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Molecular and functional characterisation of lactic acid bacteria from Malabari goat milk

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Abstract

Malabari goats, a recognized breed native to Northern Kerala, India, represent a valuable yet underexplored source of autochthonous lactic acid bacteria (LAB) with potential applications in functional food development. This study aimed at the molecular and functional characterization of LAB isolated from raw Malabari goat milk. Raw milk samples collected from 20 animals in Wayanad district yielded 12 presumptive LAB isolates. Nine isolates were molecularly identified by 16S rRNA gene sequencing and found to belong to three species: *Lactiplantibacillus plantarum*, *Leuconostoc lactis*, and *Lactococcus lactis*. Among the isolates studied, two isolates, ADMG1 (*L. plantarum*) and ADMG10 (*Lactococcus lactis* subsp. *lactis*), demonstrated superior technological performance, including rapid milk coagulation, proteolytic activity, and exopolysaccharide production. These isolates were selected for evaluation of their probiotic characteristics. ADMG1 consistently demonstrated better acid tolerance at pH 3.0, stronger bile tolerance at 0.3% bile salts, and higher ACE inhibitory and cholesterol assimilation activities (23.81%) compared to ADMG10. Both isolates tolerated 0.5% pancreatin, exhibited bile salt hydrolase activity, showed moderate cell surface hydrophobicity (20–25%), and demonstrated appreciable DPPH free radical scavenging activity (44.85% and 40.09%, respectively). These findings help address a notable knowledge gap regarding the probiotic and technological potential of LAB associated with indigenous goat breeds in Kerala. The results highlight ADMG1 as a promising candidate for further development as a starter culture for fermented goat milk products with functional health benefits.

Keywords: Malabari goat milk, lactic acid bacteria, 16S rRNA, *Lactiplantibacillus plantarum*, probiotics, functional dairy

1. Introduction

Lactic acid bacteria (LAB) are beneficial microorganisms found in various environments, including milk, fermented milk, fruits, vegetables, and the intestinal tracts of humans and animals. They serve as starter cultures in food fermentations and as probiotics in functional foods. LAB encompass predominant genera such as *Lactococcus*, *Streptococcus*, *Enterococcus*, *Lactobacillus* and *Bifidobacterium*, displaying phylogenetic heterogeneity due to co-evolution with hosts from different taxonomic groups. The prevalence of LAB varies across microbiomes based on location and environmental conditions.

India, with the largest goat population globally, holds a significant share of goat milk production. Goat milk is recognized for its therapeutic properties and is rich in bioactive components with diverse beneficial activities^[1]. Despite this, there remains untapped potential for value addition to goat milk, such as through the production of fermented milk products and other functional derivatives. However, sensory acceptance and microbiological quality pose challenges, with the strong flavor of goat milk being a deterrent for many consumers. Traditional fermentation processes have been reported, involving diverse LAB in raw goat milk contributing to distinct sensory characteristics in fermented milks and cheese^[2]. Leveraging the diverse autochthonous microflora in goat milk as starter cultures presents an opportunity for developing novel functional foods.

The demand for goat milk has risen due to its health benefits and higher digestibility compared

to bovine milk. Goats are easily reared in limited spaces with minimal expense. Among the recognized goat breeds in India, the Malabari Goat, prevalent in Northern Kerala, stands out. The breed is small to medium sized with a milk yield of 0.5 -1 litre/day [3]. However, scientific knowledge regarding autochthonous LAB in Malabari goat milk is lacking. Therefore, data on the molecular and functional diversity of LAB in this breed's milk would be valuable for developing novel fermented milk products using autochthonous flora.

2. Materials and Methods

2.1 Isolation and characterisation lactic acid bacteria

Raw milk samples drawn from Malabari goats (n=20) in Wayanad district of Kerala were collected in sterile 50 ml containers and transported to the laboratory at 4 °C. The samples were serially diluted in normal saline and suitable dilutions were plated in De Man-Rogosa and Sharpe Agar (MRS Agar). The plates were incubated at 37 °C for 24-48 h. Spindle shaped sub surface colonies per sample reaching to a total of 20 colonies were selected and were screened for Gram staining, catalase and oxidase tests [4]. Only Gram positive, catalase negative and oxidase negative isolates were considered for further analysis. Cultures were preserved in MRS broth (Hi Media, Mumbai, India) supplemented with 30% (v/v) glycerol at -20 °C.

2.2 Evaluation of technological properties

Nine isolates of presumptive lactic acid bacteria were evaluated for milk coagulation, proteolytic activity and exopolysaccharide production. To determine the milk coagulation ability 1% (v/v) of culture was inoculated to sterile reconstituted skim milk and incubated at 37 °C for 24 h. After incubation, tubes were examined for coagulum formation. The cultures were screened for proteolytic activity in skim milk agar medium (2%w/v) [5]. Overnight grown culture (20µL) was placed on skim milk agar wells (diameter 8 mm) and incubated at 37 °C for 72h. Formation of a clear zone around the wells indicated proteolytic activity. For determination of lipolytic activity the lactic acid bacteria cultures were inoculated on agar spot of MRS supplemented with Tween-80 (5%). The plates were incubated at 35 °C for 72 h. The formation of an opaque area around the agar spot indicates lipolytic activity [6].

The ability of starter cultures to produce exopolysaccharides (EPS) by streaking cultures on to brain heart infusion agar containing sucrose (5% w/v) and incubated at 37 °C for 24 h. The formation of slimy and shining black colonies within 24 hours of incubation was suggestive of EPS production [7].

2.3 Molecular Characterization

Genomic DNA was extracted from overnight bacterial cultures using the GenElute™ Bacterial Genomic DNA Kit (Sigma – Aldrich, USA., Cat No. NA2110) following the manufacturer's instructions. DNA quantity and purity were assessed using a NanoDrop spectrophotometer.

Molecular identification was performed by amplification of the 16S rRNA gene using universal primers 27F (5' AGAGTTTGATCCTGGCTCAG 3') and 1492R (5' GGTTACCTTGTTACGACTT 3') [8]. PCR was carried out in a thermal cycler (Prima Trio, HiMedia) under the following conditions: initial denaturation at 94 °C for 3 min; 30 cycles of denaturation at 94 °C for 30 s, annealing at 55 °C for 45 s, and extension at 72 °C for 1 min; followed by a final extension at 72 °C for 7 min. Amplified products were

resolved on 1.5% agarose gel stained with ethidium bromide (0.5 µg/mL) and visualized under UV illumination.

PCR products were sequenced at GenSpec Pvt. Ltd., Kochi, India, and analyzed using BLAST against the NCBI GenBank database for species identification based on sequence similarity.

2.4 Evaluation of Probiotic Properties

2.4.1 Acid and bile tolerance

Acid tolerance was assessed by inoculating 1% overnight cultures into PBS adjusted to pH 1.5, 3.0, and 7.2 using 1N HCl. Cultures were incubated at 37 °C for 3 h, and growth was monitored by measuring OD at 600 nm at regular intervals [9]. For determination of bile tolerance overnight cultures (100 µL) were inoculated into MRS broth containing 0.3% and 0.6% bile salts, with bile-free MRS as control. Incubation was carried out at 37 °C for 4 h, and growth was assessed spectrophotometrically at 600 nm.

2.4.2 Pancreatin tolerance

Cultures (100 µL) were inoculated into MRS broth with and without 0.5% pancreatin and incubated at 37 °C for 48 h under shaking conditions. Growth was measured at 0, 24, and 48 h using OD at 600 nm [10].

2.4.3 Bile salt hydrolase (BSH) activity

BSH activity was determined using MRS agar supplemented with 0.5% taurodeoxycholic acid and CaCl₂ (0.37 g/L). Wells (8 mm) were loaded with 100 µL overnight cultures and incubated anaerobically at 37 °C for 24 h. Precipitation zones around wells indicated BSH activity.

2.4.4 Antioxidant activity (DPPH assay)

Cell-free supernatant (2 mL) was mixed with 2 mL of 0.2 mM DPPH solution and incubated in the dark for 30 min. Absorbance was recorded at 517 nm [11]. Ethanol served as blank and DPPH solution as control. Radical scavenging activity was calculated as:

$$\% \text{ inhibition} = (A_{\text{control}} - A_{\text{sample}}) / A_{\text{control}} \times 100$$

2.4.5 Cell surface hydrophobicity

Cells from 20 h cultures were washed in PBS and adjusted to OD₆₀₀. Suspension (3 mL) was mixed with 1 mL hydrocarbon (n-hexadecane or toluene), vortexed for 2 min, and allowed to separate for 1 h. OD was measured before and after phase separation [12].

$$\text{Hydrophobicity (\%)} = (\text{OD}_{\text{initial}} - \text{OD}_{\text{final}}) / \text{OD}_{\text{initial}} \times 100$$

2.4.6 ACE inhibitory activity

ACE inhibition was determined using hippuryl-histidyl-leucine (HHL) substrate and rabbit lung ACE [13]. Reaction mixtures containing substrate, buffer, and trichloroacetic acid filtrate were incubated at 37 °C for 30 min. The reaction was terminated with HCl, extracted with ethyl acetate, and hippuric acid was quantified at 228 nm.

$$\text{ACE inhibition (\%)} = 1 - (C - D / A - B) \times 100$$

Where,

A is the absorbance in the presence of ACE and without sample

B is the absorbance without ACE and sample

C is the absorbance with ACE and sample

D is the absorbance with the sample but without ACE

2.4.7 Cholesterol assimilation

MRS broth supplemented with 0.3% oxgall and 10% buffalo serum (60 mg/dL cholesterol) was inoculated and incubated at 37 °C for 24 h. Cholesterol was extracted from supernatant using ethanol–KOH–hexane–o-phthalaldehyde method and quantified at 550 nm ^[14].

$$\text{Cholesterol reduction (\%)} = (A_{\text{control}} - A_{\text{sample}}) / A_{\text{control}} \times 100$$

3. Results

3.1 Isolation of lactic acid bacteria from raw goat milk

A total of 12 isolates were presumptively identified as lactic acid bacteria (LAB) from raw goat milk samples. Of these, two isolates (ADMG1 and ADMG10) were Gram-positive rods, while the remaining ten were Gram-positive cocci. All isolates were catalase and oxidase negative, a defining characteristic of LAB. The absence of these enzymes reflects their microaerophilic or anaerobic metabolism and lack of reliance on oxygen as a terminal electron acceptor ^[15].

Regarding functional traits, eight isolates (ADMG1, ADMG2, ADMG3, ADMG4, ADMG5, ADMG8, ADMG10, and ADMG12) exhibited proteolytic activity, indicating their ability to hydrolyse casein and contribute to flavour development in fermented products. Such proteolytic LAB are also associated with the generation of bioactive peptides with antioxidant, antimicrobial, and anti-inflammatory properties, enhancing their value in functional dairy applications ^[16].

Exopolysaccharide (EPS) production was observed in six isolates (ADMG1, ADMG4, ADMG8, ADMG10, ADMG11, and ADMG12). EPS-producing LAB are important for improving texture, viscosity, and stability of fermented dairy products, and may also enhance bacterial survival during gastrointestinal transit, supporting probiotic functionality. Only two isolates (ADMG1 and ADMG10) demonstrated rapid milk fermentation within 12 hours, indicating strong starter culture potential. Morphologically, the presence of both Gram-positive cocci and rods aligns with earlier reports of LAB diversity in goat milk and traditional fermented products ^[17, 18].

Table 1: Technological characteristics of LAB from raw goat milk

Isolate No.	Proteolytic activity (zone diameter in mm)	Lipolytic activity Tween 80 (5%)	Milk coagulation	EPS Production
ADMG1	25mm	46 mm	+	+
ADMG2	23mm	36 mm	+	-
ADMG3	24mm	12 mm	+	-
ADMG4	30mm	30 mm	+	+
ADMG5	24mm	0	+	-
ADMG6	26mm	26 mm	+	-
ADMG7	23mm	25 mm	+	-
ADMG8	25mm	29 mm	+	+
ADMG9	26mm	41 mm	+	-

+ positive; - negative

3.2 Molecular characterization using 16S rRNA gene sequence

In the present study, 9 isolates were identified up to species level using a 1465 bp PCR amplified product of 16S rRNA gene sequence. Out of the 9 LAB isolates one showed 99%

sequence homology with the existing *Lactiplantibacillus plantarum*, 5 towards *Leuconostoc lactis* species and 3 *Lactococcus lactis* species reported in the NCBI. The NCBI accession number of the sequences is given in Table.2

Table 2: List of lactic acid bacteria identified by 16Sr RNA sequencing

Sl. No.	Strain name	Species identified	Accession no
1	ADMG1	<i>Lactiplantibacillus plantarum</i>	OQ931333
2	ADMG2	<i>Leuconostoc lactis</i>	OQ931336
3	ADMG3	<i>Leuconostoc lactis</i>	OQ931337
4	ADMG4	<i>Lactococcus lactis</i>	OQ931341
5	ADMG5	<i>Leuconostoc lactis</i>	OQ931342
6	ADMG6	<i>Leuconostoc lactis</i>	OQ931476
7	ADMG7	<i>Leuconostoc lactis</i>	OQ931777
8	ADMG8	<i>Lactococcus lactis sub sp lactis</i>	OQ931778
9	ADMG9	<i>Lactococcus lactis sub sp lactis</i>	OQ931781

Based on these results of technological and molecular characterisation, the isolates ADMG1 and ADMG10 were selected for evaluation of probiotic attributes.

3.3 Evaluation of probiotic attributes

3.3.1 Acid tolerance test and bile tolerance test

The ability of two selected isolates (ADMG1 and ADMG10) to grow at different pH conditions (pH 1.5, pH 3.0 and pH 7.2) was evaluated by measuring the optical density (600 nm)

of the isolates at 0 [th] hour, 1 [st] hour, 2 [nd] hour and 3 [rd] hours of incubation. Both the isolates exhibited pH tolerance at varying pH. The results are given in Table 3.

At pH 1.5, both the isolates were not able to tolerate acid. At pH 3.0, the isolate ADMG1 showed excellent growth up to three hours of incubation whereas no comparable growth was observed in the case of ADMG10 at all these hours. At pH 7.2, the isolate ADMG1 showed an increase in growth up to one hour and thereafter the growth decreased slightly.

Table 3: Acid tolerance of LAB strains at pH 1.5, 3.0 and 7.2

ISOLATES	pH	OD (0 h)	OD (1 h)	OD (2 h)	OD (3 h)
ADMG1	1.5	0.5834±0.015	0.5354±0.008	0.5564±0.002	0.5724±0.004
	3.0	0.6257±0.0003	0.7031±0.0003	0.8102±0.0014	0.8899±0.0003
	7.2	0.714±0.0002	0.9769±0.0003	1.0069±0.0005	0.9469±0.0002
ADMG10	1.5	0.5348±0.0005	0.4958±0.005	0.3753±0.003	0.4063±0.014
	3.0	0.1062±0.0002	0.1021±0.0002	0.0932±0.0004	0.0979±0.0002
	7.2	0.1137±0.0001	0.0969±0.0001	0.0692±0.0002	0.0888±0.0003

Acid tolerance is a key probiotic trait. At pH 1.5, ADMG1 showed a gradual decline in growth over 3 h, while ADMG10 exhibited a sharper reduction, indicating higher sensitivity to acidic conditions. At pH 3.0, ADMG1 maintained better growth than ADMG10, whose poor performance raises concerns about its survival in acidic fermentation environments. LAB capable of sustaining activity at low pH are preferred for probiotic and fermentation applications due to their role in flavour development, texture improvement, and preservation [19].

At neutral pH (7.2), both isolates showed positive growth trends, with ADMG1 demonstrating more consistent performance. Overall, ADMG1 displayed stronger acid tolerance across all pH conditions, suggesting better adaptability to gastrointestinal and fermentation environments. This supports findings by Tambekar and Bhutada [20], emphasizing that acid tolerance is crucial for probiotic survival through gastric transit and effective colonization.

The ability of the two selected isolates (ADMG1 and ADMG10) to tolerate bile salts at 0.3 per cent and 0.6 per cent levels were evaluated by measuring the optical density (600 nm) of the isolates at 0 [th] hour, 2 [nd] hour and 4 [th] hours of incubation. At both bile concentrations, the isolate ADMG1 showed comparatively higher tolerance to bile than the isolate ADMG10. The results are given in Table 4.

At 0.3 per cent bile concentration, the isolate ADMG1 showed good growth up to four hours ADMG10. Similarly at 0.6 per cent bile concentration, the isolate ADMG1 showed better growth up to four hours whereas the isolate ADMG10 showed no increase in growth.

Table 4: Bile tolerance of LAB at different bile concentrations

Isolates	Bile concentration (%)	OD (0 h)	OD (2 h)	OD (4 h)
ADMG1	0.3	0.061±0.004	0.406±0.051	0.6665±0.0175
	0.6	0.1565±0.0025	0.167±0.001	0.172±0.002
ADMG10	0.3	0.0325±0.0015	0.035±0.011	0.0705±0.0005
	0.6	0.1765±0.0005	0.17±0.001	0.177±0.002

At a bile concentration of 0.3 per cent, the isolate ADMG1 exhibited a gradual increase in growth during the incubation period. This notable growth suggests that the isolate ADMG1 possessed strong bile tolerance, which is critical for survival and activity in the gastrointestinal tract, where bile salts are present. Conversely, ADMG10 showed relatively lesser growth. At 0.6 per cent bile, both the isolates showed low growth performance. These results indicate a lack of metabolic activity or growth of LAB in the presence of higher bile concentrations. The ability of ADMG1 to maintain metabolic activity and promote growth in the presence of bile salts indicates its potential as a probiotic strain, which is in line with findings from Al-Saleh [21].

3.3.2 Pancreatin tolerance test

The ability of two selected isolates (ADMG1 and ADMG10) to tolerate pancreatin at 0.5 per cent concentration were evaluated by measuring the optical density (600 nm) of the isolates after 0 [th] hour, 24 [th] hour and 48 [th] hours of incubation at 37°C in a shaker incubator. Both the isolates showed growth during the incubation period with the isolate ADMG1 having better performance. The results are given in Table 5.

Table 5: Pancreatin tolerance of LAB (0.5% Pancreatin)

ISOLATES	OD (0 h)	OD (24 h)	OD (48 h)
ADMG1	0.072±0.002	1.089±0.002	1.0945±0.0005
ADMG10	0.054±0.001	0.7175±0.005	0.7205±0.0065

At 0.5 per cent pancreatin, both the isolates ADMG1 and ADMG10 showed consistent growth. Both the isolates showed a steady increase in growth upto 24 hours and thereafter remained stationary. This indicates that while pancreatin is highly effective in promoting substrate breakdown initially, the rate of degradation slows after the first 24 hours, suggesting a plateau in enzyme activity or substrate availability. The enzymatic activity of pancreatin is composed of proteases, lipases, and amylases and it allows for effective breakdown of complex molecules. The static growth after 24 hours may indicate a slowdown in enzyme efficiency as the substrates are being depleted. This aligns with Khagwal [10] who emphasized the importance of optimizing reaction conditions for maximal enzymatic activity.

3.3.3 Bile salt hydrolase activity

Bile salt hydrolase activity was done using agar well assay. Both the isolates ADMG1 and ADMG10 gave precipitation zones around the wells (Fig.1). The results are given in Table 6.

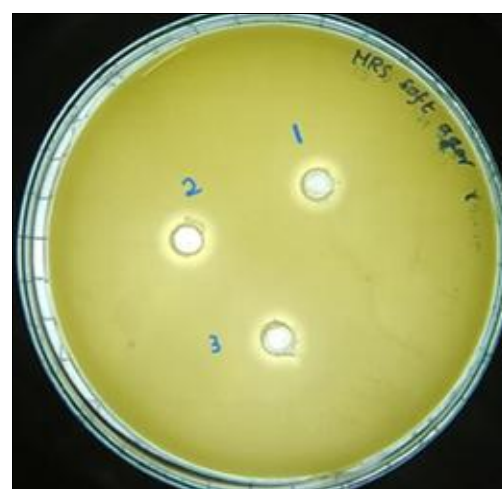
**Fig 1:** Zones of precipitation for BSH activity

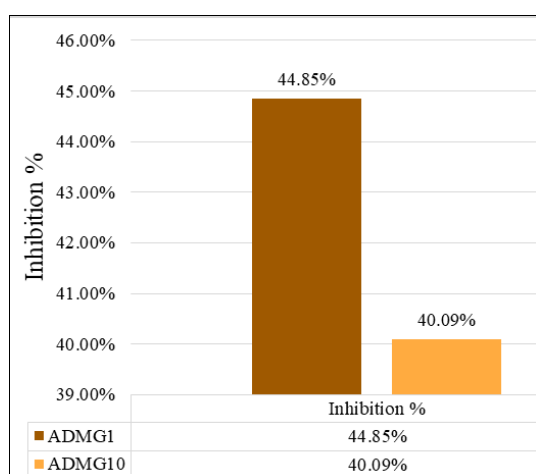
Table 6: Bile salt hydrolase activity of LAB

ISOLATES	BSH activity (zone in mm)
ADMG1	12±0.07
ADMG10	13±0.4

The zones of precipitation for both ADMG1 and ADMG10 are comparatively similar. Tanaka ^[22] explored the activity of bile salt hydrolases in 300 strains of LAB and reported a strong correlation between the habitat of a genus or a species and its bile salt hydrolase activity. He also observed that LAB from intestines and faeces have better bile salt hydrolase activity than those isolated from milk or vegetables. The similarity in the activity of the isolates may be attributed to their same niche from which they have been isolated.

3.3.4 Antioxidant potential

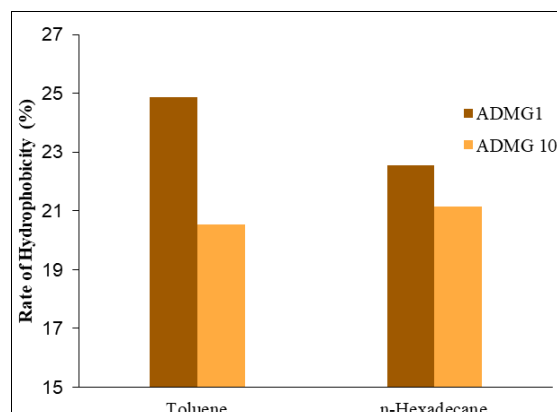
Antioxidant potential of the selected two isolates ADMG1 and ADMG10 were done using DPPH free radical scavenging assay. The isolates ADMG1 and ADMG10 showed an inhibition of 44.85 and 40.09 per cent respectively (Fig 2). The isolate ADMG10 showed more DPPH free radical scavenging activity compared to ADMG10. The production of bioactive compounds by LAB, such as phenolics or flavonoids are known to contribute to antioxidant properties ^[11]. Antioxidant properties of LAB are associated with several health protective effects ^[23].

**Fig 2:** Antioxidant potential of LAB

3.3.5 Bacterial adhesion to hydrocarbons

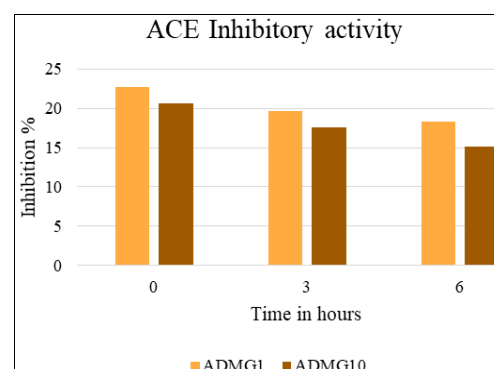
The test for bacterial adhesion to hydrocarbons of the two isolates ADMG1 and ADMG10 were done using two different hydrocarbons (n-Hexadecane and Toluene). The rate of hydrophobicity of the isolate ADMG1 against the n-Hexadecane and Toluene was found to be 22.558 per cent and 24.859 per cent respectively, whereas the isolate ADMG10 showed rate of hydrophobicity of 21.149 per cent and 20.539 per cent against n-Hexadecane and Toluene respectively (Fig 3). Both the isolates ADMG1 and ADMG10 showed moderate hydrophobicity, with ADMG1 demonstrating a slightly higher affinity for non-polar solvent (Toluene). Probiotics with adhesion rates to hydrocarbons between 20-30 per cent are considered moderately hydrophobic and have the potential for effective adhesion to host tissues ^[24]. Both ADMG1 and ADMG10 fall within this range, suggesting they may both possess adequate surface hydrophobicity to adhere to epithelial surfaces. However, the slightly higher hydrophobicity observed for ADMG1 with toluene indicates that it may have a more strong interaction with the intestinal

environment, possibly contributing to enhanced colonization and probiotic effects. This higher hydrophobicity may give ADMG1 a competitive advantage in probiotic applications, where adhesion to host tissues is crucial for providing health benefits such as immune modulation and pathogen exclusion ^[25].

**Fig 3:** Rate of hydrophobicity of LAB

3.3.6 ACE inhibitory activity

The ACE inhibitory activity of the two isolates ADMG1 and ADMG10 were done at zeroth, third and sixth hours of incubation. Both the isolates showed ACE inhibition at these intervals. At zeroth hour, the isolates ADMG1 and AGMG10 showed 22.675 per cent 20.63 per cent inhibition respectively. After three hours of incubation the inhibition potential of ADMG1 reduced to 19.6215 per cent and that of ADMG10, to 17.559 per cent. After six hours of incubation, the inhibition per cent of both the isolates showed reduction. The ACE inhibitory activity of ADMG1 and ADMG10 after six hours of incubation was found to be 18.3467 per cent 15.1185 per cent respectively (Fig 4). Both the isolates demonstrated more than 15 per cent inhibition throughout the testing period, with decreasing inhibition over time. ACE inhibitors are significant for their ability to regulate blood pressure by preventing the conversion of angiotensin I to the vasoconstrictor angiotensin II, and thus, strains exhibiting ACE inhibitory activity have potential applications in functional foods for cardiovascular health ^[26]. Throughout the testing period, ADMG1 consistently exhibited higher ACE inhibitory activity than ADMG10. This difference could be due to the specific proteolytic enzymes produced by the isolate ADMG1. The peptides generated by ADMG1 may have a higher affinity for inhibiting ACE compared to those produced by ADMG10. Certain lactic acid bacteria (LAB) are capable of producing bioactive peptides that exhibit ACE inhibitory properties ^[27].

**Fig 4:** ACE Inhibitory activity of LAB

3.3.7 Cholesterol assimilation

The cholesterol assimilation potential of both the isolates were calculated based on the reduction in cholesterol in the medium. The isolate ADMG1 showed a cholesterol reduction of 23.81 per cent whereas the isolate ADMG10 showed 22.095 per cent (Fig 5). The cholesterol reduction percentages for isolates ADMG1 (23.81 per cent) and ADMG10 (22.095 per cent) demonstrated that both isolates have a considerable ability to reduce cholesterol, with ADMG1 being slightly more efficient. The percentage reduction achieved by ADMG1 and ADMG10 align with findings from previous research, where different bacterial strains were shown to exhibit cholesterol-lowering capabilities through mechanisms such as assimilation of cholesterol during growth, bile salt deconjugation, and production of short-chain fatty acids [28]. Bacterial strains exhibiting higher bile salt hydrolase (BSH) activity were more effective in reducing cholesterol levels [29].

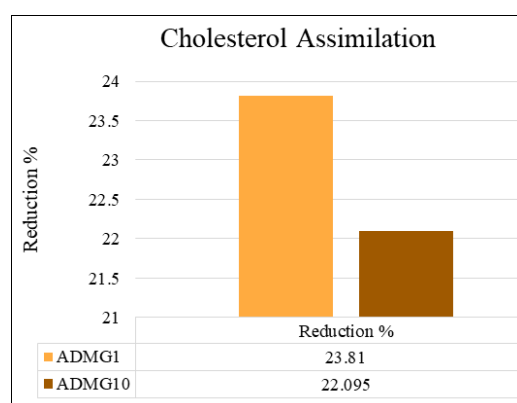


Fig 5: Cholesterol assimilation of LAB

4. Conclusion

This study documented the first characterization of autochthonous lactic acid bacteria (LAB) from raw Malabari goat milk in Northern Kerala. Twelve presumptive LAB isolates were obtained, and 16S rRNA gene sequencing identified nine isolates belonging to *Lactiplantibacillus plantarum*, *Leuconostoc lactis*, and *Lactococcus lactis*. Two strains, ADMG1 (*L. plantarum*) and ADMG10 (*L. lactis* subsp. *lactis*), were selected for detailed probiotic evaluation due to strong technological traits such as rapid milk coagulation, proteolysis, and exopolysaccharide production. Both isolates exhibited desirable probiotic characteristics, with ADMG1 showing superior performance. It tolerated acidic conditions (pH 3.0) and bile salts (0.3%), indicating good gastrointestinal survivability. Both strains tolerated pancreatin (0.5%) and exhibited bile salt hydrolase activity, suggesting potential roles in cholesterol metabolism. Moderate antioxidant activity was observed through DPPH scavenging, with ADMG1 (44.85%) outperforming ADMG10 (40.09%). Cell surface hydrophobicity (20–25%) indicated moderate adhesion potential. Both isolates also showed ACE inhibitory activity and cholesterol assimilation ability, with reductions of 23.81% (ADMG1) and 22.10% (ADMG10). Overall, ADMG1 demonstrated stronger functional and probiotic properties, making it a promising candidate for starter culture development in fermented Malabari goat milk products.

Conflict of Interest

Not available

Financial Support

Not available

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