

Supplementary Material

Table S1. Standards for interpreting the inhibition zone diameters for antibiotics used in this study. Results were recorded as: R (resistant), MS (moderately susceptible), or S (susceptible).

Antibiotic	Mechanism of action	Concentration (µg/disc)	Zone of inhibition			Reference
			R	MS	S	
Penicillin	Inhibitor of cell wall synthesis	10	≤ 19	20 – 27	≥ 28	Charteris et al. [1]
Oxacillin		5	≤ 14	15 – 19	≥ 20	Sharma et al. [2]
Ampicillin		10	≤ 12	13 – 15	≥ 16	Charteris et al. [1]
Vancomycin		30	≤ 14	15 – 16	≥ 17	
Gentamicin	Inhibitor of protein synthesis	10	≤ 12	–	≥ 13	Charteris et al. [1]
Tetracycline		30	≤ 14	15 – 18	≥ 19	
Erythromycin		15	≤ 13	14 – 17	≥ 18	
Streptomycin		10	≤ 11	12 – 14	≥ 15	
Chloramphenicol	Inhibitor of nucleic acid synthesis	10	≤ 14	15 – 19	≥ 20	Sharma et al. [2]
Mupirocin		200	≤ 14	15 – 19	≥ 20	
Rifampicin	Inhibitor of nucleic acid synthesis	30	≤ 14	15 – 19	≥ 20	Charteris et al. [1]
Nalidixic acid		30	≤ 13	14 – 17	≥ 18	

Table S2. The source of origin along with the incubation condition where the 22 LAB isolated from.

Name	Growth condition	Source
<i>L. plantarum</i> 41G	30 °C	Prosciutto
<i>L. plantarum</i> 41E		
<i>L. sakei</i> 41D		
<i>L. sakei</i> 42C		
<i>L. curvatus</i> 40A		
<i>L. curvatus</i> 41A		
<i>L. plantarum</i> 41O	37 °C	
<i>L. plantarum</i> 41P		
<i>P. acidilactici</i> 40J		
<i>P. acidilactici</i> 40I		
<i>L. coryniformis</i> subsp. <i>torquens</i> 42L		
<i>L. coryniformis</i> subsp. <i>torquens</i> 42M		
<i>L. plantarum</i> 13A	30 °C	Pancetta
<i>L. plantarum</i> 37F		
<i>L. sakei</i> 38F		
<i>L. sakei</i> 39F		
<i>L. curvatus</i> 15A		
<i>L. curvatus</i> 15E		
<i>L. plantarum</i> 38I	37 °C	
<i>L. plantarum</i> 37I		
<i>L. coryniformis</i> subsp. <i>torquens</i> 14I		
<i>L. coryniformis</i> subsp. <i>torquens</i> 15I		

Table S3. Average mean concentration of organic acid (mmol/L) and standard deviation (SD) of organic acids produced by LAB, obtained from three independent experiments.

	Lactate		Acetate		Propionate	
	Mean	SD	Mean	SD	Mean	SD
<i>L. plantarum</i> 41G	117.13	0.53	41.25	0.61	3.92	0.16
<i>L. plantarum</i> 41E	114.99	0.09	41.49	0.06	3.65	0.03
<i>L. plantarum</i> 41O	158.02	0.22	46.77	0.07	3.61	0.03
<i>L. plantarum</i> 41P	157.09	0.29	46.78	0.03	3.43	0.05
<i>L. plantarum</i> 13A	131.20	0.17	43.82	0.03	4.90	0.04
<i>L. plantarum</i> 37F	106.67	0.14	40.94	0.05	3.26	0.02
<i>L. plantarum</i> 38I	133.13	0.13	45.16	0.07	2.81	0.01
<i>L. plantarum</i> 37I	138.91	0.42	45.84	0.04	2.97	0.04
<i>L. sakei</i> 41D	80.19	1.95	37.74	0.20	0.00	0.00
<i>L. sakei</i> 42C	68.75	0.08	37.68	0.04	0.00	0.00
<i>L. sakei</i> 38F	81.90	0.02	37.65	0.05	0.00	0.00
<i>L. sakei</i> 39F	81.60	0.20	37.81	0.08	0.00	0.00
<i>L. curvatus</i> 40A	71.14	0.02	37.03	0.03	0.00	0.00
<i>L. curvatus</i> 41A	74.82	0.05	36.86	0.07	0.00	0.00
<i>L. curvatus</i> 15A	78.07	0.10	36.86	0.32	0.00	0.00
<i>L. curvatus</i> 15E	75.79	0.23	36.50	0.31	0.00	0.00
<i>L. coryniformis</i> subsp. <i>torquens</i> 42L	86.87	0.05	37.56	0.21	0.00	0.00
<i>L. coryniformis</i> subsp. <i>torquens</i> 42M	79.37	0.01	37.35	0.04	0.00	0.00
<i>L. coryniformis</i> subsp. <i>torquens</i> 14I	89.89	0.18	37.43	0.03	0.00	0.00
<i>L. coryniformis</i> subsp. <i>torquens</i> 15I	88.54	0.18	37.33	0.14	0.00	0.00
<i>P. acidilactici</i> 40J	88.08	0.05	38.40	0.02	0.00	0.00
<i>P. acidilactici</i> 40I	88.53	0.06	38.35	0.05	0.00	0.00

Table S4. Amino acid sequences that encode *bsh*, *mub* and *fbp* genes in probiotic candidate strains.

Isolate	Gene	Amino acid sequence
<i>L. plantarum</i> 38I,	<i>bsh</i>	MCTSLTYLDTDNHRYFARTMDPFTTPWWRPIFLPRRYPWPTGLATTRMTQYAILGGG RLPDHFKAICLMADGINEAGLMCAELYLPHAVEYATQPQVNQINLTPQAFINWALGE
<i>L. plantarum</i> 41G		HQSVAAVIADLPSVNLVGASWGGDTGEVYPFWYLSDAHTSVVIEPTGGPLTAQPN PAGVLNTNPVLDHQRRLNLYLAISGNQITTATRQAAQHVIQTKQPLPSGPIPTDRFIH MALRRLGTPQLAPQQVPTTLFRWLQEVSPLYHADRRHLISHNYTHYRCLITLATRTY RFIPRTTGHEQRLTLTPEMAATWRTPYLFPAD
	<i>bsh</i>	MCTSLTIQTTAGDQFLARTMDFAELGGRPVAIPRNHHFDSVTNADGFDSFYSFVGT GRDLNGYIFVDGVNEHGVSAAALYFSGQAHFTQQTAKAGKVNLPHEVLMWILGNV KSTAELGERIADLNMEAAPLLNIVVPLHWIISDKSGSTYVLELENDGVHYMKNPV GVMTNTPDFEWHLKNLSNYVNLQPGPHPSRQYGDMTVNPFGPGTGALGMPGDYTS VARFVRTVFMREHTDAVTTDAEAVNALSHMLNSVEIPKGVKMQDNGTPDYTQYRA YMSMNEPAFYMQPYADQTIRVELTPALMTAAQPTEFELKTTQQFRLAN
	<i>bsh</i>	MCTAITYQSYNNYFGRNFDEYEISYNEMVTITPRKYPLVFRKVENLDHHYAIIGITADV ESYPLYYDAMNEKGLCIAGLNFAGYADYKKYDADKVNITPFEIPLWLLGQFSSVREV KKNIQKLNLVNINFSEQLPLSPLHWLVADKQESIVIESVKEGLKIYDNPVGVLTNPN FDYQLFNLNNYRALSNSTPQNSFSEKVDLDSYRGMMGLPGDLSSMSRFVRAAFT KLNSLPMQTESGSVSQFFHILGSVEQQKGLCEVDGKYEYTISSCCDMNKGVYYYR TYDNSQINSVNLNHELDTTTELISYPLRSEAQYYAVN
	<i>bsh</i>	MCTSLTYTSHGGHFLARTMDFNVDFTETRIMFMPRHVTGDLGDFTTYGFIGAG RQLNHEIFTDGVNECGVSIAALYFPNHAIYQPHSNQDKIDLAPHDFVAWVLGKITSV ADLRERVKDVQLISSTAELINEIPPLHIFIISDQTGETAVLEPTSGELRLLNNPVGVLTN PNLKWLQLNLSKYGTLTNERPLNKFINYQPGSQGPGTGALGLPGDYTSMSRFARTV FLKHYAQVPATTDVTNLLQHILNAVTIPKGAKVAANGQATYTEYRSYMDLNHQTY ALELYENPGVIQQVNLTDLLEKQTVPLEYALSRTPHVQLLTPDIATLPAH
	<i>mub</i>	LKPNNVNNQNKRHQSRWVITSATAMILTTIASQAAAADDVTTTNEPTNSQLNT NTQVNATQVNLKADTSTSVDISTIKSDQSABAATSPPTSTGPSEHSSSVNTNPQQSAN PASQSQATTSESTPTTDIKHTQTAPAQTASASTTEPTTESNTESATDSQAKATTND QASKQPSQQAVPASSNSTTIEVNTQSATSSASTDDKIVTNVNQEKVLKTNQPVVRA ISRTASENINDWMPNTLLQQEVLSQLRKQNSRTWNSAADITKADMLLTTYYGKD TYIDGKTSYSLEGLQYATNLTVWLNNNLNAPSGSYSSDVTDISPLANLQKLQVVNI QQNRIMDISPLANLKNLTEVDAAYNHISDFSPLKGFKNLKGTFSNQFITLPPAYISADN NIATLAIDCYLPDGSKVQLPKNNVGGETVFYKNGQLYVRWYFNGAGGGNYDSNGHI YYTNMKPQQPGLTGFNGTTVIPMDYYFMTAASDGNNFVVVRPYVLAATAAPIT VKYVDALTGESLVTDLTLNGIVQPYTTQRIDDELNPYDFTNIVGNASGVFTADAQ TVTYYYTRKDAGDITHMVDTNGNLVYEPQILPGKHNGLNAYNLDAPTFDHFKLQQ TIGNAAGVFTTDQPSITFVYVRLDAGNITVKYQDKQGHQLKPDKTVSGSQLGQTYT TEPLGIENYTLMTTPANATGTFTDQEQTIVYVYVRRDAGQIVVKYQDSAGNPLAPDK LLDGKEQLGTAYQTAISIPNFYLVATPANATGTFSTDTQTVIYQYTRSNAGHITVKY QDANGTTLAPDDILTGNQQLGRPYQTNAKTIENYRLFQTPANATGQFSDQAQTVIYV YTREDAGDITVQYLDENGQQLAADMVLSGQQQLGPYETSPNINGYTVKSTQGNT TGTYTAQPQRVYIYERTAGQPVTAKYQDQDGKSIHPDVHSGYLGDNYSTEQLAI DGYTFKTVQGDVNGTFTAKTVTYVYERTAGLPVTVKYLDEHGKSIHPDVVLSGY LGDSYTKQLVIDGYTFKAVQGDVSGTFGTTAKTVTYVYENTPTIPDTQGTVTV HYVTKDGIKLNEPTVLSGKTGTTYQTVPLFTDHELVGQPNATGLFTADNVDTVY VYQATDTAGTDDIIDPPEEQPQTPVETPNEPQTTVTPQDPRIKPTQPAVAVKPA ATVKPALKPAAQASLVKTTSPVTEHSAQLPQTDEQTGKLAVALGLLSVVTFGFYG KHRQS
	<i>mub</i>	VSFLDRLKGMLQALNSTEATSATEAPRSIAAQTAAPTVNQTEALVLVHLDQDG NELQAADMIACTIGEEIHPAVSITGYHLVIEGLTRWFPTPQASITLTYERQAGQPV WMYAYDIRRELIGRPTMYRGKLGTPYEVSAVTAGFKLLRSVGDVTGEYTTTSKT

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 GKQVHTYIEPYGRYLTTVTHGDTVNLIERMADDNGVVWYRLQDGQYLPGRYLTKL
 DPPFA
mub
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 SVASQNDTTQAVATSAKVQSRAASVDTTATVQQATPTVTAPTSSATPKVSEATLT
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mub
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 DGVQGNFTDKDETITLMYSPGGIMFASAPQTINFQNPITGKSESYGASYDTGLVIQD
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mub
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	<i>fbp</i>	MSFDGLFTHAMVTELRLQTLVGGRISKINQPYQNELELTIRANRKNHPVLLSADPTYPR IQTTCIPYVNPAVPTNFAMMMRKYLQGAIVTDVSQVANDRVVHLTVTTRNELGDAE TLTLIEIMARHSNVILDNQTKIIDVIKHVGADQNRYRLLLPGATYIEPPKQDKQDP FTPNTDFHTLVDYDNPEDVLAKQLQQHYQGFRDSAQQLAADLHQPGNLDHHYQA FLAQFDQPQATLITLPNNKTMFAAGLFTFGKATRQFDSSLSSLLDFYYADAAQRERV QQQAGNLIRVVVKNNLKKNRNKLKLEKTLANTKQADELRLKGEILTTYLHEVKRG MTEITLPDYDHNAPLKIQLSNQLSPSRNAQKYFSRYQKQKNAVGFGVGEQISLTQAEI DYLDNIQTQIELASPADITEIREELTQQGQLKQHKTKKKQRSSRKPSQPQEFTASDGTP IFVGKNNRQNDQLTLKTARKSDYWLHTQKIPGSHVIIHSDDPSDQTLTEAANLAAYF SKARDSATVPVDYVQVRRIRKPNGAKPGFVIYEGQKTLVYSPNAELVEQLTPHA
	<i>fbp</i>	MTTTTDVDLVQTGLAHLIHTRKQIESLTALKALDHPVSDLQLKGTLKTYASQIEG HHHFVELPDYQGHQLSIKLDIKKSIENAEODYFHRYHKSKRGQATVQQNLATAKTEL YQQLATQAAFDPNPQAVAALKQTLIAAGAIPHTVLHSSKAPTPAHPPRFYTHDHVL VEVGKNSRQNDHLLTARKDYYWMHAGGEIPGSHVVIHSNHPSEQLQEAAVLTAY YSKGRQMNRVPDVLTVGQMRPKGAKAGLVTSGPARTITVVPDATLAADLRDQ EDIHHAD
<i>P. acidilactici</i> 40J	<i>bsh</i>	MCTSIELTAENGAKFWGRTMDLAMTMFGEDGGAESVITTIPAEAKIASQLTDWTAK YATMGVGVKGTPILFDGNEAGLAGDLQVLFESTADSLENLKQRGLTPLMNTEFVTY VLTHFKSVAEIREHYQELGLADQATQVNGQGFTFPLHYNFVDESGDGVVLEPVENG AFKLYDSVGVTNSPEYSWHTTLRNLYLGLTDVDVKDPRNYKNGVTLPIEGGTGY GMAGLPGSYTSPARFVRSFTIANAMDDFAADRGIAQLYAAFRPVIPEGIERKTADAPI SDYTRYWSGYDLRKRAVYVQTGLGLAFTKQTLNADAQEISYTTIDRGDYVHEV
	<i>mub</i>	LGTNHYQRFNYGRKWFITSVGVТИGLNVLLSPISVAASDQVSKSTYPASSPQIAPQ EAASRPPRLDYWGSSASAISSADPHHYFWGNKHHHHHHCHATVSVRYVDQ SGHLLGTGQAYCPHGPYVGEPYVSQPRSINKYRVLVTAPDSLPTGRRLNKDGDNMG VTYIYAPIYHFKAKTINETIHYVDKNGQTVAPTHVAQPIFTVTVDNLAEVHTKNYFSN TSTDFQMDQGNPRDSENWHSGTQATFTEVPDPLPHGYQLTDPAKDAVPATPVTAP STDLNITVRYQLKKKTAIRWIDDRTGKIVSSKTVNVDVKHPQANLTETFDHQDYRL VSSDLPQGSLSLTFDEIKESGHLYEVHLRSQTTPVLPVAEVKPTSEMSSSSQPVTPPALAP AEQRPALPVSPQRATPAIQPAVAGRHPQQLSKSLSSSSRPQSAQSQPRYPVPTGTIP LAVNDQQPAPVPDLLARLNKWFYFPRDHHPVLAFFDWNNHVQKIIKNGDTKSHT QLGQVWYKMSGRLVMGQRVRKSPGSL
	<i>mub</i>	MFDSACANLNKNDLSSHWNNTSNTNMNYMFEACGVSRDLHIDMSNVTRYDRMLTA MSNLRLVVLGKKTIAAGAHLSEPSFIYTFRNWWAVAGGTEDNPLGKQQYTSHELM LYNPSMADTYVIRPFKTINEDQDVTQTIHYVNKNGQMLPDHTETRRYSRKGHQNP DTGEIYWEPWKIADGENTYFDPVYSPKISGYTPDIRVVDKTIIDDELREKGGIEVTY SPNALTGVTYWDDEDNKKVSTGSLNGSTDDEGNFVINVPAHYEIDPENNPGYVD GQTVHFTWSAKDGANDFTVYLRHKHRVDPDDPEWSKETTVNETVHYVDNQG KTVYPDTSAMLTYHREVVIDEVNNNSVISRGEWPDTSNKFAGFDTPIVDGYVADHA HIEAQTVAKPGKPNQDITLTVVYYPDVDPEYPIVPGTPVDPVPDSPEYPAGMD VNDLNKDLTETIHYVDKDGKQVAPDRTITVHYTRKGHVFQKQDGATISYDPWEAD EDYPAVDSPVIDGMFPDKQTVAEVGDNSKDDDFEVKVTTYPSDVPDVDPDNPIAPDT PVDPSPDSDPDPAGVDVNDLNKDLTETIHYVDKVGNGQVAPDQKVTVHYTRKAHV HFNQDGTAEVTYDPWVADGNYPSVDSPVVDGMVPDPTVKEVDGDSVSADFEVTV IYHGSDIDVDPDHPiapDTPVDPSPDSDPSYPSGVVDLNUKDVTETIHYVDKDGKQV APDKTVTVHYTRKGHVFHNQDGTAEVTYDPWKADSDYPAVDPSPVVDGMVPDPTPT VKEVDGDSVNADFEVTVIYHGSDIDVDPSPDPTVDPDPDNPSPDYPAGVDVNDL NKDVTETIHYVDKNGKQVAPDCKTVTVHYTRKGHVFHNQDGSAEVTYDPWKADGD

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<i>L. coryniformis</i> subps. <i>torquens</i> 42L,	<i>bsh</i>	MTGQSTTWRSNYATLGVGLTNSLVLVDGINECGLAGDLQVLMECGRASADDLEQR GLQPILGEELVTYILTQCKDVAAVKELAATLALVDQPSFMQTAQIPAHYTFIDPTG AMVVLESTDNGTFKLYDSVGVLTNSPDYHTTNRNYSLDNLNKAKKTVGADLE LEPIENGTHGFFGMPGDYTPSRFRVATLIAKNIDPFASSAGIPMLYNTFSSVMIPKG LGRTPQHETVTDYTQYWGYDLTARKLYVQDYACPTFTSKALDQTTDTITYTPIDLT FQTNEI
<i>L. coryniformis</i> subps. <i>torquens</i> 14I	<i>mub</i>	VNFLKRLKAFFNPQQVATAQLPMGPDYQPIARRPILLPSPTRQAYLPISSHQPSIH VQPDSFVIVFYFTETGERLAKPQIISGVRGQAFKFTVHQFDYYISRIENYHGYFVYPR AIQLIYAQQPAAPVIVFHFDENHLLTPPEYLVGQLGQHYETHFLDSQLYRVQHVTT NQVGHFSEQTQIVTYSYRPRVIRWANRYLTGFVRLTMPVTSYREPGKAALAQQLPTN TIWRVYQKVQTTDRQWTYDLGGQWIATDHTERVEYYQQPKQQVIAAPLFQQAAVIP GSRRAVVDFIPQRSLRTWTQPYGDAANYLQHGQIVNIIHLILSNNSVWYELEDHTW LEEHYLRLLSAGHDFTSPIKRLQ
	<i>mub</i>	VQLKTLEINGFKSFADKTVIQFDHGITGIVGPNGSGKSITEAIRWALGEQSAKSLRG GKMPDIIFAGSSERKPLNRAEVTLTFDNDHQLKSDYDEVSVTRILYRDGTSAFYLNQ KSCRALKDIVNLFMDSGLGRESFSIISQGKIAIFNSKPEDRRGIIEAAGVVKYKQRKK EADSQLSATADNLHRVSDIIAELAQVPLKEQSSLAKDYLQQKKQLDQITKTLV QIESRAAAKKEQQQALKTAQENVILARRNQTDQTKVTAQKEQQQKNTQRLDILQQ DQLRITKQQAEQALSGQAELAGERRVAQNKLADLTAELKTQQQQLAEQQVLTTEKT ALQQADADLKKQQLVQNYTQAQQVDEATIKRKVEALRQQYIDQLQQQTTLHNEA AYLAREQQQTKVDEKQQAEQAAALQQTAELAAQVKTAEKTATQLKKQRTQQQQ QQQQLTTQVQHDQQQYDQQQQQWYQALAIMQKVEAKQASLAEMKEDYSGFYAG VRSILQHKTQLTGVIGAVAELLTVPAKYNQALEAILGGQLQAVVVSDEAAGKRSINY LKQQHLGRATFLPLSVMQPQQLNSTMQQIAQQPGFIGVAADLVKFAPEHANVMRH LLGRIVIATDLTAIAIKLALLQHVRVIRTVLEGDILNPGGAMTGGGRTKQNGLLAREQ EQRDLTAQLAQMKQQLATKEQALQALKAQIEAANQQLSTTDEQLQQQLARQELENQ AILKDLTRQQAQLVRQQQAVAYTSQQNDATADQQQKYLANQQQAKKVAATIEKI QADLAAQQAAALASWQENQAATASQRQQAQTDLAVAQEQQQKQRQQTNREHVEQQS ILQAAMVRNQQQCDQLTQLNNTQTKDHASNAADLKRAAEQLAQIDVQIKTVKEQR EVLAATLQQQQQLAHAQAVYQQQTAQQRIEATLASLNSLNHALTQLESDynLS FEAAKQAALPTDVAELQQQQKLLKGLADLGEVNIGAIAEYERVSQRYEFLLAQRE DLLSAREQLTTMTEMQEVSPRFKATFDATAKAFATIFPPQMFGGGQASLSLDPAN LLTTGIEITAQPPGKKLQLQLSLLSGGERALTAITLLFAIIHVRPVPLCILDEVEAALDEA NVERFGRFLQRYDQQTQFVVITHRKGTMAMDVLFVAMQESGVSHMVSVALED VKTEAHA
	<i>fbp</i>	MSFDGVFTHTMVNELSPLLTGARLSRISQPYPNELIITVRANRHNPPLSAHPSYAR LQITEIPFVNPEKPTNFTMLRKYLDGAILKSISIKQIDNDRVVHLTFTARNEIGDQESLV

LIIEMMGRHSNIVLVNQADQRIIDTIRHVAHDQNRYRLLLPGATYIAPPQQNEADPFT
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QGILTQIDLAAPKDLQDIQAELRQQGYLRTKSQQKQRPKLSQPETFYASDGTKILVG
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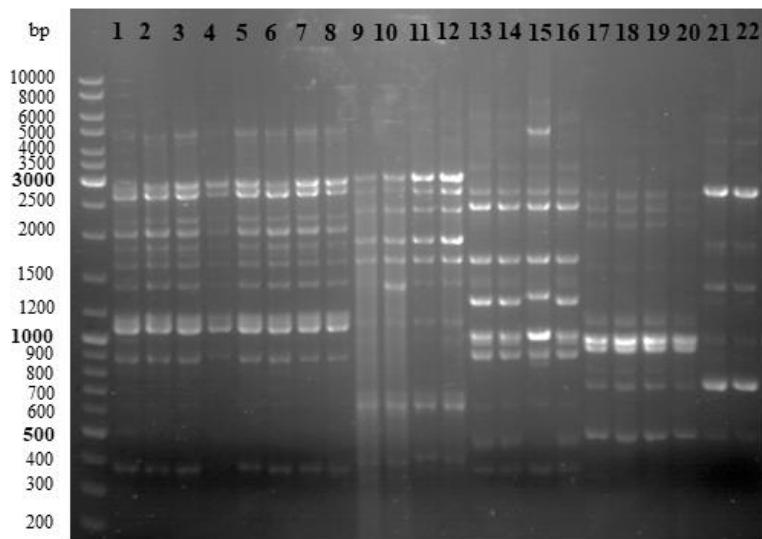


Figure S1. (GTG)₅-PCR DNA fingerprints of LAB isolates obtained from prosciutto and pancetta. Lane 1-8: *L. plantarum* strains 41G; 41E; 41O; 41P; 13A 37F; 38I; and 37I. Lane 9-12: *L. sakei* strains 41D; 42C; 38F; and 39F. Lane 13-16: *L. curvatus* strains 40A; 41A; 15A; and 15E. Lane 17-20: *L. coryniformis* subsp. *torquens* strains 42L; 42M; 14I; and 15I. Lane 21-22: *P. acidilactici* 40J and 40I. The first lane was GeneRuler DNA Ladder Mix (Thermo Fisher).

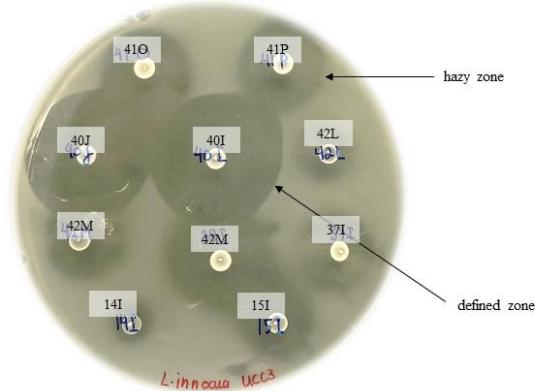


Figure S2. Representative spot-on-lawn agar plate of LAB isolates against *L. innocua* UCC3 indicator. The zone of inhibition formed by *P. acidilactici* 40 J and 40I were defined, whereas the zone of inhibition produced by *L. plantarum* 41P, 41O, 38I, 37I, *L. coryniformis* subsp. *torquens* 42M, 42L, 14I, 15I were hazy or less defined.

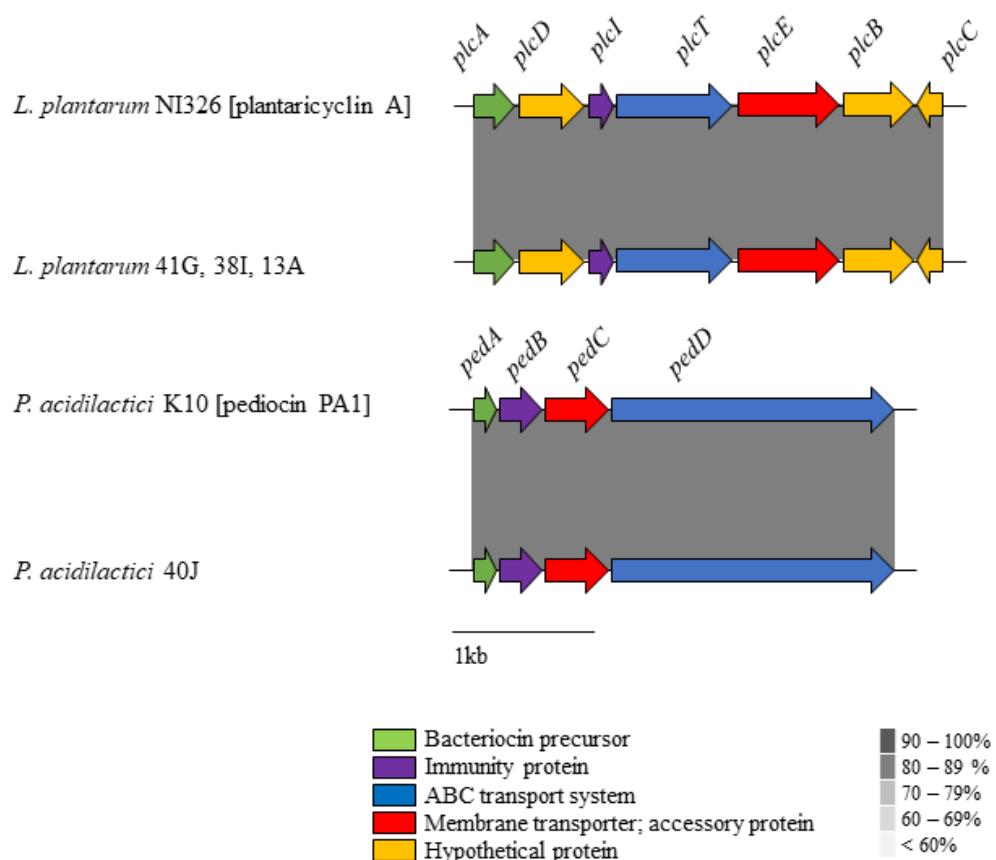


Figure S3. Schematic representation of the gene clusters involved in the production of previously studied strains of LAB (*L. plantarum* NI326, *P. acidilactici* K10) with bacteriocin producing strains isolated in this study (*L. plantarum* 41G, 38I, 13A, *P. acidilactici* 40J).

Reference

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