

Supplementary Table S1. Dietary composition and nutrient levels of the experimental diets (as fed basis)

Ingredients	%	Nutrient content ^c	Value
Corn	58.98	Metabolizable energy (MC/kg)	2.60
Soybean meal (43)	18.22	Crude protein (%)	15.50
Limestone powder (10-20 mesh)	9.73	Crude fibre (%)	2.94
DDGS	8.47	Calcium (%)	3.70
Rice bran meal (15.1%)	2.00	Total phosphorus (%)	0.47
Corn germ cake (16.7%)	0.79	Salt (%)	0.36
Rice bran oil	0.60	K (%)	0.62
Bone Calcium hydrogen phosphate	0.50	Na (%)	0.20
NaCl	0.25	Cl (%)	0.2
Methionine	0.12	Lysine (%)	0.75
Lysine sulfate (70%)	0.10	Methionine (%)	0.37
mineral premix ^a	0.10	<i>DL</i> -Methionine (%)	0.63
Choline chloride (50%)	0.10	Threonine (%)	0.58
Multi-vitamins ^b	0.03	Tryptophan (%)	0.16
Thermostable phytase (20000)	0.01	Isoleucine (%)	0.60
Total	100.00	Valine (%)	0.72

^a Mineral premix provided the following per kg of diets: Cu, 7,000mg; Fe, 78,000mg; Zn, 65,800mg; Mn, 85,000; I, 550mg; Se, 300mg.

^b Multi-vitamins provided the following per kg of diets: VA, 4,000 IU; VD3, 1,500 IU; VK3, 15,000 mg; VE, 95,000 IU; VB1, 10,000 mg; VB2, 30,000mg; VB6, 15,000 mg; VB12, 120 mg; Nicotinamide, 50,000mg; D biotin, 500mg; folic acid, 800 mg; D pantothenic acid, 45,000; Choline, 500 mg.

^c The values of metabolizable energy, available phosphorus, and amino acids are calculated, and others are measured values.

DDGS: Distillers Dried Grains with Solubles

Supplementary Table S2. Genes associated with plantaricin in the LP18 genome

query	Description	Preferred_name
CHROMOSOME_1_2585	LytTr DNA-binding domain	plnD
CHROMOSOME_1_2587	-	plnF
CHROMOSOME_1_2592	CAAX protease self-immunity	plnU

Supplementary Table S3. Genes associated with antibiotic resistance in the LP18 genome of the CARD database

Contig	NZ_CP016270.1_52	NZ_CP016270.1_1972
Start	53399	2061681
Stop	54136	2061989
Orientation	+	-
Cut_Off	Strict	Strict
Pass_Bitscore	50	75
Best_Hit_Bitscore	86.7	75.1
Best_Hit_ARO	vanY gene in vanB cluster	qacJ
Best_Identities	31.33	40.2
ARO	3002956	3007014
Model_type	protein homolog model	protein homolog model
SNPs_in_Best_Hit_A		
RO	n/a	n/a
Other_SNPs	n/a	n/a
Drug Class	glycopeptide antibiotic	disinfecting agents and antiseptics
Resistance		
Mechanism	antibiotic target alteration	antibiotic efflux
AMR Gene Family	vanY; glycopeptide resistance gene cluster	small multidrug resistance (SMR) antibiotic efflux pump
Percentage Length of Reference Sequence	91.42	95.33
ID	gnl BL_ORD_ID 603 hsp_num:0	gnl BL_ORD_ID 4661 hsp_num:0
Model_ID	556	5730

Supplementary Table S4. Genes associated with virulence factors in the LP18 genome of the VFDB database

VFclass	Virulence factors	Related genes	Lactiplantibacillus plantarum 18(Prediction)
			NZ_CP016270.1
Adherence	BslA	bslA	-
	Listeria adhesion protein(Listeria)	lap	orf02247
	Streptococcal plasmin receptor/GAPDH(Streptococcus)	plr/gapA	orf02888
Enzyme	Immune inhibitor A metalloproteinase	Undetermined	-
		inhA	-
	Pho	plcA	-
	Phosphatidylinositol-specific phospholipase C (PI-PLC)	pipIc	-
	Sphingomyelinase (SMase)	sph	-
	Streptococcal enolase(Streptococcus)	eno	orf00802
Immune evasion	B. cereus exo-polysaccharide (BPS)	bpsA、bpsB、bpsC、bpsD、 bpsE、bpsF、bpsG、bpsH、 bpsX	-
	Hyaluronic acid (HA) capsule	hasA、hasB、hasC	-
	Polyglutamic acid capsule	capA、capB、capC、capD、 capE	-
	Capsule(Streptococcus)	cps4I	orf00192
		cps2T	orf00201
		rmlA	orf00206; orf00222
		rmlB	orf00208
		rfbD	orf00209
		epsE	orf00215
		cpsY	orf00747
	Polysaccharide capsule	Undetermined	orf02158; orf02819; orf02860
Iron acquisition	Bacillibactin	dhbA、dhbB、dhbC、dhbE、 dhbF	-
	Hal	hal	-
	IlsA	ilsA	-
		asbA、asbB、asbC、asbD、 asbE、asbF	-
Regulation	AcpAB	acpA、acpB	-
	AtxA	atxA	-
	PagR-XO1	pagR-XO1	-

	PagR-XO2	pagR-XO2	-
	PlcR-PapR quorum sensing	papR、 plcR	-
	LisR/LisK(Listeria)	lisR	orf00468
Secretion system	Type VII secretion system	essC、 esxB、 esxL	-
	T6SS-II(Klebsiella)	clpB	orf00786
Toxin	Anthrax toxin	Cya、 Lef、 pagA	-
	Anthrolysin O/Cereolysin O/Hemolysin I	alo	-
	Cereulide	cesA、 cesB、 cesC、 cesD、 cesH、 cesP、 cesT	-
	Certhrax	cer	-
	Cytotoxin K (Hemolysin IV)	cytK	-
	Hemolysin II	hlyII	-
	Hemolysin III homolog	Undetermined	-
	Hemolysin III	hlyIII	-
	Hemolytic enterotoxin HBL	hblA、 hblC、 hblD	-
	Insecticidal crystalline toxins	Cry、 Cyt、 vip	-
	Non-hemolytic enterotoxin (Nhe)	nheA、 nheB、 nheC	-
	Phytotoxin phaseolotoxin(Pseudomonas)	cysC1	orf00351
	Hemolysin(Clostridium)		orf00522
Antiphagocytosis	Capsule(Enterococcus) Capsule(Klebsiella)	cpsI	orf00227
		gnd	orf00466
			orf00916
		cpsJ	orf02568
Bile resistance	Bile-salt hydrolase(Listeria)	bsh	orf02198
Invasion	Cell wall teichoic acid glycosylation protein(Listeria)	gtcA	orf01556
Manganese uptake	Pneumococcal surface antigen A / Metal binding protein SloC(Streptococcus)	psaA	orf00123
Phagosome arresting	Nucleoside diphosphate kinase(Mycobacterium)	ndk	orf02475
Protease	Trigger factor(Streptococcus)	tig/ropA	orf01024
	Serine protease(Streptococcus)	htrA/degP	orf02301
Stress adaptation	Catalase(Neisseria)	katA	orf02226
Surface protein anchoring	Lipoprotein diacylglyceryl transferase(Listeria)	lgt	orf02858
Table saved from VFDB (http://www.mgc.ac.cn/VFs/) [Fri Jul 7 11:13:13 2023]			

Supplementary Figure S1. Prediction of CRISPR structural positions in the LP18 genome

