

**Lactacaseibacillus paracasei GM-080 Ameliorates Allergic Airway Inflammation  
in Children with Allergic Rhinitis: From an Animal Model to a Double-Blind,  
Randomized, Placebo-Controlled Trial**

En-Kwang Lin, Wen-Wei Chang, Jhih-Hua Jhong, Wan-Hua Tsai, Chia-Hsuan Chou  
and I-Jen Wang

## Supporting information

**Table S1** CRISPR loci, prophage-like clusters, and bacteriocin gene in the GM-080 genome.

CRISPR loci								
Position		Length	Repeat consensus			Repeat length	Spacers number	
1076933-1078354		1421	GCTCTTGAAGTATTGATTCGACATCTACCTGAGAC			36	21	
Prophage								
Locate	Length	Completeness <sup>a</sup>	Score	Region	Position	Protein Number	GC (%)	
Chr	44.6Kb	intact	130	760-45436	info_outline	63	45.05	
	30.7Kb	intact	130	798774-829567	info_outline	28	43.58	
	13.6Kb	incomplete	20	1781477-1795130	info_outline	12	45.38	
	31.5Kb	intact	130	2386341-2417905	info_outline	43	44.26	
	34.1Kb	intact	141	2757738-2791893	info_outline	47	45.64	
	39.6Kb	intact	144	2867742-2907382	info_outline	54	45.29	
	64.6Kb	intact	137	3075976-3140658	info_outline	95	44.55	
Bacteriocin								
Locate	AOI <sup>b</sup>	start	end	Class	Organism	Uniprot	PMID	Sequence
Chr	AOI_01	126251	129165	143.2;LSEI_2386	Carnobacterium piscicola	P38582.1	-	MDIKSQTLTYLNLSEAYKDPEVKANEFSLKLVVQCAGKLTASNSE NSYIEVISLLSRGISSYYLSHKRIIPSSMLTIYTQIQKDIKNGNIDTE KLRKYEIAKGLMSVPYIY

<sup>a</sup> Prediction of prophage region: intact (score > 90), questionable (score 70–90) or incomplete (score < 70)

<sup>b</sup> AOI, area of interest. These are potential clusters responsible for the production of RiPPs and other bacteriocins.

**Table S2** Minimum inhibitory concentrations (MICs) of *L. paracasei* GM-080 toward eight antimicrobials and their microbiological cutoffs.

Antibiotics	EFSA cut-off <sup>a, b</sup>	GM-080 MIC <sup>a</sup>
Ampicillin	4	2~4
Gentamicin	32	2~4
Kanamycin	64	32~64
Streptomycin	64	8~16
Erythromycin	1	0.25
Clindamycin	1	0.0625~0.125
Tetracycline	4	1
Chloramphenicol	4	4

<sup>a</sup> g/L

<sup>b</sup> according to ref 17

**Table S3** EggNOG functional annotations of *L. paracasei* GM-080.

Functional Categories	Gene	egg NOG annotation	Brite
Amino acid transport and metabolism (E)	dppA	D-aminopeptidase	Bacterial chemotaxis
	pepA	M42 glutamyl aminopeptidase	Glutathione metabolism
	yxwO	ABC transporter	L-cystine transport
Carbohydrate transport and metabolism (G)	agaD	PTS system mannose/fructose/sorbose family IID component	Galactose metabolism
	kdul	Catalyzes the isomerization of 5-dehydro-4-deoxy-D- glucuronate to 3-deoxy-D-glycero-2,5-hexodiululonate	Pentose and glucuronate interconversions
	kdgK	pfkB family carbohydrate kinase	Pentose phosphate pathway
	ahaA	PTS system fructose IIA component	Biosynthesis of secondary metabolites
	xyIP	MFS/sugar transport protein	Glycosidases
	lacE	Phosphotransferase system, EIIC	Galactose metabolism
	lacG	Belongs to the glycosyl hydrolase 1 family	lactose/L-arabinose transport
	lacF	PTS system, Lactose/Cellobiose specific IIA subunit	
Replication, recombination and repair (L)	recT	RecT family	DSBR (double strand breaks repair)
	pi112	PDDEXK-like domain of unknown function (DUF3799)	prophage pi1 protein 12
	tnpA1	PFAM transposase, IS204 IS1001 IS1096 IS1165 family protein	Chromosome and associated proteins
	tnp1216	DDE domain	
	cas2	CRISPR	CRISPR-associated protein Cas2
	cas1	CRISPR	CRISPR-associated protein Cas1
	cas9	CRISPR	CRISPR-associated endonuclease Csn1
	int3	Belongs to the 'phage' integrase family	Spliceosome
	pi346	IstB-like ATP binding protein	DNA replication protein DnaC
	tnpR	Resolvase, N terminal domain	
	is18	Integrase core domain	putative transposase
	yqaJ	YqaJ-like viral recombinase domain	
	rusA	Endodeoxyribonuclease RusA	DNA repair and recombination proteins
Cell wall/membrane/envelope biogenesis (M)	rfbP	Bacterial sugar transferase	undecaprenyl-phosphate galactose phosphotransferase
	rgpAc	Domain of unknown function (DUF1972)	rgpA; rhamnosyltransferase
	mprF	lysyltransferase activity	Two-component system

**Table S4.** Putative IMa and CpG-containing ODN<sup>b</sup> contents in *L. paracasei* strains.

			GM-080	BCRC 16100	L9 <sup>c</sup>	HD1.7 <sup>c</sup>	Lpc10 <sup>c</sup>
Code	Sequence	Genome size (bp)	3,140,923	3,029,023	3,076,440	3,039,280	3,052,120
IM1	TTAGGG	Frequency	292	276	187	184	193
		No. copies per 10 <sup>6</sup> bases	93	91.1	60.8	60.5	63.2
IM2	TTTCGTTT	Frequency	103	78	54	52	59
		No. copies per 10 <sup>6</sup> bases	32.8	25.8	17.6	17.1	19.3
IM3	TCAAGCTTGA	Frequency	4	4	3	2	3
		No. copies per 10 <sup>6</sup> bases	1.3	1.3	1.0	0.7	1.0
ODN2216	GACGATCGTC	Frequency	1	3	ND <sup>d</sup>	ND	ND
		No. copies per 10 <sup>6</sup> bases	0.3	1	ND	ND	ND
ODN2336	ACGACGTCGT	Frequency	1	1	ND	ND	ND
		No. copies per 10 <sup>6</sup> bases	0.3	0.3	ND	ND	ND

<sup>a</sup> ODN, oligonucleotides.

<sup>b</sup> IM, immunosuppressive motif

<sup>c</sup> Information of three reference *Lactobacillus* strains were obtained from Mazhary Z et al., Inform. Med. Unlocked. 2020;18:100280.

<sup>d</sup> ND, not determined