

**S1 Table. Distribution of *fosX* in *Listeria* spp.** FosX orthologs (73-91% identity, 100% coverage over 133 residues) are encoded in all *Listeria* “*sensu stricto*” species except *L. seeligeri*. FosX homologs (63-66% amino acid sequence identity, i.e. similar to the level of homology with FosX proteins from more distantly related bacteria) are encoded in a different chromosomal location in the “*Paenilisteria*” clade except *L. grandensis* (in *L. cornellensis* and *L. rocourtiae* the gene is truncated). More distant homologs are encoded in *Murraya grayi* (55% identity, truncated) and “*Mesolisteria*” spp. (23-55%). The *fosX*-like genes in the “*Paenilisteria*”, “*Mesolisteria*” and *Murraya* clades probably represent evolutionary paralogs. FosX homologs from other *Firmicutes* and  $\alpha$ -*Proteobacteria* bacteria originally described in ref. [23] are included for reference.

Species	Classification <sup>a</sup>	Strain	<i>Lm</i> serovar, lineage	NCBI RefSeq / Accession no.	Aa identity (%)	Coverage (%)	Amino acids
<i>L. monocytogenes</i>	<i>Listeria</i> “ <i>sensu stricto</i> ”	EGDe	1/2a, LII	WP_010989789.1	100 <sup>b</sup>	100	133
		P14	4b, LI	LT795753	92 <sup>b</sup>	100	133
		10403S	1/2a, LII	WP_014600911.1	95 <sup>b</sup>	100	133
		SLCC 2755	1/2b, LI	WP_003726635.1	92	100	133
		SLCC 2372	1/2c, LII	WP_010989789.1	100	100	133
		L99	4a, LIII	WP_012581185.1	93	100	133
		HCC23	4a, LIII	WP_012581185.1	93	100	133
		F2365	4b, LI	WP_003726635.1	92	100	133
		H7858	4b, LI	WP_003726635.1	92	100	133
		SLCC 2376 <sup>b</sup>	4c, LIII	WP_003730577.1	96 <sup>b</sup>	100	133
		SLCC 2378	4e, LI	WP_003726635.1	92	100	133
		ATCC 19117	4d, LI	WP_003726635.1	92	100	133
		SLCC 7179	3a, LII	WP_010989789.1	100	100	133
		SLCC 2479	3c, LII	WP_010989789.1	100	100	133
		SLCC 2540	3b, LI	WP_003726635.1	100	100	133
<i>L. innocua</i>	“	CLIP11262	“	WP_003762632.1	89	100	133
<i>L. marthii</i>	“	FSL S40-120	“	WP_010989789.1	91	100	135
<i>L. welshimeri</i>	“	SLCC5334	“	WP_011702500.1	89	100	133
<i>L. ivanovii</i>	“	PAM 55	“	WP_014093062.1	73	100	133
<i>L. seeligeri</i>	“	SLCC3954	“	—	—	—	—
<i>L. weihenstephanensis</i>	“ <i>Paenilisteria</i> ”	FSL R9-0317	“	WP_036061641.1	65	97	133
<i>L. riparia</i>	“	FSL S10-1204	“	WP_036101082.1	63	97	133
<i>L. cornellensis</i>	“	FSL F6-969	“	EUJ2945.1	66	57	79
<i>L. rocourtiae</i>	“	FSL F6-920	“	EUJ44943	63	53	73
<i>L. booriae</i>	“	FSL A5-0281	“	WP_036087766.1	63	97	133
<i>L. newyorkensis</i>	“	FSL A5-0209	“	WP_030689544.1	66	99	133
<i>L. grandensis</i>	“	FSL F6-0971	“	—	—	—	—
<i>L. grayi</i>	<i>Murraya</i>	FSL F6-1183	“	WP_036103975.1	55	50	76
<i>L. fleischmannii</i>	“ <i>Mesolisteria</i> ”	FSL S10-1203	“	WP_036061826.1	23	48	99
<i>L. aquatica</i>	“	FSL S10-1188	“	WP_036073138	34	43	100
<i>L. floridensis</i>	“	FSL S10-1187	“	WP_036098293	55	30	130
<i>Mesorhizobium loti</i>	<i>Rhizobiales</i>	NZP2014	“	WP_064991938.1	63	98	139
<i>Brucella melitensis</i>	<i>Rhizobiales</i>	S66	“	WP_004687281.1	58	98	139
<i>Clostridium botulinum</i>	<i>Clostridiales</i>	Kyoto	“	WP_012705368	56	98	137
<i>Desulfotobacterium</i>	<i>Clostridiales</i>	TCP-A	“	WP_018213323.1	63	98	137

<sup>a</sup> Classification of *Listeria* based on phylogenomic clades as per ref. [25].

<sup>b</sup> The FosX amino acid sequence differs in 10 positions between strains EGDe (serovar 1/2a) and P14 (serovar 4b), defining two major lineage-related sequence types; see S3 Table. There are exceptions, for example FosX from strain 10403S (serovar 1/2a, lineage II) differs by five amino acid substitutions with the EGDe sequence. *L. monocytogenes* lineage III strains define a third FosX sequence type, in turn with internal sequence polymorphisms. See Fig 1.