Supplementary Information

A Bacteriolysin of *Lactococcus piscium* is potentially involved in mediating contact-dependent antagonism against *Listeria monocytogenes*

Raouf Tareb¹, Sandrine Rezé¹, Manar Harb¹, Laurence Dubreil², Veronique Monnet³, Joanna Björkroth⁴, Delphine Passerini⁵, Francoise

Leroi⁵, Marie-France Pilet^{1*}.

² Oniris, INRAE, APEX, PAnTher, Nantes, France

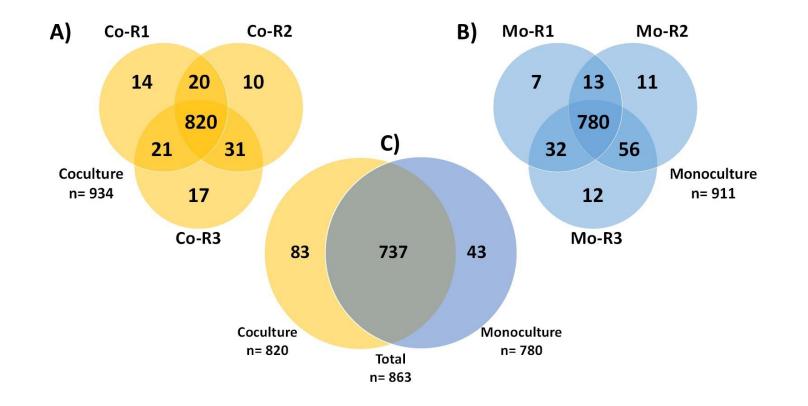
³ PAPPSO, Micalis Institute, INRAE, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France

⁴ Department of Food Hygiene and Environmental Health, Faculty of Veterinary Medicine, University of Helsinki, Helsinki, Finland

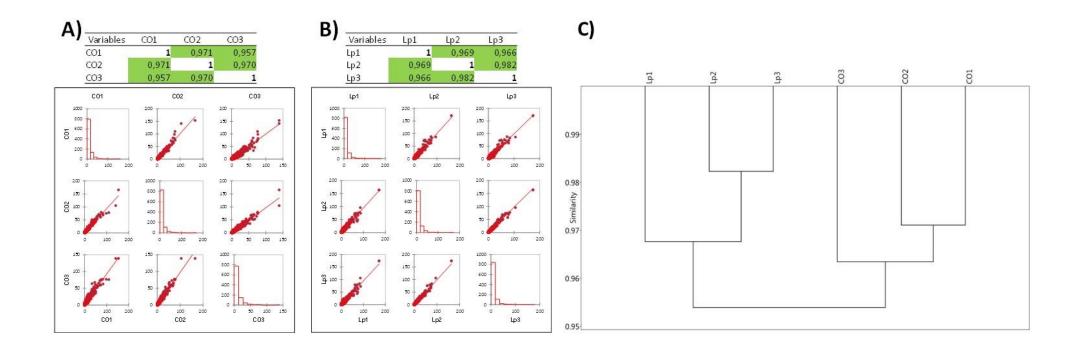
⁵ Ifremer, MASAE, Nantes, France

*Corresponding author

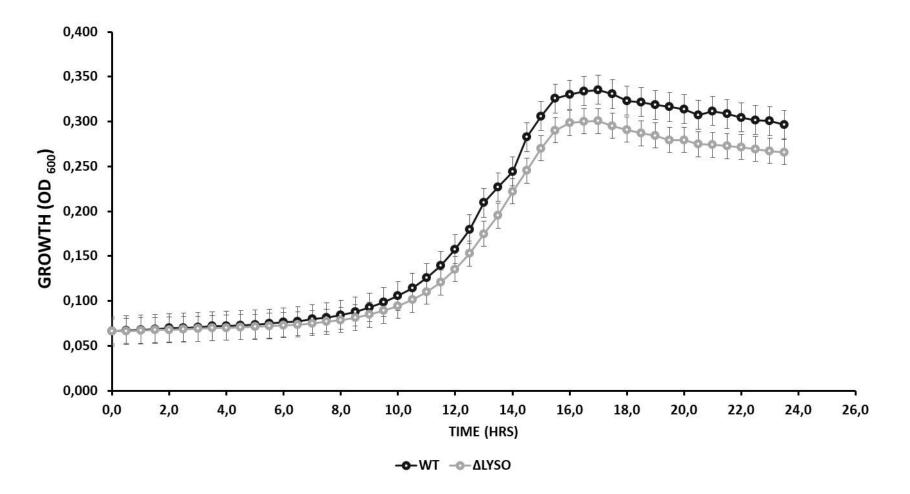
¹ Oniris, INRAE, SECALIM, Nantes, France



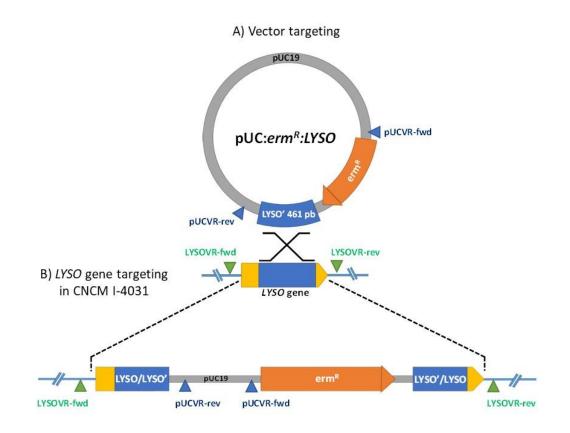
Supplementary figure S1. Venn diagram illustrating protein identification of *L. piscium* CNCM I-4031 overlaps among the three biological replicates (R1–R3) in coculture (**A**) and monoculture (**B**) conditions, (**C**) overlap of protein identified in at least two out of the three biological experiments between the both culture conditions and some of the mutually exclusively identified proteins. The total numbers of proteins are indicated for each condition outside the diagram, and the numbers of proteins exclusively detected in each condition or shared between them are indicated within the diagram.



Supplementary figure S2. Pearson correlation coefficient values of biological replicates for coculture (A) and monoculture (B) conditions, demonstrating reproducibility. Hierarchical clustering analysis of non-normalized spectral counts for identified *L. piscium* CNCM I-4031 proteins from both coculture and monoculture conditions utilizing a correlation matrix (C).

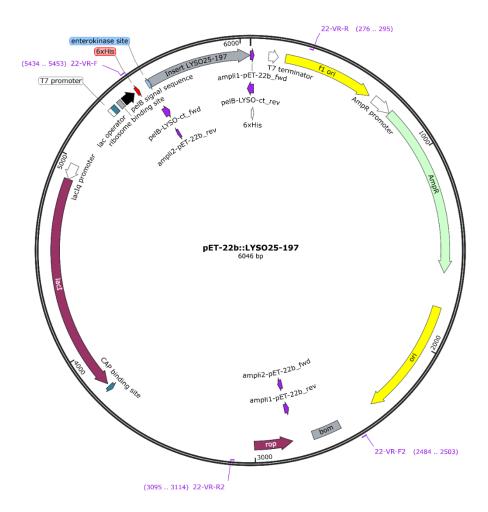


Supplementary figure S3. The growth curves of the CNCM I-4031 wild-type strain (WT) and the isogenic $\Delta LYSO$ strain in MSMA medium at 26°C.

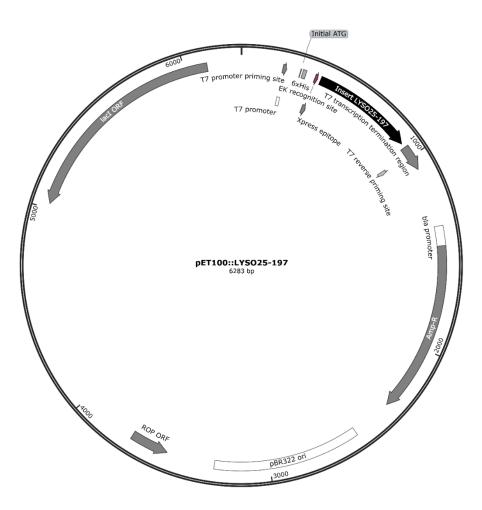


C) Targeted interruption of LYSO gene in CNCM I-4031

Supplementary figure S4. Interruption of *LYSO* gene using suicide vector pUC: erm^R :*LYSO*. (A–C) Schematic view of homologous recombination producing a mutant *L. piscium* CNCM I-4031 Δ *LYSO*. Disruption of *LYSO* gene in CNCM I-4031 wild-type (WT) by suicide vector pUC: erm^R harbouring 461 bp of *LYSO*. The mutant strain shows resistance to erythromycin by inserting a cassette containing erm^R . The primers for sequencing the insert and characterizing CNCM I-4031 WT and Δ *LYSO* are indicated as a blue or green triangle.



Supplementary figure S5. pET100 plasmid carrying the sequence encoding for truncated LYSO protein (residues between 25aa -197aa) that lacks the native signal peptide.



Supplementary figure S6. pET-22b plasmid carrying the sequence encoding for truncated LYSO protein (residues between 25aa -197aa) that lacks the native signal peptide.

Supplementary Table S1. Summary of the 863 *L. piscium* CNCM I-4031 proteins present only in all three datasets. The proteins are grouped according to predicted localization.

Predicted localization			Number of identified proteins	Number in the <i>L. piscium</i> CNCM I-4031 genome	Percent identified
Cytoplasmic proteins		Cytoplasmic proteins	693	1577	44%
Cell envelope proteins	Membranome		85	414	21%
		LPXTG anchored	2	8	25%
	ne	Lipid anchored	27	49	55%
		N-terminally anchored (No CS)	39	108	37%
	Surfaceome	N-terminally anchored (with CS)	7	19	37%
	Su	C-terminally anchored (with CS)	0	1	
		Secretory (released) (with CS)	10	29	34%
	Total surfaceome		85	214	40%
Total of cell envelope proteins			170	628	27%
Total proteome			863	2205	39%

Supplementary Table S2:	Strains,	plasmids and	primers use	d in this study.
--------------------------------	----------	--------------	-------------	------------------

Strains	Description	Reference
Lactococcus piscium CNCM I-4031	Bioprotective Strain for Seafood Products	1
Listeria monocytogenes ScottA	Clinical Isolate from a Food-Borne Listeriosis Outbreak	
E. coli 5-alpha	Derivative of the popular DH5a. It is T1 phage resistant and endA deficient for high-quality plasmid preparations	
E. coli Lemo21(DE3)	Tunable T7 Expression Strain for difficult targets: membrane proteins, toxic proteins and proteins prone to insoluble expression	
Plasmids	Description	Reference
pHSP02	Plasmid carrying erythromycin resistance gene (Erm ^R)	3
pUC19	Standard <i>E. coli</i> vector with a multiple cloning site (MCS) for DNA cloning	
pET100	Protein expression vector with an ampicillin resistance marker, for inducible expression of an N-terminally 6xHis- tagged protein	
pET-22b(+)	Protein expression vectors that encodes a signal sequence for inducible expression of proteins in the periplasm	
pUC: <i>erm^R:LYSO</i>	pUC19 carrying erythromycin resistance gene and a 461 bp internal fragment of <i>LYSO gene</i> of strain CNCM-I 4031	
pET100:: <i>LYSO</i> ₂₅₋₁₉₇	pET100 carrying the sequence encoding for truncated LYSO protein (residues between 25aa -197aa) that lacks the native signal peptide	
pET-22b::LYSO25-197	pET-22b carrying the sequence encoding for truncated LYSO protein (residues between 25aa -197aa) that lacks the native signal peptide	
Primers		Reference
Knockout mutants	Sequence (5' to 3')	Reference
Erm ^R gene	fwd: aaacgacggccagtgGGGCCCTAGTTTAGAAAAAG rev: ATAAGAGCGCTAGGGACC	
LYSO- internal fragment (full-length 461 nt)	fwd: tccctagcgctcttatTCCAGCGGACTTCTTTTG rev: tgaccatgattacgccaCGATGACTTTGTGACCCAAAC	
pUCVR: primers for sequencing the insert and characterizing wild-type and LYSO mutant	fwd: AGGGTTTTCCCAGTCACGAC rev: TTAGGCACCCCAGGCTTTAC	
LYSOVR: Primers for characterizing wild- type and LYSO mutant	fwd: TAGCGGATATAGCCCACAGC rev: TGAAGATGCGGAAACTGTCG	

Gene expression in pET22b			
ampli1-pET22b	fwd: ACTCGAGCACCACCACCAC	This study	
	rev: aaacctctgaCACATGCAGCTCCCGGAG	This study	
ampli2-pET-22b	fwd: gctgcatgtgTCAGAGGTTTTCACCGTC	This study	
	rev: CTTGTCGTCGTCGTCATAC	This study	
pelB-LYSO ₂₅₋₁₉₇	fwd: tgtatgacgacgacgacaagGAAAACGTGAAAAGCGTG	This study	
perB-L15025-197	rev: ggtggtggtggtgctcgagtTTACCAGTTAAACAGCTG		
22-VR1 : primers for sequencing the insert	fwd: CATGGGAGGGTCACATCACC	This study	
22-VK1 : primers for sequencing the insert	fwd: TGGCGAGAAAGGAAGGGAAG	This study	
22-VR2 : Primers for characterizing plasmid	fwd: TACCGCCTTTGAGTGAGCTG	This study	
22-VK2 . 1 rimers for characterizing plasmia	fwd: TCCAGTAACCGGGCATGTTC	This study	
RNA expression analysis by RT-qPCR			
<i>rpoB</i> gene	fwd: CGAGTTTGTAGATGGTGCGG	This study	
тров gene	rev: AAGGGCCATTTCTCCACCTT	This study	
Back game	fwd: TTCGGAAACACTTTGGCCTG	This study	
<i>RecA</i> gene	rev: TGGCTCTGAAACTTTAGGGGT	This study	
<i>PLY</i> gene	fwd: TTCGGAAACACTTTGGCCTG	This study	
	rev: ACAGCAAGTGCTGACGAAGT	This study	
LYSO gene	fwd: GGACTGGTGTGCAAGCCTAT	This study	
LISO gene	rev: GGCGCAACAACATCTTTGGA	This study	

1. Saraoui, T. et al. Inhibition mechanism of Listeria monocytogenes by a bioprotective bacteria Lactococcus piscium CNCM I-4031. Food Microbiology 53, 70–78 (2016).

2. Briers, Y., Klumpp, J., Schuppler, M. & Loessner, M. J. Genome sequence of Listeria monocytogenes Scott A, a clinical isolate from a food-borne listeriosis outbreak. Journal of Bacteriology 193, 4284–4285 (2011).

3. Huang, C. et al. CRISPR-Cas9-assisted native end-joining editing offers a simple strategy for efficient genetic engineering in Escherichia coli. Applied Microbiology and Biotechnology 103, 8497–8509 (2019).