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EVALUATING THE ANTIBIOTIC POTENTIAL OF METABOLIC PEPTIDES DERIVED FROM *LACTOBACILLUS PLANTARUM* USING IN SILICO APPROACH

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SUMMARY

The increasing resistance of microorganisms to conventional antibiotics resulted in rising interest in the use of probiotic microorganisms and their antimicrobial metabolites as alternatives to antibiotics. Lactobacillus species are generally considered to be safe probiotic microorganisms. This study evaluated the antibiotic potential of metabolic peptides derived from *Lactobacillus plantarum* using computational methods. Genomic data on *Lactobacillus plantarum* with accession no. GCA_001434175.1 was retrieved from sequence raw archive of National Center for Biotechnology Information for analysis. Genome assembly was done using the database of Bacterial Viral Bioinformatics Resource Centre. Metabolic peptides were identified using antiSMASH server. Antimicrobial regions of the metabolic peptides were predicted using the database of Collection of Antimicrobial Peptides (CAMPR3). The antimicrobial regions were evaluated for antibiotic activity using the Antibiotic prediction server. The identified metabolic peptides were T3PK3, terpene precursor, terpene, RiPP-like and cyclic lactone- auto inducer. Various regions of the metabolic peptides indicated antimicrobial probabilities of 0.87, 0.78, 0.89, 0.95 and 0.97 respectively. Findings of this study demonstrated antimicrobial potential of metabolic peptides derived from Lactobacillus plantarum.

Keywords: *Lactobacillus; Metabolic peptides; Antibiotic potential and Computational methods*

INTRODUCTION

Public health threat posed by antibiotics resistance resulted in increasing interest in the use of probiotic microbes and their metabolites as alternatives to antibiotics (Dunne *et al.,* 2001). The use of antibiotics as growth promoters and disease prevention in the livestock industry contributed to the development of antimicrobial resistance (Mahizan *et al.,* 2019). Lactobacillus species are generally considered to be safe probiotic microorganisms. Antibiotics have been used extensively as growth promoters to improve performance and prevent infection in poultry industry; however, the practice increases the risk of emergence of antibiotic-resistant microorganisms (Khan *et al.,* 2024). Feed supplementation with probiotics is reported to effectively replaced antibiotics for improved productivity of livestock (Slizewsska, *et al.,* 2021).

Some diseases of the gastrointestinal tract have been attributed to compromised intestinal flora which can be remedied with probiotic microorganisms. Anti-microbial potential of lactobacillus strains against pathogenic microbes has been demonstrated (Parisa *et al.,* 2014). Probiotic supplementation has demonstrated improved weight gain, feed intake and feeding conversion ratio in broiler chickens. Probiotics are suitable alternatives to antibiotics due to their ability to modulate immune system, antibiotic activity and growth promoting factor (Arsene *et al.,* 2021).

The use of probiotics minimizes exposure to antibiotic residue in animal products and the environment thereby preventing the risk to public health. The use of probiotics as feed additives enhanced healthy gut micro flora and improved livestock productivity (Anee *et al.,* 2021). Positive effects on carcass weight and meat quality of sheep and goats have also been reported (Nie *et al.,* 2022).

The probiotic components and secondary metabolites of Lactobacillus strains have been identified, however, data on computational assessment of the antibiotic potential of the metabolic peptides are lacking. Therefore, the objective of this study is to evaluate the antibiotic potential of *Lactobacillus plantarum* derived metabolic peptides using silico approach.

MATERIALS AND METHODS

Data retrieval and genome assembly:

Genomic data on *Lactobacillus plantarum* with accession number GCA_001434175.1 was retrieved from the data base of National Centre for Biotechnology Information. Genome assembly was done using the database of Bacterial Viral Bioinformatisc Resource Center (BV-BRC). The analysis was done using the SRR run accession number and auto assembly option to obtain the fasta contiq of *Lctobacillus plantarum* as described by (Olson *et al.,* 2023).

Identification of metabolic peptides and antibiotic activity prediction:

The AntiSMASH server (Bacterial version 4) was used for identification of secondary metabolites as described by (Blin *et al.,* 2023). The contiq fasta file obtained from genome assembly was used for the analysis. CAMPR3 database was used to predict the antimicrobial potential of regions of protein sequence of the secondary metabolic. The prediction was done using the Support Vector Machine option (Waghu *et al.,* 2016). The Antibiotic potential of the protein sequence obtained from CAMPR3 was predicted using Anti-bacterial Prediction server as described by (Sneh *et al.,* 2007).

RESULTS AND DISCUSSION

The identified metabolic peptides derived from *Lactobacillus plantarum* are shown in Table 1. Antimicrobial regions within metabolic peptides derived from *Lactobacillus plantarum* are shown in Table 2. Predicted antibacterial activity of metabolic peptides are shown in Table 3.

The antimicrobial activity of *Lactobacillus plantarum* has been attributed to production of antimicrobial metabolites, the probiotic microbes also compete with pathogenic microorganisms for nutrients and attachment sites, thereby preventing colonization of the intestine by pathogenic microbes (Parisa *et al.,* 2014). The production of lactic and organic acids is also reported to play a significant role in the antimicrobial activity of Lactobacillus strains. Probiotic microbes increase the production of volatile fatty acids, nutrient digestibility and feed conversion ratio. Decrease colonization of gastrointestinal tract by pathogenic microbes have been demonstrated following use of probiotics thereby reducing environmental pathogenic pollutants. The growth of other GIT microbes is suppressed by probiotic microorganisms (Waters and Bassier, 2025). Lactobacillus strains have induced growth of beneficial microbes, secretion of antimicrobial agents and enhanced immune response (Yang *et al.,* 2025).

Terpenes and their derivatives have demonstrated potent antimicrobial activity exhibiting bacteriostatic and bactericidal action against pathogenic microbes (Mahizan *et al.,* 2019). Terpenoids are reported to exhibit antimicrobial action by inhibiting oxygen uptake and oxidative phosphorylation in microorganisms. RiPPs have demonstrated antimicrobial activity against a wide range of pathogenic microbes. RiPPS have been used in food industry to suppress spoilage and pathogenic bacteria, thereby extending shelf life and ensuring safety of products (Han and Won, 2024). Lactobacillus strains have been used extensively in the fermentation of foods and are generally regarded as safe.

CONCLUSION

Metabolic peptides T3PK3, Terpene precursor, Terpene, RiPP-like and Cyclic lactone auto inducer) were identified in the evaluated *Lactobacillus plantarum* strain. Antibiotic activity was demonstrated by various regions of metabolic peptides. This study demonstrated the probiotic potential of metabolites derived from Lactobacillus plantarum. The use of Lactobacillus strains as probiotic additives in livestock feeds is recommended.

Table (1): Metabolic peptides derived from *Lactobacillus plantarum* using antiSMASH server.

Metabolic peptides	Amino acid sequence
T3PK3	MKVGIDKLHFATSHLYVDMAELATARQAEPDKYLIGIGQSKMAVIPPSQDVVTLAANAAAPMLTATDIAAIDLLVVGTESGIDNSKASAIYVAKLLGLSQRVRTIEMKEAC YAATAGVQLAQDHVRVHPDKKALVIGSDVARYGLNTPGEPTQGGGAVAMLISADPKVLVLGTESSLLSEDVMDFWRPLYHTEALVDGKYSSNIYIDYFQDVFKNYLQ TTQTSPDALTALVFHLPYTKMGLKALRSVLPLVDAEKQAQWLAHFEHARQLNRQVGNLYTGSLYLSLLSQLLTDPQLQPGNRLGLFSYGSGAEGEFYTGVIQPDYQ TGLDHGLPQRLARRRRVSVAEYEALFSHQLQWRADDQSVSYADDPHRFVLTGQKNEQRQYLDQQV
Terpene precursor	MATKFHLSKLTPMNKQLLTEFESKWRPQINQYLDEQLQACSDQSTLTDAMRYSVLAGGKRLRPLLTLAILDTFDITTTAANLRASVAVELMHTYSLIHDDLPAMDNDQ LRRGEPTNHVKFGEDVAILAGDALQPLTFEWIADSGLPASIVANQTLALAQATGPRGMVAGQIADVLGAGQHLALPALQQLHREKTGALIHYAVQAGLIQAQVQPAVQ ELLLQYADAYGLAFQIYDDILDVTSTPAQLGKATHKDADEHKNTYPGLLGLAGARTALEQAVTAAQTALVKASAASQRGMGLLAAFLTYFTD
Terpene	MFYSFFDPTYLLVIIGLIISMAASGYVNRTFRHYDAYRSQSGTTGTDAARFILSQSGINDVGVQKISGDLTDNYNGQTKILSLSEATADSTSVAAIGVAAHECGHAVQDHVNYW PMRLRTALVPITNIGSSLSLPLIIIGVLLSYNQTLIHIGILLFSLALLFQLVTLPVEFNASRRALQILSDGQVLTRDEVPMVRKVLVAAALTYVAAALSTFLQLLRLIILFGGNRDDN
RiPP-like	MFPIYLYEDNAEQRDNYCKTVNNTIMINEFAMELRVATDDQKIILADLNQQQDGLFFLDMEIGEDKQTGLELASRIRATIPLAKIVFITTHDELSFVTLERRIAPLDYILKDQSADLITQRIIKDINVVQNE LKKTNSQRKDVFNYKLGTRYFSLALDDVILLSTSKLRPGSVQLHAINKVAEFPGNLNALEEKYPQFFRCDKSSLVNLNHLRSFDYKEKELLLDGEIRCKASFRKSRELNKLLRDN
Cyclic lactone – auto inducer	MEKPEQKLLLYKLSDRLFAAIQKNLQLERRQALLVKLGIDTVLNVIPKLIITIILALLLHELVPVLVFMGSFLVLRGFAYGRHLESDLLCTILTIFVFVGVPYVIGTGISE VYRLLLSLIFVIIISIFAPADTVKNPITSKSLRKKLKRRAIGLSLILSLLQIVSNNYFGTIILIAMALAALLLMPYERRENYERKNV

Table (2): Predicting antimicrobial regions within metabolic peptides using CAMR3.

Secondary metabolites	Position	Amino acid sequence	AMP PROBABILITY
T3PK3	81-100	GIDNSKASAIYVAKLLGLSQ	0.879
Terpene precursor	144-163	GLPASIVANQTLALAQATGP	0.778
Terpene	48-67	AARFILSQSGINDVGVQKIS	0.898
RiPP-Like	36-55	VATDDQKIILADLNQQQDGL	0.953
Cyclic lactone-auto inducer	151-170	AIGLSLILSLLQIVSNNYFG	0.975

Table (3): Predicting antibacterial peptides using Anti BP server.

Peptide	Score	Antibacterial activity
DNSKASAIYVAKLLG	0.99	Yes
PASIVANQTLALAQA	1.00	Yes
DDQKIILADLNQQQD	0.72	Yes

REFERENCES

Anee, I.J., Alam, S., Begum, R.A. and Khandakar, A.M. (2021). The role of probiotics in animal health and nutrition. *Journal of Basic and Applied Zoology*, 82(52): 3-16

Arsene, N.M.J., Davares, A.K.L, Andrewna, S.L. and Khilifi, I. (2021). The use of probiotics in animal feeding for safe production and as potential alternative to antibiotics. *Veterinary World*, 14 (2): 319-328

Blin, K., Shaw, S., Medema, M.H. and Weber, T. (2023). The AntiSMASH database version 4: Additional genome and BGCs new sequence-based scale and more. *Nucleic Acid Research*, 51 (1): 586- 589.

Dunne, C., Omahony, L. and Murphy, L. (2001). In vitro selection criteria for probiotic bacteria of human origin: Correlelation with in vitro findings. *The American Journal of Clinical Nutrition*, 73 (2):386-392

Han, S.W. and Won, H.S. (2024). Advancement in the application of ribosomally synthesized and post translationally modified peptides (RIPPs). *Biomolecules*, 14(4): 479

Khan, U., Rahman, S.M., Khan, S. and Hossain, K.M. (2024). Effects of probiotics on productive performance and serum lipid profile as substitute of antibiotics. *Science Progress*, 107(3): 1-23

Khan, a., Ahmed, T. and Muktar, N. (2024). Optimizing GUT health in the era of antimicrobial stewardship. *World Poultry Science*, 80: 1-20

Mahizan, N.A., Yang, S.K., Limoo, C., Song, A.A., Chang, C.M. and Lai, K.S. (2019). Terpene derivatives as a potential agent against antimicrobial resistance pathogens. *Molecules*, 24 (14): 263

Nie, C., Hu, Y., Chen, R. and Chen, H. (2022). Effects of probiotics and Chinese medicine polysaccharides on meat quality, muscle fiber type and intramuscular fat deposition in lambs. *Italian Journal of Animal Science*, 21 (1): 811-820

Olson, R.D, Rida, A., Thomas, B. and Rick, L.S. (2023). Introducing the Bacterial and Viral Bioinformatics Resource Centre. *Nucleic Acid Research*, 51(1): 678-689

Parisa, S., Chinchin, S., Ramasamy, K., Juan, B. and Yin, W.H. (2014). Probiotic potentialof Lactobacillus strains with antimicrobial activity against some human pathogens. *Biomedical Research International*, doi: 10.1155/2014/927268

Slizewska, K., Chlebiz, A. and Nowak, A. (2021). Probiotic properties of new Lactobacillus strains intehded to be useful as feed additives in monogastric animals. *Probiotics Antimicrobial Proteins*, 13: 146-162

Sneh, L., Sharma, B.K. and Reghava, G.P.S. (2007). Analysis and prediction of antibacterial peptides. *BMC Bioinformatics*, 8, 263

Waghu, F.H., Barai R.S., Gurang, P and Idicula, T.S. (2016). CAMPR3: a database on sequences, structures and signatures of antimicrobial peptides. *Nucleic Acid Research*, 44: 1094- 1997

Waters, C.M. and Bassier, B.C. (2025). Quorum sensing. Cell to Cell Communication in bacteria. *Annual Review of Cell and Developmental Biology*, 21: 319-346

Yang, L., Yang, W., Lin, J., Zhang, W. and Liu, R. (2025). Evaluation of probiotic properties and complete genome analysis of Lactobacillus bacteria isolates fromcrested ibis Nipponia Nippon feces. *Frontiers in Microbiology*, 16: 1-16