Supplementary Material

Wall teichoic acids restrict access of bacteriophage endolysin Ply118, Ply511, and PlyP40 cell wall binding domains to the *Listeria monocytogenes* peptidoglycan

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Table S1. Primers used for PCR amplification and sequencing

Purpose	Primer	Sequence (5' → 3') [1]
construction of Δ*lmo0959*	lmo0959_f_del_A	ATCA<u>GAGCTC</u>AGCAATGTAATGAAAATTGAGC
(Δ*tagO1* construct for serovar 1/2a)	lmo0959_r_del_B	CGATAGGAGCGAATTAGCGGTGTAAGTAATACG
	lmo0959_f_del_C	CACCGCTAATTCGCTCCTATCGCCCATTAC
	lmo0959_r_del_D	ATCA<u>GGATCC</u>GGTTGAGCCATTTCACTC
construction of Δ*lmo2519*	lmo2519_f_del_A	ATCA<u>GAGCTC</u>AACACCTTAACGCGGAGC
(Δ*tagO2* construct for serovar 1/2a)	lmo2519_r_del_B	CAGTAGGTATCATTATGCATCGAAAACGAAAATAAAAAG
	lmo2519_f_del_C	CGTTTTCGATGCATAATGATACCTACTGCAAAG
	lmo2519_r_del_D	ATCA<u>GGATCC</u>GCGTATTTGTTTGGACG
construction of Δ*LMO1042_0979*	lmo0979_f_del_A	ATCA<u>GAGCTC</u>GTTACGGCGACCGTG
(Δ*tagO1* construct for serovar 4b)	lmo0979_r_del_B	GCGATATGTGCTAATTAGCGGTGTAAGTAATACGGAC
	lmo0979_f_del_C	CTTACACCGCTAATTAGCACATATCGCCCATTAC
	lmo0979_r_del_D	ATCA<u>GGATCC</u>GGTTGAGCCATTTCACTC
construction of Δ*LMO1042_2492*	lmo2492_f_del_A	ATCA<u>GAGCTC</u>GTACACGACACATCGATAGTGATATC
(Δ*tagO2* construct for serovar 4b)	lmo2492_r_del_B	GCAGTTGGTATCCGACCAATCTTAAATTTACTTC
	lmo2492_f_del_C	GTAAATTTAAGATTGGTCGGATACCAACTGCAAAGCTAATC
	lmo2492_r_del_D	ATCA<u>GGATCC</u>TAAGGATTTTGTGGAGCATGC
pLiv2 construct for strain EGDe	lmo0959_pLiv2_for	ATAA<u>GGATCC</u>AATTTGCGGGGAGGACTAG
	lmo0959_pLiv2_rev	ATCA<u>CTGCAG</u>CAATCTCTAATCTATTTTTTCTTCTTTTG
pLiv2 construct for strain WSLC 1042	lmo0979_pLiv2_for	ATAA<u>GGATCC</u>AAAAATTTGCGGGGAGG
	lmo0979_pLiv2_rev	ATCA<u>CTGCAG</u>TCTCTAATCTATTTTTTCTTCTTTGG

[1] Restriction sites in sequences are underlined.

Figure S1: *Listeria* TagO1 and TagO2 homologues are highly similar and related to *Bacillus* and *Staphylococcus* proteins. The TagO1 and TagO2 amino acid sequences of *L. monocytogenes* strains EGDe and F2365 were aligned with the TagO proteins from *S. aureus* MN8 (GenBank sequence: accession no. ZP_06948960), and *B. subtilis* 168 (NP_391433). Black boxes indicate identical amino acids in all six proteins; residues conserved in five or four strains are indicated by dark and light grey background shading, respectively. Alignment was performed using CLC Main Workbench (Aarhus, Denmark). For *Listeria* gene identities, see Figure 1.