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Relationship between incidence of probiotics and presence of pathogenic bacteria in milk products

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ABSTRACT

Milk and dairy products hold a prominent place in the Egyptian diet; however, their contamination by pathogenic microorganisms constitutes a significant public health concern. Bacterial contamination of fermented dairy items is particularly critical, as it compromises both the safety of the end products and facilitates the transmission of foodborne pathogens to the population. Therefore, this study was conducted for the investigation of the incidence of probiotic and potentially pathogenic bacteria in dairy products with a focus on the relationship between the presence of probiotic and pathogenic microorganisms. Ninety samples, including Rayeb, yogurt, and cheese, were analyzed. The samples were collected randomly from different localities in Assiut city, Egypt. All microorganisms were isolated in corresponding media, and the resulting colonies were purified through repeated subculture. They were preliminarily identified based on Gram staining, morphology, and biochemical tests. Molecular identification was then performed using PCR. The results obtained showed that the occurrence of *LactoBacillus*, *Bifidobacteria*, *Enterococcus*, *Salmonella*, *E. coli* and *S. aureus* was 60.0%, 33.3%, 30%, 05, 0% and 46.7% for Rayeb, 36.67%, 20%, 33.3%, 10%, 0 % and 26.7% for yogurt and 26.7%, 0%, 6.66%, 30%, 20% and 70% for Karish cheese. PCR screening revealed that Rayeb contained 66.67, 0, 0, 0, 0 and 37.5, and yogurt contains 36.36, 0, 0, 0, 0 and 0, and Karish cheese 54.54, 0, 9.5, 11.11, 16.67, and 0 for *LactoBacillus*, *Bifidobacteria*, MRSA, *Salmonella*, *E. coli*, and *Enterococcus*, respectively. Two representative lactic acid-containing samples from each product were sequenced, and sequencing revealed the presence of *Enterococcus faecium* strain R21 with accession number (PX661676) and *LactoBacillus plantarum* SN13T with accession number (PX661677) from Rayeb, *Bacillus cereus* Y3 with accession number (PX661678), and *Bacillus manliponensis* Y11 with accession number (PX661679) from yogurt, and *Weissella viridescens* K6 (PX661680) and *MetaBacillus halosaccharovorans* K7 with accession number (PX661681).

Introduction

Milk is a protein-rich and easily digestible food, with an abundance of minerals, energy, and bioactive components, including hormones, growth factors and vitamins such as riboflavin (Anema, 2020). Milk and dairy products have historically been recognized as fundamental components of a balanced diet due to their significant contributions of energy, protein, and essential minerals including calcium (Pereira, 2014; Tunick & Hekken, 2015). Research indicates that the consumption of milk and dairy products offers health benefits related to musculoskeletal development and the mitigation of various chronic conditions, including diabetes, hypertension, obesity, and certain cancers (Tunick & Hekken, 2015). Yogurt is a nutritious dairy food renowned for its significant health-promoting properties (Serafeimidou *et al*., 2012). Fermentation processes enhance the proliferation of beneficial microflora, including lactic acid bacteria (LAB), which has led to the belief that milk may serve as a biological preservative (Tesfaye *et al*., 2011). Furthermore, Karish cheese, recognized as a widely consumed dairy product in Egypt, is characterized by its low-fat content and its significant concentrations of calcium and protein (Todaro *et al*., 2013).

Pathogenic contamination of milk and dairy products is a critical determinant of food safety and public health (Shen *et al*., 2021). The ingestion of contaminated dairy products can lead to foodborne illness, presenting serious health hazards to consumers and contributing to substantial economic burdens (Kadariya *et al*., 2014). Disease outbreaks linked to dairy consumption are frequently attributed to a defined set of pathogens, notably *Escherichia coli*, *Salmonella* spp., O157:H7 *Listeria monocytogenes*, *Staphylococcus aureus*, *Campylobacter jejuni*, *Clostridium botulinum*, and *Brucella* spp. (Fox *et al*., 2016; Gould *et al*., 2014; Cummings *et al*., 2012).

One of the most common enteric bacteria in humans and warm-blooded animals is *E. coli*, which is frequently utilized as an indicator organism for fecal contamination (N'guessan *et al*., 2015). Its detection in cheese and raw milk is strongly linked to inadequate hygiene standards during production or handling (Ombarak *et al*., 2016). Although numerous *E. coli* strains are commensal, specific pathogenic variants are established etiological agents in foodborne disease. These include Verocytotoxin-producing *E. coli* (VTEC), notably serotype O157:H7, as well as enteroinvasive (EIEC), enterotoxigenic (ETEC), enteroaggregative (EAggEC), enteropathogenic (EPEC), and diffusely adherent (DAEC) *E. coli* (Baylis, 2009; Willis *et al*., 2022). *E. coli* is recognized as one of the predominant pathogens in foodborne outbreaks, associated with major health concerns ranging from symptoms like abdominal pain, vomiting, and diarrhea to severe conditions such as hemorrhagic colitis (FDA, 2024).

Moreover, research by Gould *et al*. (2014) identified *Salmonella* spp. as the pathogen most isolated from dairy products, demonstrating its highest prevalence (34%) in cheeses made from unpasteurized milk. Consumption of such raw milk cheese has been linked to disease outbreaks involving rare *Salmonella* strains (CDC, 2008; Van Cauteren *et al*., 2009), as well as with infections occurring at very low infectious doses (Van Duynhoven *et al*., 2009).

The nutrient-rich, neutral-pH environment of milk and dairy products renders them susceptible to contamination by *S. aureus* (Osman *et al*., 2020). Although *S. aureus* is a principal producer of thermostable enterotoxins, research indicates that at temperatures between 10°C and 25°C, it fails to generate enough Staphylococcal Enterotoxin C (SEC) to induce food poisoning (Valihrach *et al*., 2013). Notably, *S. aureus* can persist in raw milk through various stages of processing, subsequently contributing

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to a spectrum of infectious and foodborne illnesses (Shen *et al*., 2021).

In contemporary food science, functional dairy products have become a significant focus of research and development, largely due to their capacity to deliver enhanced nutritional and health advantages. Synbiotic dairy foods, which synergistically combine probiotics and prebiotics, are of particular interest. Their appeal stems from documented positive effects on host microbiota, metabolic functions, and immune function (Tadesse, 2012). The term probiotics refers to live microorganisms in low doses that can exert a favorable function on the host microbiota and health. The probiotic microorganisms comprise bacteria like *LactoBacillus*, *Bifidobacterium*, *Bacillus*, *Pediococcus*, *Lactococcus*, and yeasts of the genus Saccharomyces, which confer many health benefits to the host. Probiotics are live microorganisms that help to treat various pathologies, including Inflammatory Bowel Disease (IBD) (Ulcerative colitis and Crohn's disease), Constipation, Diabetes Mellitus (DM), Hypertension (HTN), Irritable Bowel Syndrome (IBS), and Diarrhea (acute antibiotic-related), and it also helps to treat allergic conditions (Hill *et al*., 2014).

Probiotic dairy products, such as yogurt, are associated with anticarcinogenic properties and exhibit antagonistic activity against various pathogens (Srilakshmi, 2018). Probiotics are defined as viable microorganisms, predominantly bacterial genera like *Bifidobacteria*, *Lactococci*, and *Lactobacilli* (Kerry *et al*., 2018). Among lactic acid bacteria (LAB), strains of *LactoBacillus*, *Streptococcus thermophilus*, and *Bifidobacterium*, are most utilized. Notably, *LactoBacillus* and *Bifidobacterium* strains are favored for their resilience to gastric acidity, pancreatic enzymes, and bile salts, as well as their ability to colonize the gastrointestinal tract and successfully adhere to the intestinal mucosa (Soccol *et al*., 2010).

This study aimed to investigate the incidence of probiotic and potentially pathogenic bacteria in selected dairy products (Rayeb, yogurt, and Karish cheese) collected from Assiut city, Egypt, and to evaluate the relationship between the presence of probiotic microorganisms and pathogenic bacteria using both conventional microbiological methods and molecular identification techniques (PCR and sequencing).

Materials and methods

A total of 90 random samples of Rayeb, Karish cheese, and Yoghurt (30 for each) were gathered from different supermarkets and shops in Assiut City, Egypt. During period from September 2024 to February2025 The collected samples were subsequently transferred in ice boxes to the Food Safety laboratory in Veterinary Medicine, Assiut University and kept for 48h in the refrigerator at 4°C till examined.

Isolation and identification of samples

One ml from Rayeb and yogurt or 1g from karish cheese was enriched in Tryptic Soya Broth or BPS (HI Media, India) (9 ml) and incubated at 37°C for 24 h. for *E. coli*, *Salmonella* and *Enterococci* and De Man Rogosa Sharpe (MRS) broth (9ml) for *LactoBacillus* and MRS with 0.25% L-cysteine for *Bifidobacterium* and incubated at 37ºC for 24 hours in Co2 incubator, then were cultured in cultural media prepared following the manufacturers instruction and sterilized as:

Mannitol Salt Agar (MSA) for isolation of *S. aureus*, later recognized by biochemical identification rendering to Quinn *et al*. (2002). MacConkey and Eosin Methylene Blue (EMB) for *E. coli* isolation, then affirmed by biochemical tests (IMVIC) as stated by Quinn *et al.* (2002).

MRS agar for *LactoBacillus* and incubated at 37ºC for 48 - 72 h in Co2 incubator. The emerged colonies were further purified and were subjected to biochemical and morphological characterizations (Soltan Dallal *et al*., 2016).

MRS agar with 0.25% L-cysteine for *Bifidobacteria* and incubated at 37ºC for 48-72 hours in Co2 incubator (Zinedine & Faid, 2007).

Salmonella Shigella (S.S.) agar for *Salmonella*, then incubation for 24 h at a temperature of 37 °C. Suspected *Salmonella* was subjected to biochemical tests (Cruickshank *et al*., 1975). *Enterococcus* was isolated on bile azide agar (Martin *et al*., 2005).

Molecular characterization of strains

Bacterial genomic DNA was isolated from overnight cultures by suspending several colonies in 300 µL of sterile deionized water. The suspension was boiled for 10 minutes in a water bath and subsequently centrifuged at 4000 rpm for 17 minutes. The resulting supernatant, containing the template DNA, was collected and stored at -20°C. Target gene amplification was performed via PCR using specific primers under optimized cycling conditions (Table 1). Amplification products were separated by electrophoresis on a 1.5% agarose gel (Applichem, Germany) using 1x TBE buffer at 5 V/cm. Gels were visualized and documented using an Alpha Innotech (Biometra) gel documentation system, and the data were analyzed with computer software (Ahmed *et al*., 2009).

Sequencing of the PCR product

PCR products were purified with a QIA quick PCR Purification Kit (Qiagen, Valencia). Bigdye Terminator V3.1 cycle sequencing kit (Perkin-Elmer) was used for the sequence reaction, followed by purification via Cen-

Table 1. Primer sequences, target genes, amplicon sizes and cycling conditions

Specificity	Primers sequences	Amplified segment (bp)	Primary Denaturation	Amplification (35 cycles)			Final extension	Reference
				Secondary denaturation	Annealing	Extension		
LactoBacillus (16s rRNA)	TGGAAACAGRTGCTAATACCG GTCCATTGTGGAAGATTCCC	232bp	95 ˚C 1min	95 ˚C 30sec	50 ˚C 1 min	65 ˚C 2min	72 ˚C 10min	Byun *et al*. (2004)
Bifidobacteria (16s rRNA)	GGGTGGTAATGCCGGATG CCACCGTTACACCGGGAA	523bp	94 ˚C 30sec	95 ˚C 30 sec	54 ˚C 1 min	65 ˚C 15 min	72 ˚C 10 min	Kok *et al*. (1996)
Salmonella (invA)	GTGAAATTATCGCCACGTTCGGGCAA TCATCGCACCGTCAAAGGAACC	284	94˚C 5 min.	94˚C 30 sec.	55˚C 30 sec.	72˚C 30 sec.	72˚C 10 min.	Oliver*et al*. (2003)
S. aureus (Nuclease gene)	GCGATTGATGGTGATACGGT AGCCAAGCCTTGACGAACTAAAGC	279	95ºC 5 min	95ºC 30 min	55ºC 30 sec	72ºC 1 min	72ºC 6 min	Brakstad *et al*. (1992)
MERSA (MecA)	AAAATCGATGGTAAAGGTTGGC AGTTCTGCAGTACCGGATTTGC	533	95ºC 3 min	94ºC 30 sec	55ºC 30 sec	72ºC 1 min	72ºC 6 min	Faisal (2019)
E. coli (stx1)	GAAGAGTCCGTGGGATTACG AGCGATGCAGCTATTAATAA	130 bp	95ºC 3 min	94 ˚C 20 sec	50 ˚C 20 sec	70 ˚C 12sec	72ºC 6 min	Pollard *et al*. (1990)
Enterococci (16s rRNA)	TACTGACAAACCATTCATGATG AACTTCGTCACCAACGCGAAC	112	94 ˚C 2 min	94 ˚C 15 sec	55 ˚C 15sec	72 ˚C 45sec	72 ˚C 5 min	Ke *et al*. (1999)

tri-Sep spin columns. Sequencing was conducted on an Applied Biosystems 3130 Genetic Analyzer (Hitachi, Japan). Initial sequence identity was assessed through a BLAST® analysis (Basic Local Alignment Search Tool) (Altschul *et al*., 1990) against GenBank accessions. Sequence alignments and identity determinations were carried out using Lasergene DNAStar software, version 12.1 (Thompson *et al*., 1994). Phylogenetic analysis was performed in MEGA7 (Tamura *et al*., 2013), employing maximum likelihood, neighbor-joining, and maximum parsimony methods.

Results

Bacterial and biochemical analysis

Samples collected were identified based on their cultural, microscopical, and biochemical properties (Table 2).

Molecular Characterization

PCR Amplification

All biochemically confirmed isolates were subjected to molecular detection using PCR (Table 3) and illustrated in Figures 1, 2, 3, 4 and 5.

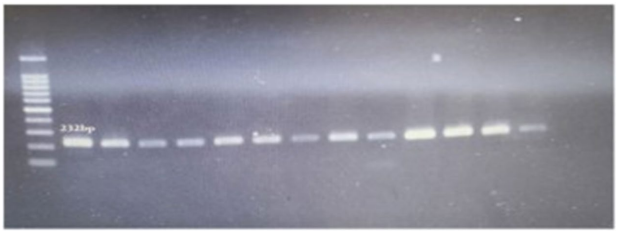

Figure 1. Agarose gel electrophoresis of the obtained PCR product of 16s rRNA.

Sequencing the PCR products

Two representative lactic acid-containing samples from each product were sequenced, and Sequencing revealed the presence of *Enterococcus faecium* strain R21 with accession number (PX661676) and *LactoBacillus plantarum* SN13T with accession number (PX661677), from Rayeb, *Bacillus cereus* Y3 with accession number (PX661678), and *Bacillus manliponensis* Y11 with accession number (PX661679) from yogurt, and *Weissella viridescens* K6 (PX661680) and *MetaBacillus halosaccharovorans* K7 with accession number (PX661681) as shown in Table 4.

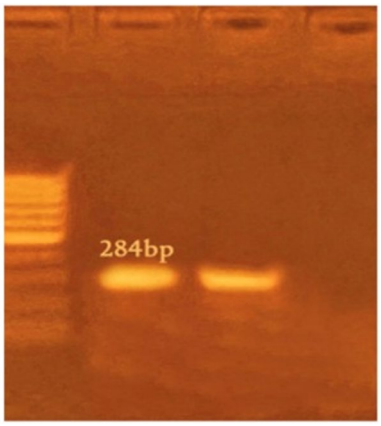

Figure 2. Agarose gel electrophoresis of the obtained PCR product for the *inv*A gene.

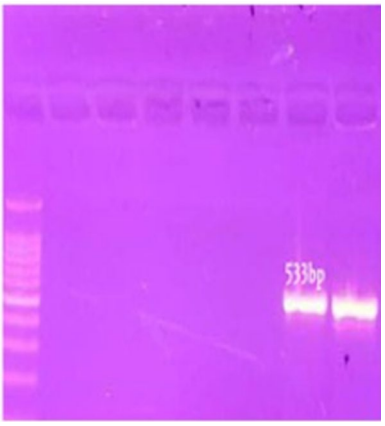

Figure 3. Agarose gel electrophoresis of the obtained PCR product for the *Mec*A gene.

Table 2. Percentages of microorganisms in dairy product samples.

The examined sample	Samples No.	Positive samples											
		LactoBacillus		*Bifidobacterium*		*S. aureus*		*Salmonella*		*E. coli*		*Enterococcus*	
		No	%	No	%	No	%	No	%	No	%	No	%
Rayeb	30	18	60	10	33.3	14	46.7	0	0	0	0	16	30
Yogurt	30	11	36.67	6	20	8	26.7	2	10	0	0	10	33.3
Cheese	30	11	36.67	0	0	21	70	9	30	6	20	2	6.66

Table 3. Molecular identification of the isolates.

	Lactic acid bacteria			*Bifidobacteria*			MRSA			*Salmonella*			*E. coli*			*Enterococcus*		
	No	+ve	%	No	+ve	%	No	+ve	%	No	+ve	%	No	+ve	%	No	+ve	%
Rayeb	18	12	66.67	10	0	0	14	0	0	0	0	0	0	0	0	16	6	37.5
Yogurt	11	4	36.36	6	0	0	8	0	0	2	0	0	0	0	0	10	0	0
Cheese	11	6	54.54	0	0	0	21	2	9.5	9	1	11.11	6	1	16.67	2	0	0

Table 4. Strains result from Sequencing the PCR products.

Type of sample	Strain	Accession number
Rayeb	*Enterococcus faecium strain R21*	PX661676
	LactoBacillus plantarum SN13T	PX661677
Yogurt	*Bacillus cereus Y3*	PX661678
	Bacillus manliponensis Y11	PX661679
Kariesh cheese	*Weissella viridescens K6*	PX661680
	MetaBacillus halosaccharovorans K7	PX661681

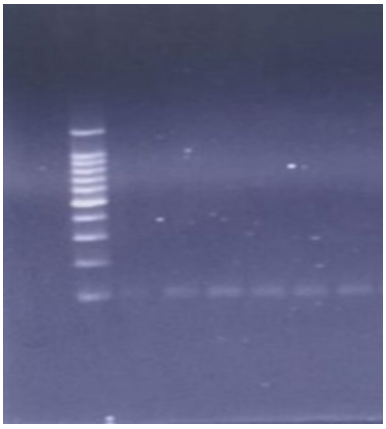

Figure 4. Agarose gel Electrophoresis of the PCR product for the *Enterococci* gene.

Figure 5. Agarose gel electrophoresis of the obtained PCR product for the *stx*1 gene.

Discussion

Analysis of 30 Rayeb samples revealed the presence of *LactoBacillus* in 18 (60%). This finding is consistent with the 68.1% reported by Soomro and Masud (2007) but is higher than the rates documented by Abd El Gawad *et al*. (2010) and Abd-Allah *et al*. (2024) (46.25%).

For yogurt, *LactoBacillus* was detected in only 11 out of 30 samples (36.67%). This result agrees closely with the 36.98% prevalence found by Samuel *et al*. (2016). However, it is lower than the figures from Abd-Allah *et al*. (2024) (46.67%), Bhattacharya and Das (2010) (50%), and Shruthy *et al*. (2011) (50%), while being higher than the 11% reported by Haghshenas *et al*. (2016).

Among cheese samples, 11 of 30 (36.7%) tested positive for *LactoBacillus*. This prevalence is lower than the 59.77% identified by Zommara *et al*. (2023).

All isolated strains displayed typical phenotypic characteristics of *LactoBacillus*: they were Gram-positive, catalase-negative, non-motile, and produced small, whitish-creamy colonies on MRS agar. These phenotypic identifications were subsequently confirmed by molecular analysis, as presented in Tables 2,3 and Figure 1. The overall prevalence rates observed in this study were lower than those reported by Ebrahim (2017) and lower than the results of Abd-Allah *et al*. (2024).

Table 2 shows that 6 out of 30 yogurt samples, (20%) contain *Bifidobacteria*. This result is lower than that of Ebrahim (2017), 54%. Out of 30 rayed samples, only 10 (33.3%) contain *Bifidobacterium*. Conversely, Ebrahim (2017) indicates that 60% of the rayeb samples give a positive result. All cheese samples gave a negative result, in contrast to Milani *et al*. (2019) and Zomorodi *et al*. (2011) who isolated *Bifidobacterium* from cheese.

The low prevalence of *Bifidobacteria* among the examined samples can likely be attributed to non-optimal manufacturing parameters. These conditions appear to compromise the microorganism's viability, leading to its low incidence in commercial products (Juliana, 2006).

Bifidobacterium spp., *LactoBacillus* viability in final products is influenced by a multiplicity of interrelated factors. Key determinants include the specific bacterial strain used, physicochemical conditions (such as pH, dissolved oxygen, and hydrogen peroxide levels), the accumulation of inhibitory metabolites like lactic and acetic acid, and post-production storage temperature (Shah & Ravula, 2000; Talwalkar & Kailasapathy, 2024).

Enterococci are prevalent in a variety of fermented dairy foods (Ogier & Serror, 2008). Among the species identified in milk products, *E. faecium* and *E. durans* are frequently reported (Franz *et al*., 1999). In this study, *Enterococcus* was isolated from rayeb, yogurt and cheese in percentages of 30, 33.3 and 6.66%. Due to the convergence of phenotypic characteristics between *Enterococci* and some species of lactic acid bacteria, such as *Lactococci*, reliance on biochemical and morphological analysis alone is insufficient. Thus, molecular identification serves as the confirmatory standard Table 3 and Fig. 4.

Dairy products constitute a favorable substrate for microorganisms, representing a public health hazard (Zakary *et al*., 2011). The contamination pathway is multifaceted, encompassing the animal, operational environments, utensils, additives, and personnel across the production continuum (Garedew *et al*., 2012). This microbial burden directly compromises shelf life, arising from a combination of the product's intrinsic physicochemical parameters and external contamination incurred during processing and packaging stages (Hosny *et al*., 2011).

The prevalence of *S. aureus* in the examined samples, as shown in Table 2, was 46.7% in rayeb, 26.7% in yogurt, and 70% in cheese. This result is lower than the rates reported by EL-Kholy *et al*., (2018), who isolated *S. aureus* from 72% of plain yogurt, 48% of fruit yogurt, 48% of rayeb, and 72% of mish samples, and by Abdulrahman and Sanmi (2021), who recovered the bacterium in 88% of samples, all of which were coagulase-positive. Conversely, a lower incidence of 26.6% was documented for Staphylococcus species in Karish cheese by Eid and Etalawy (2014).

The observed variation in the incidence of *S. aureus* across studies may be attributed to differences in geographic regions, farm management systems, hygiene standards, and sample sizes applied at farms and milk collection centers. The elevated level of *S. aureus* contamination in dairy products is primarily associated with environmental contamination, the use of low-quality raw milk, and inadequate hygienic practices by workers, including individuals who are ill or asymptomatic carriers, in addition to unsanitary conditions during production and marketing processes (Araujo *et al*., 2002).

The recorded result in Table 2 indicated the occurrence of *E. coli* 0, 0 and 20% in rayeb, yogurt and cheese, respectively. These results are lower than those obtained by Atef *et al*. (2017) in laban rayeb (55%) and yoghurt (40%), respectively, and those obtained by Elbastawesy *et al*. (2025) in yogurt (12.5%) and rayeb (7.5%), and higher than those recorded before by Hegab *et al*. (2020), and Abd El Latif *et al*. (2022) in yogurt but similar in rayeb. In contrast, a higher result was recorded by Elbastawesy *et al*. (2025) for cheese (14.3%).

The current study found no *Salmonella* in fermented milk products, a result consistent with several previous reports. For example, no *Salmonella* was detected in yogurt by Mohammed (2019) and Kamel *et al*. (2023), nor in Rayeb by Samet-Bali *et al*. (2016), Beukes *et al*. (2001), and Abdel-Rahman *et al*. (2009). In contrast, a higher prevalence of 10% (specifically *S.* Typhimurium) in yogurt was reported by Amin and El-Sherif (2018). According to El Bagoury *et al*. (2019), contrasting findings were reported, with no *Salmonella* species detected in samples of either Kariesh or Domiati cheese.

The reduced contamination rates observed in fermented dairy products may be strongly attributed to the protective activity of diverse probiotics and their metabolites, including organic acids, lysozymes, and bacteriocins (Cirat *et al*., 2024). This antimicrobial effect is notably apparent when comparing products like rayeb and yogurt, which harbor a complex consortium of probiotics against cheeses produced with a more restricted starter culture.

By Molecular confirmation, as shown in Table 3, this study indicates that higher levels of probiotic microorganisms (*LactoBacillus*, *Enterococcus*) are associated with a reduced prevalence of pathogenic bacteria (*S. aureus*, *E. coli*, *Salmonella*), highlighting their inhibitory potential. Such

interactions emphasize the role of probiotics in enhancing microbial safety and quality of dairy products. However, the absence of *Bifidobacteria* after molecular investigation indicates that other bacteria can grow in its selective media; therefore, sequencing of some PCR strains was done for randomly selected *LactoBacillus*-positive samples.

To avoid possible misclassification, genetic sequencing was used for reliable identification of LAB, which showed the presence of *Enterococcus faecium* and *LactoBacillus plantarum* in two randomly selected rayeb samples. These genera, along with *Streptococcus* and *Micrococcus*, are recognized as common bacterial constituents of milk (Richter *et al*., 1992; Kim *et al*., 2000; Chye *et al*., 2004).

The recorded result in table 4 showed two randomly selected yogurt samples underwent further analysis, revealing the presence of *Bacillus cereus* in one, which is unpredictable, and *Bacillus manliponensis* in the other. The latter has been identified as a novel member of the *Bacillus cereus* group (Jung *et al*., 2011) and is employed as a probiotic in animal feed and as a food additive, including in dairy applications. Interest in *Bacillus* spp. for functional foods has grown due to their resilience, notably their ability to survive harsh gastrointestinal conditions and remain stable during food processing, storage, and in pharmaceutical formulations. Sequencing confirmed the presence of *Weissella viridescens* in Karish samples. This species is recognized as an opportunistic pathogen implicated in celiac disease and human bacteremia (Kulwichit *et al*., 2007; Kamboj *et al*., 2015). Despite its prevalence in fermented foods, it remains a documented, though infrequent, cause of sepsis (Sharma *et al*., 2018). Additionally, *MetaBacillus halosaccharovorans* was identified in a Karish sample, corroborating a prior finding in camel milk (Drici *et al*., 2025). As extremotolerant, spore-forming bacteria, Meta*Bacillus* species likely enter the production chain via environmental contamination, and their spores present a processing challenge due to their heat resistance (Patel & Gupta, 2020).

Conclusion

This study concludes that selected probiotic strains effectively inhibit pathogenic bacteria in dairy products through competitive exclusion and antimicrobial compound production. Their efficacy is influenced by strain specificity, product matrix, and storage conditions. While promising for enhancing food safety, further in situ and clinical research is needed to optimize applications and validate direct health benefits. Ultimately, integrating probiotics offers a natural strategy to boost the microbiological safety and functional value of dairy products.

Conflict of interest

The authors have no conflict of interest to declare.

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