Probiotic Lacticaseibacillus of human origin to tackle colistin resistant Klebsiella pneumoniae



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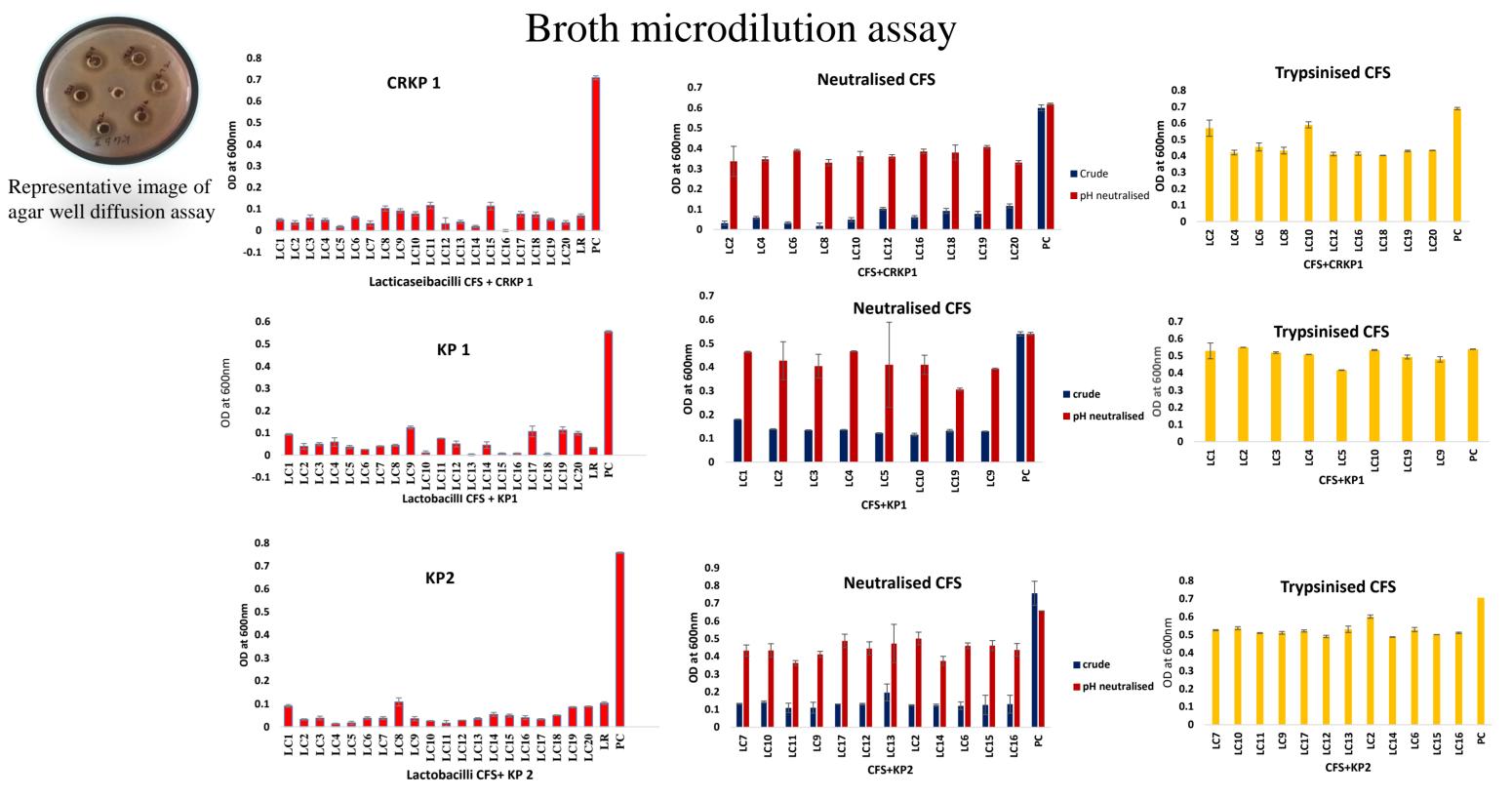
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INTRODUCTION

- Infectious diseases caused by multi-drug resistant bacterial pathogens are a major threat to public health globally and are responsible for ~ 4.95 million deaths yearly (Murray, 2022).
- Probiotics are an alternate strategy to combat antibiotic resistance by protecting from infections as well as a complementary approach alongside antibiotics.
- Probiotics are considered to be "health-friendly bacteria" that help to restore the gut microbial composition.
- They exert antimicrobial effects through competitive exclusion, production of antimicrobial substances, modulating immune response and inhibiting pathogen



Pathogens used in the study are colistin resistant *K.pneumoniae* CRKP 1, KP1 and KP2 (colistin MIC ≥64 µg/ml)



RELEVANCE OF THE WORK

- Escalating colistin resistance among K. pneumoniae made current treatment regimes more complicated.
- Present study aims to evaluate the prophylactic potential of probiotics against colistin resistant Klebsiella
- Human-origin probiotics were selected as it has prolonged survivability in gut and genome based screening for antibiotic resistance will erase the possibility of resistance transfer

OBJECTIVES

- ✤ Isolation and characterization of probiotic bacteria of human origin
- Assessment of antibacterial property of potential probiotic strain against colistin resistant *K.pneumoniae*
- Genome analysis, safety evaluation and anti-infectious property of selected probiotic against pathogen in *in vivo* models

METHODOLOGY

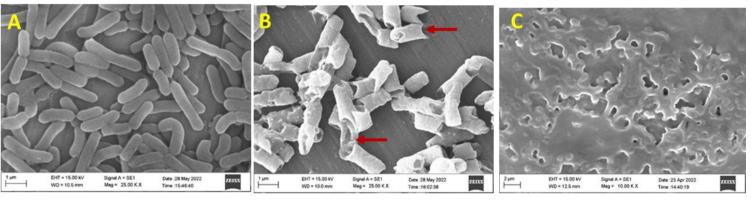
Sample collection, screening and selection of probiotics Identification, Gastric tolerance, Virulence testing and antibiotic susceptibility

Antibacterial activity and adhesion assay **Broth microdilution, SEM imaging and cell line adhesion ability**

• Twenty Lacticaseibacilli were selected based on probiotic characterization

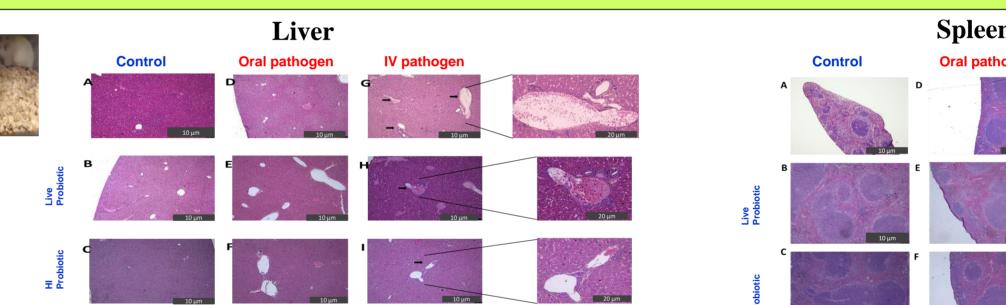
K.pneumoniae CRKP1 was selected for downstream studies as it is hypervirulent and whole genome sequenced Antibacterial activity was evaluated and two isolates (LC 10 and LC 2) showed suspected proteinaceous substances, among which LC 10 showed more adhesion

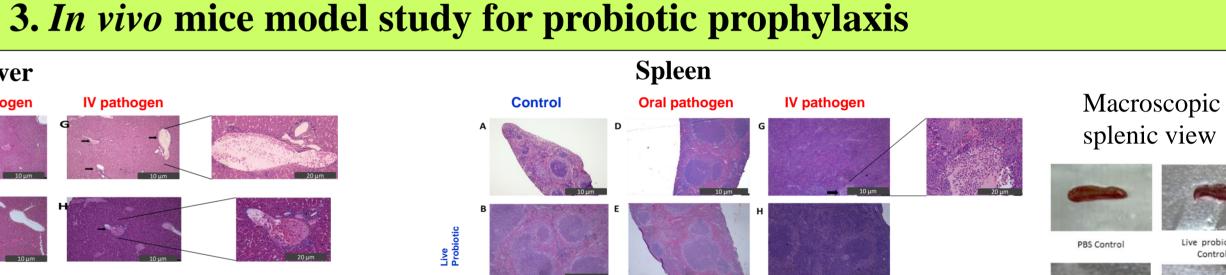
Lacticaseibacilli isolates	% Adhesion	
LC10 (infant feces)	31 ± 2	
LC2 (infant feces)	12 ± 2	
L. rhamnosus GG	26 ± 3	



Cell adhesion assay: LC10 showed good adhesion to CaCo-2 cells in vitro.

Scanning electron microscopy: A- untreated cells, B- 10⁸ CFU /ml pathogen treated with lactobacilli cell free supernatant (CFS, LC10) for 6h, C- 3x10⁸ CFU/ml treated with CFS for 24h







In vivo studies **Microbiological analysis and Histopathological imaging**

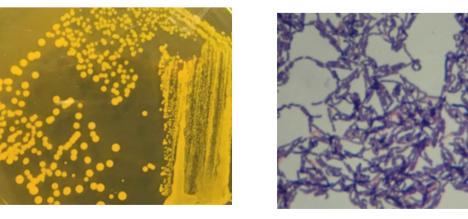
Genome analysis Genome sequencing, screening of AMR genes, prediction of bacteriocin

RESULTS

1.Sample collection and probiotic characterisation

Subjects data				
Total no: of subjects	40			
Infant age	0-6 months			
Subjects with normal delivery	25			
Subjects with cesarean section	15			
Infants with breast feeding only	30			
Infants with bottle as well as breast fed	10			
Antibiotics after delivery	Cephalosporins			

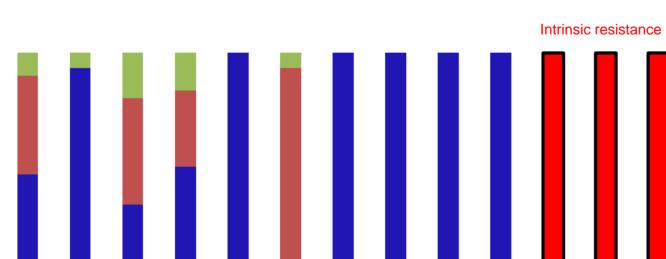
Probiotic characterisation



Lacticaseibacilli colonies Gram positive bacilli

N 1 2 3 4 5 6 7 8 9 10 11 12 13

Antibiotic susceptibility of Lacticaseibacilli



Oral pathogen treated mice - sinusoidal haemorrhage and congested blood vesse

IV challenged mice - dialated and congested blood vessels , severe neutrophilic and macrophage infiltration in many blood vessels, partly thrombosed portal vessels having mixed population of inflammatory cells. Probiotic prophylactic + IV pathogen challenge - one lesion of periportal focal haemorrhagic necrosis and neutrophilic infiltration

nactivated probiotic+IV pathogen challenge - neutrophilic infiltration in one blood vessel and also dialated and partly thrombosed portal vessels



pathological changes as compared to pathogen treated grou



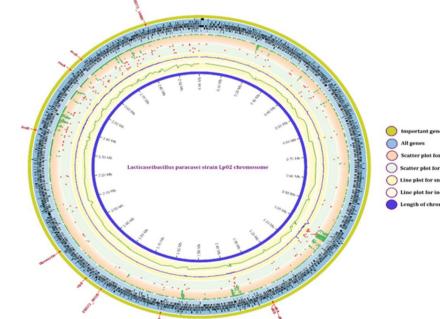
• Safety evaluation of *L. paracasei* LC10 showed promising results with no translocation to other organs • Microbiological analysis proved that live probiotic administration was more effective as compared to heat inactivated Lactobacilli in terms of pathogen reduction.

4. Whole genome sequencing of *Lacticaseibacillus casei* LC10

Tools	Genes identified
ResFinder (Antibiotic resistant genes)	No antibiotic resistance genes detected
CARD analysis	No antibiotic resistance genes detected
VirulenceFinder (Virulence/genes)	No virulence genes detected
PlasmidFinder	No plasmids detected
Tox Finder	Toxin genes not detected
ANTISMASH	Ripp like proteins detected in region 2

and 3 with similarity percentage less

than 50% with existing bacteriocins



Circos plot illustrating the distribution of SNPs and INDELs across the "L. paracasei strain Lp02 chromosome" with each concentric circle (track) representing the quality and depth of each class of variant as compared to the L. paracasei LC10. The important genes were indicated in the outer track

Location: 2,887,4	439 - 2,911	1,610 nt. (total: 2	24,172 nt) Show	pHMM detection rules used	Download region SVG Download region GenBank file	
				代訳P-like		
2.888.000	2,890,00	2,892,00	0 2,894,000		2,609,000 2,608,000 2,610,000	
Legend:						
Reference: BGC0	0000619	1: 155-6278			_	
Reference	RiPP- like	Similarity	Туре	Compound(s)	Organism	AntiSMASH analysis
BGC0000619.1	1	0.41	RiPP (gassericin T	Lactobacillus gasseri	
BGC0001602.1	1	0.41	RiPP	gassericin-T	Lactobacillus gasseri	
BGC0001388.1	1	0.41	RiPP	gassericin E	Lactobacillus gasseri	
BGC0000617.1	1	0.33	RiPP	coagulin	Bacillus coagulans	
BGC0000231.1	1	0.20	Polyketide	griseusin	Streptomyces griseus	
BGC0000624.1	1	0.20	RiPP	salivaricin CRL1328 α peptide, salivaricin CRL1328 β peptide	Lactobacillus salivarius	
BGC0000228.1	1	0.19	Polyketide	granaticin	Streptomyces violaceoruber	
BGC0000234.1	1	0.19	Polyketide	jadomycin	Streptomyces venezuelae ATCC 10712	
BGC0001229.1	1	0.18	RiPP	SBI-06990 A1, SBI-06989 A2	Streptomyces bingchenggensis BCW-1	

CONCLUSION

□ All the isolates exhibited desirable probiotic characteristics like tolerance to gastric conditions such as pH, bile and 0.5% phenol.

L. paracasei LC 10 and LC 2 showed promising antimicrobial activity against Colistin resistant K. pneumoniae in vitro.

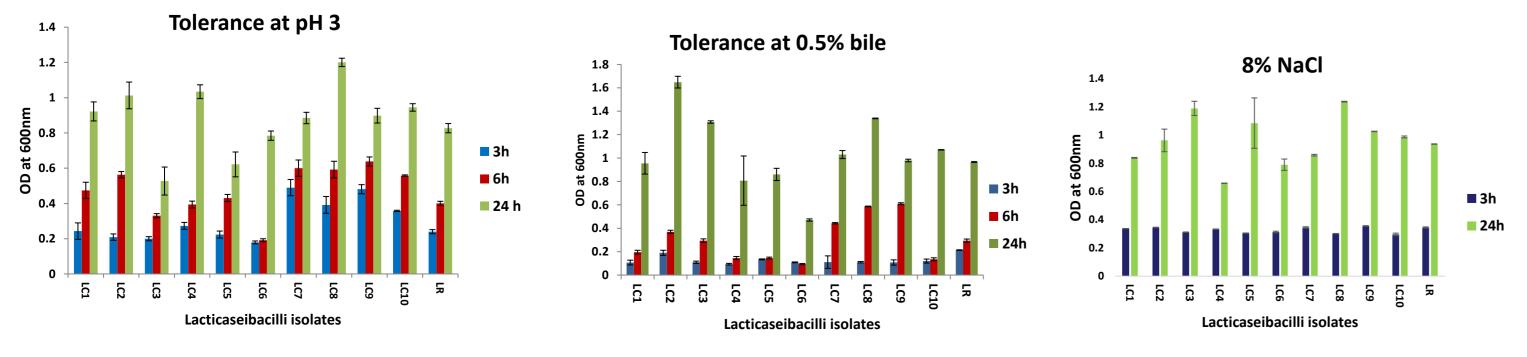


16 S rRNA Gene amplification: Lane M - 100bp ladder,

N-negative control, Lane 1–13-Lacticaseibacilli isolates

1500bp

INTER-Intermediate, RES-Resistant, SEN- Sensitive. AMP-ampicillin, Van-Vancomycin, CIP-ciprofloxacin, IMP-imipenem, MT-metronidazole, CTX-cefotaxime, GEN-gentamicin, TET-tetracycline, COL-colistin, MET-methicillin, C-chloramphenicol, E-erythromycin, AZM-azithromycin, LZ-linezolid



Representative image showing tolerance to acid, bile and sodium chloride L.rhamnosus ATCC 53103 was used as control strain

SEM imaging indicated morphological changes like pore formation on the cell surface of CFS treated K. *pneumoniae* which is similar to bacteriocin activity.

□ In vivo studies proved the administration of L. paracasei LC10 was effective in terms of pathogen reduction and improved histopathological changes in colistin resistant *K. pneumoniae* challenged mice. U Whole genome analysis of *L. paracasei* LC10 revealed that the strain is devoid of antibiotic resistance genes, plasmids and virulence genes and also predicted the presence of thermostable cyclic class II bacteriocin.

Key message:

Development of a probiotic formulation having prophylactic activity against colistin resistant *K.pneumoniae* is a promising strategy to tackle emerging AMR.

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