessl B, Guinane CM, et al. (2013) Tn6188 - A Novel Transposon in Listeria monocytogenes Responsible for Tolerance to Benzalkonium Chloride. PLoS ONE 8(10): e76835. doi:10.1371/journal.pone.0076835
Type of publication	Article (peer-reviewed)
Link to publisher's version	10.1371/journal.pone.0076835
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Download date	2024-05-05 22:32:50
Item downloaded from	https://hdl.handle.net/10468/2364



Figure S2

<i>L. mono.</i> EGD-e	1	-----ATGTTGACACATGAAATATCAGAGAATGAAAAACCACGC
<i>L. mono.</i> F2365	1	-----ATGTTGATACATGAAATATCAGAGAATGAAAAACCACGC
<i>L. mar.</i> FSL S4-120	1	-----ATGTTAATTAAATGAAATTCTCTGGAAAATGAAAAACCGCGT
<i>L. inn.</i> Clip11262	1	-----ATGCTAGTAATGAAATCTCGGAAAATGAGAAGGCCACGA
<i>L. wel.</i> SLCC5334	1	-----ATGCTTACAAGTGAGATTCAGAAAGCGAAAAACCACGT
<i>L. iv.</i> FSL F6-596	1	-----ATGTTTCAACGAAATTTCAGGAAATGAGAAGCCCTCGC
<i>L. seel.</i> SLCC3954	1	-----ATGCTAGCAACGAAATTTCAGGGAGCGAAAAGCCCGT
<i>L. gr.</i> DSM20601	1	-----ATGCAAATGAAAGAAATGCAGATTGATAAACCTCGA
<i>B. smi.</i> 7_3_47FAA	1	-----TTGTCAAAAGAATCGCTAGGATCCATAACGTTCCACGTGAAGATCGGCCCGG
<i>B. coag.</i> 36D1	1	-----TTGGAAAAATGCTGATCAAAGATTTCCTGAGAAAGACCGGCCCGT
<i>B. subt.</i> 168	1	-----TTGGTCATACACGATCTGCCATTAAAGACTCAAAGATTCCAATGAAAGAAAAGCCAAGG
<i>B. weih.</i> KBAB4	1	-----ATGAAACGGTATTCGTGATGTTGAGAGAAGAACGCCACGG
<i>S. aur.</i> COL	1	-----TGAAAATTAAAGAAATGGTAACCTTCAGAAATGCCAAGA
<i>S. aur.</i> 71193	1	-----TGAAAATTAAAGAAATGGTAACCTTCAGAAATGCCAAGA
<i>E. faec.</i> DO	1	-----TTGGGAAAACGATTGATCAAAGAAATACCTACTAGCTTTACCAAGG
consensus	1*.*.....*.....**....*
<i>L. mono.</i> EGD-e	40	GAAAAACTTCAGAATTATGGTATAGAAGGACTTTCATCTCGGAACCTGGTTGCTTTAATT
<i>L. mono.</i> F2365	40	GAAAAGCTACAGAATTATGGGATAGAAGGACTTTCATCTCGGAATTGGTTGCTTTAATT
<i>L. mar.</i> FSL S4-120	40	GAAAAGTTACAGAATTATGGGATAGAGGCCTTTCTTCGGAGTTAGTTGCTTTAATT
<i>L. inn.</i> Clip11262	40	GAAAATTACAAAATTATGGGATAGAGGCCTTTCGACTTCGGAGTTAGTGGCATTAAATT
<i>L. wel.</i> SLCC5334	40	GAAAACTTCAAAATTATGGGATAGAGGCCTTTCTTCAGAATTAGTCGCATTATC
<i>L. iv.</i> FSL F6-596	40	GAAAATTACAAAATTATGGTATAGAGGCCTTTCTACTTCAGAATTAGTCGCATTATC
<i>L. seel.</i> SLCC3954	40	GAAAAGCTACAAAATTATGGCATTAAGGCACTTCAGAATTAGTCAGAGCTTGTGCGATAATA
<i>L. gr.</i> DSM20601	40	GAAAATGCAGACAAGAGGGCAAGCGCAACTTACCAATAACGGAACCTTGTGCGATATA
<i>B. smi.</i> 7_3_47FAA	55	GAACGACTGATATTAAAGGAGCCACAGCTTGTCCAACCATGAATTGATGCCATTCTT
<i>B. coag.</i> 36D1	49	GAACGGTTGATCCGCACAGGAGCGAGGCTCTCCAAATCAGGAACCTGGCCATTTTA
<i>B. subt.</i> 168	61	GAACGGCTCTGAAAGTCGGAGCCGAGAACTTAGCGAATCATGAACTTTGGCTATATA
<i>B. weih.</i> KBAB4	43	GACGTTTATTGTTAGAAGGAGCAGGAAGTTATCGAATCGAGAACTTCTTGCACTTTA
<i>S. aur.</i> COL	40	GAACGTTTGTAAAGCCATGGTCAAAAGCTTTCAACAGAATTATTAGCTATATA
<i>S. aur.</i> 71193	40	GAACGTTTGTAAAGCCATGGTCAAAAGCTTTCAACAGAATTATTAGCTATATA
<i>E. faec.</i> DO	49	GAACGTATGAAATTATGGCGGGAAAGCTTATCGGATCAGGAGCTTGTGCAATCTA
consensus	61	***....*.....*....*.....*.....*.....*.....*.....*.....*.
<i>L. mono.</i> EGD-e	100	ATTGAAACAGGAACTAAAAATGAGTCAGTTTGACGATAGCTAATCGAATCATCATGAAG
<i>L. mono.</i> F2365	100	ATTGAAACAGGGACTAAAAATGAGTCAGTTTGACGATAGCTAATCGAATCATCATGAAA
<i>L. mar.</i> FSL S4-120	100	ATTGAAACTTGGAACGAAAATGAGTCAGTTAACAAATGCAAATCGAATTATTATGAAA
<i>L. inn.</i> Clip11262	100	ATTGAAACTTGGAACGAAAACGGAATCAGTTAACAAATTGCTAATCGAATTATGATGAAA
<i>L. wel.</i> SLCC5334	100	ATTGAAACAGGCACAAAAATGAATCGGTTAACAAATAGCAAATAGAATTATCATGAAA
<i>L. iv.</i> FSL F6-596	100	ATTGAAACAGGCACGAAAATGAGTCAGTTAACATCGCGAACCGTATTATTATGAAA
<i>L. seel.</i> SLCC3954	100	ATTGAAACAGGAACGAAAATGAGTCAGTTGACAATTGCTAATCGGATTATTATGAG
<i>L. gr.</i> DSM20601	100	TTGAAACGGGAACGAAAGAAGATTCCGTTTATCATAGCCAATAAAATCATCTTAAA
<i>B. smi.</i> 7_3_47FAA	115	CTTCAGTCGGGGACAAAAGAAGAGTCGCTCTGCACCTGGCAAATCGGCTATTAAATCAG
<i>B. coag.</i> 36D1	109	CTCCGTACCGGACGAAAAGAAGATCGGTGCTCGACCTTGCCAAACAGACTGATCCGCCAT
<i>B. subt.</i> 168	121	TTGCGGACAGGGACTAAACACGAATCTGTTTGGACCTGTCAAACCGGCTGCTGCGCTCA
<i>B. weih.</i> KBAB4	103	CTCAGAACGGTTCTAAAGAAGAACGGTTAACGTTATCAGATAATATTCTCCATCAT
<i>S. aur.</i> COL	100	ATTAACACCGGAAGAAAAGGATTCTCGAGTATTGACATTAGTAATGAACTGCTTAAATCT
<i>S. aur.</i> 71193	100	ATTAACACCGGAAGAAAAGGATTCTCGAGTATTGACATTAGTAATGAACTGCTTAAATCT
<i>E. faec.</i> DO	109	CTGCGTACCGGTCAACACCCTTATAGTGTGATGTCGATTGCTGGAAATCTGTAAAACG
consensus	121	.*.....*....*.....*.....*.....*.....*.....*.....*.....*.....*.

<i>L. mono.</i>	EGD-e	280	ATCGTAACGGAGCAGGAAGAA-----GTGTTCTTAGGTGTCCCAGAAGATGCAGTAAAA
<i>L. mono.</i>	F2365	280	ATCGTAACGGAGCAGGAAGAA-----GTGTTCTTAGGTGTCCCAGAAGATGCCGTAAAA
<i>L. mar.</i>	FSL S4-120	280	TAGTAACAGAACAAAGAGGAG-----GTTGTTCTTAGGTGCCCTGAAGATGCCGTAAA
<i>L. inn.</i>	Clip11262	280	TAGTTACGGAACAAAAGAA-----ATTGTCATTAGATGTCGGAGAAGATGCCGTGAAA
<i>L. wel.</i>	SLCC5334	280	ATTGTAACTAATCAAGAGAA-----ATTGTTATTAGATGCCCTGATGACGCCGTGAAA
<i>L. iv.</i>	FSL F6-596	280	TAGTAACGGAGCGTGAAGAA-----ATTGTCATTAGATGTCAGGGATGCAAGCAGAAA
<i>L. seel.</i>	SLCC3954	280	TTAGTGACAGAGCGCAGAGAA-----ATTGTAATAAGATGCCCTGACGATGCAGTAAA
<i>L. gr.</i>	DSM20601	280	CTGCAAAGTGAATCAGAAAAAAATAATATTAGCGATCAGAACATCCAAAGATGCAGTGTCC
<i>B. smi.</i>	7_3_47FAA	295	AGTCTTTCATAGACGAAACGG-----TATGTTATCCGCTCTCCCGAAGACGGTGCIAAT
<i>B. coag.</i>	36D1	289	AATTGCAAGCACGATAACACG-----TATGTAATCCGACGCCGQAAGACGGGCCAAT
<i>B. subt.</i>	168	301	AAATTAGCCAACGAAAGAACAT-----TTCTGTTATTGCGCTCCCCGGAAGACGGOGCTAA
<i>B. weih.</i>	KBAB4	283	CGTTAGAATATCAAAATAGA-----TATAGTATTGAACTCCAGAAGATTGTGCGAGT
<i>S. aur.</i>	COL	280	AGAAGAGCTGAAAAATAATCGT-----ATAAAAATAACGCAACCAAGTGATGTTGCTGAT
<i>S. aur.</i>	71193	280	AGAAGAGCTGAAAAATAATCGT-----ATAAAAATAACGCAACCAAGTGATGTTGCTGAT
<i>E. faec.</i>	DO	288	-----GACGGATCATGAAAGAGCGGCTCCACCGCTTGTACAGCTACGAATTGCCAG
consensus		301*.....*.....**.....*.....

<i>L. mono.</i>	EGD-e	394	ACCAAAAAATCAAGTAATACTATCGGCAAACGATTTTGTGGTGGTCTGAATGCTTCCATC
<i>L. mono.</i>	F2365	394	ACCAAAAAACCAGTAATACTATCGGCAAACGATTTTGTGGTGGTCTGAATGCTTCCATC
<i>L. mar.</i>	FSL S4-120	394	ACAAAGAACATCAAGTGATTATCGACAAACAACTTTGTGGTGGACTGAATGGCTCAATC
<i>L. inn.</i>	Clip11262	394	ACCAAGAACATCAAGTGATTATAGGCACAAACAACTTTGTGGTGGTTGAATGCTTCCATC
<i>L. wel.</i>	SLCC5334	394	ACTAAGAACATCAAGTGATTATAGGCACAAACAACTTTGTGGAGGATTAAATGGATCGATT
<i>L. iv.</i>	FSL F6-596	394	ACTAAAAAATCAAGTGATTACAGACAAACGATTGGTGGGGACTAAATGGATCTATT
<i>L. seel.</i>	SLCC3954	394	ACAAAAAAATCAAGTAATCTATAGACAAACAACTTTCGTGGTGGATTAAATGGATCCATC
<i>L. gr.</i>	DSM20601	400	ACACCGAACATCAAGTGTCATCGTCAGACTATCTTATCCGGCAGTTGAATGCTCTATT
<i>B. smi.</i>	7_3_47FAA	409	ACCAAAAAATCAAGTCTCCACAAACAAACCATTTTATCGGTAGTTGAATGCTTCGATT
<i>B. coag.</i>	36D1	403	ATTAAAAAACCCAGGTGATCCACCGCAGACGATTTCATCGGAAGCTTAAATGGCTCGATC
<i>B. subt.</i>	168	415	ACAAAAAAATCAAGTCATCCATAAACCGCACCGTATTATCGGAAGCCTGAATTGATCTATT
<i>B. weih.</i>	KBAB4	397	ACGAAAATCAAGTTACATAGGCACAACTTTTATGGAAGTTAAATACGTCGATT
<i>S. aur.</i>	COL	394	TCAAAAAAATGTAGTGATAAAAGAACCTGTGTTTTAAAGGTACATTAAATAGTTCGATT
<i>S. aur.</i>	71193	394	TCAAAAAAATGTAGTGATAAAAGAACCTGTGTTTTAAAGGTACATTAAATAGTTCGATT
<i>E. faec.</i>	DO	403	ACGAAGAACATCAAGTGATCTTAAAAAACAGTGTTCATCGGTTCGCTGAATCAGTCAGTC
consensus		421**.....*....*.....*.....*.....*.....*.....*.....*.....*.....*

<i>L. mono.</i>	EGD-e	634	AAGAATAAGTATATTAGTTGAAAGAAAAAGGT	TACTTT	TAA		
<i>L. mono.</i>	F2365	634	AAGAATAAGTATATTAGTTGAAAGAAAAAGGT	TACTTT	TAA		
<i>L. mar.</i>	FSL S4-120	634	AAGAATAAGTACATTAGTC	CTAAAAGAAAAAGGT	TATT		
<i>L. inn.</i>	Clip11262	634	AAAAAA	CAAATA	CATTAGTTAAAAGAAAAAGGC	TACTTT	TAA
<i>L. wel.</i>	SLCC5334	634	AAAAAATAAATATTAGTC	GAAAGAAAAAGGC	TATT	TAA	
<i>L. iv.</i>	FSL F6-596	634	AAAAAATAAGTC	CATTAGTC	CTAAAAGAAAAAGGT	TATTTC	TGA
<i>L. seel.</i>	SLCC3954	634	AAAAAATAATATAC	AGTTAAAAGAAAAAGGC	TATT	TAA	
<i>L. gr.</i>	DSM20601	640	AAGGGTTCAATT	TACCAAGTTAAAAGAA	QAGGGATATT	TT	TAA
<i>B. smi.</i>	7_3_47FAA	649	GACCAAAATA	CATTAGTTAAAAGAAAAAGGC	TACTTA	TAA	
<i>B. coag.</i>	36D1	643	GAGAAAAAATT	TGTAAGCTGAGAC	AAAAGGGTATTG	TAA	
<i>B. subt.</i>	168	655	GATAAAAATT	TGTGAGTTAAAGGAAAAGGGATATTG	T	TAA	
<i>B. weih.</i>	KBAB4	637	GACCATAAATT	TCGTGAGTTAAAGGAAAAGGT	CATATT	TAA	
<i>S. aur.</i>	COL	634	GATAATAGATT	TACCAAGTCTTG	TAGAACGCCGGT	TACTTT	GATGAAATGAT
<i>S. aur.</i>	71193	634	GATAATAGATT	TACGAGTCTTG	TAGAACGCCGGT	TACTTT	GATGAAATGAT
<i>E. faec.</i>	DO	643	CGCAAACGATATT	TAGTTGAGAGAAGAAGGAATGAT	GGAA	--GAGAAG	TAA
consensus		661*	*****	***	**	*

Figure S2: Nucleic acid based alignment of *radC* sequences from various *Firmicutes*.

The alignment was done with MAFFT (Katoh K, Toh H (2008), Brief Bioinform 9: 286-298), shading of conserved 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, NC_003210), *L. mono.* F2365 (*L. monocytogenes* F2365, NC_002973), *L. mar.* FSL S4-120 (*L. marthii* FSL S4-120, ADXF01000663), *L. inn.* Clip11262 (*L. innocua* Clip11262, NC_003212), *L. wel.* SLCC5334 (*L. welshimeri* SLCC5334, NC_00855), *L. iv.* FSL F6-596 (*L. ivanovii* FSL F6-596, ADXI01000816), *L. seel.* SLCC3954 (*L. seeligeri* SLCC3954, NC_013891), *L. gr.* DSM20601 (*L. grayi* DSM 20601, ACCR02000005), *B. smi.* 7_3_47FAA (*Bacillus smithii* 7_3_47FAA, EHL73379), *B. coag.* 36D1 (*Bacillus coagulans* 36D1, NC_016023), *B. subt.* 168 (*Bacillus subtilis* 168, NC_000964), *B. weih.* KBAB4 (*Bacillus weihenstephanensis* KBAB4, NC_010184), *S. aur.* COL_S. (*Staphylococcus aureus* COL, NC_002951), *S. aur.* 71193 (*Staphylococcus aureus* 71193, AFH69892), *E. faec.* DO (*Enterococcus faecium* DO, AFK59806).