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**EVALUATION OF BACTERIOCIN ACTIVITIES AMONG ENTEROCOCCAL DAIRY
ISOLATES FROM NORTH-WEST IRAN**

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ABSTRACT

The objectives of the study were to isolate and characterize the bacteriocin producing enterococci in 100 enterococcal dairy isolates from north-west of Iran and to determine the prevalence of enterocin structural genes among them. The obtained isolates were assessed for antibacterial action against 6 indicator strains. The PCR method was applied to detect previously identified enterocin genes. Our results showed that 11 (11%) of enterococcal isolates were considered as potential bacteriocinogenic strains. Furthermore, genes encoding diverse bacteriocins are fairly distributed among dairy enterococci. Enterocin A, enterocin LA50A/B and cytolysin were the most abundant structural genes detected in bacteriocinogenic strains. This work is the first survey on the prevalence of bacteriocin genes among dairy enterococci in Iran.

Keywords: Prevalence, Genes, Bacteriocin, Enterococci, Dairy

INTRODUCTION

Antimicrobial peptides (AMPs) produced by a variety of microorganisms are of great importance as novel antibacterial alternatives

(Haynes et al. 1999; Overbye and Barrett 2005) to combat antibiotic resistant bacteria (Johnson et al. 1999; Cornelis 2008). A

probiotic by producing antimicrobial agents such as organic acids and bacteriocins can avoid pathogens to infect the intestinal tract. Bacteriocins have bactericidal or bacteriostatic action against bacteria closely related to producer strains (**Jack et al. 1995; Nes et al. 2007a; Shin et al. 2008**).

The bacteriocins encompass a number of properties which make them exceptional candidates for becoming a new generation of antimicrobials, (i) their high potency, (ii) the narrow inhibition spectrum of some AMPs and their potential to develop pathogen-specific compounds (iii) yet other AMPs have broader activity spectra and can be applied in more common approaches, (iv) The high stability to many proteases, high temperature and pH variation, and (iv) the AMPs are open to bioengineering, leading to develop novel variants of the antimicrobials by peptide synthesis or DNA recombinant technology.

Overall, Bacteriocins are categorized into three main groups (**Klaenhammer 1993; Nes et al. 1996**). Class I or lantibiotics (from lanthionine-containing bacteriocins) consist of small post translationally modified peptides (<5 kDa) and have the unusual amino acids lanthionine and methyl-lanthionine (**Guder et al. 2000**). Class II include small (<10 kDa) heat-stable membrane active peptides which are the largest and most diverse group of

bacteriocins among Gram-positive bacteria. They are typically cationic and amphiphilic and/or hydrophobic (**Nes et al. 1996**) which are further subdivided into three subclasses (**Klaenhammer 1993**): Class IIa consists of pediocin-like peptides with a strong antibacterial activity against listeria and enterococci (**Ennahar et al. 2000**). Class IIb are included the bacteriocins whose their optimal action is rely on the action of two different peptides (**Oppegard et al. 2007**). Other bacteriocin subgroups are the leaderless peptide and the circular bacteriocin (**Nes et al. 2007a**). Class III bacteriocins or bacteriolysins are big in size (>30 kDa) and heat-labile proteins (**Cotter et al. 2005; Drider et al. 2006**).

Biosynthesis of bacteriocins generally requires four types of genes, and these are often found in the same genetic locus: (1) the structural gene(s) encoding the bacteriocin itself (2) an immunity system. The AMP producer needs to encode an immunity mechanism to keep away from being killed by its own AMP. (3) A transport system. To be active outside the cell, the AMPs should be exported across the cell envelope. 4) Genes in charge for post-translational modifications (PTMs).

The mode of action of bacteriocins differs deeply between peptides, and is often

different from classical antibiotics. In general, the bacteriocins can eradicate sensitive bacteria by two methods; in the first mechanism, they may target the cell envelope by producing pores or hindering cell wall biosynthesis. In the second method, they may act intracellularly to inhibit essential enzymatic/metabolic processes such as DNA synthesis, transcription and translation which are found only among Gram-negative bacteriocins. Conversely, both Gram-negative and Gram-positive bacteriocins are targeting the cell envelope by permeabilizing the membrane or affection the cell wall.

Enterococci from lactic acid bacteria have a significant position in human and animal health both as nosocomial pathogens and potential probiotics (Russell and Mantovani 2002; Foulquié Moreno et al. 2006; Poeta et al. 2006). Their pathogenicity arises from virulence factors such as cytolysin, gelatinase, aggregation substance, extracellular surface proteins and other adhesions. Furthermore, they can harbor multiple antibiotic resistant genes and spread resistance to other bacterial strains which is another worry with regard to use of enterococci in food fermentation or as probiotics (Franz et al. 1999; Semedo et al. 2003; Poeta et al. 2006). Most of the characterized bacteriocins from *Enterococcus* spp. belong to the group II bacteriocins.

Bacteriocinogenic strains from Iran, especially of *Enterococcus* species, are poorly described. In our previous work, we performed a survey on the prevalence of bacteriocins of *Enterococcus* spp. isolates originated from different clinical samples in North-Western Iran (Hassan et al. 2012). In the present study we aimed to investigate the prevalence of *Enterococcus* spp. isolates from dairy products of North-Western region of Iran. The antibacterial activity of the isolates, physicochemical characteristics and presence of bacteriocin genes as well as presence of certain virulence genes and antibiotic resistance pattern of bacteriocin producers have also been studied.

MATERIALS AND METHODS

Isolation and Phenotypic Characterization of the *Enterococcus* Genus

Enterococci were identified according to Manual of Clinical Microbiology (Murray et al. 2003) as follow: Milk samples collected from industrial dairy farm of West Azerbaijan provinces of Iran during 2012 to 2014 were inoculated in 20 mL of Bile Esculin Broth for 24 h at 37 °C. Then, 20 µL of cultures which had turned black as a result of growth of the enterococcal cells, were collected and plated onto Bile-Esculin sodium azaid agar. Following the incubation at 37 °C single black colonies were collected and kept in 30%

glycerol at -20 °C as well as -80 °C as stocks. The isolates were also subjected for enterococcal phenotypic characterization tests. Growth at 10 °C and 45 °C for 7 days, growth in modified Brain Heart Infusion broth (BHI, Scharlau, Spain) at apparent pH 4 and 9 containing 6.5% NaCl and Esculin hydrolysis in the presence of 40% bile salts (bile-Esculin agar, Scharlau Spain) were examined. Strains were also tested for survival at 60 °C for 30 min (Abriouel et al. 2005; Line et al. 2008).

Screening for Anti-Bacterial Activity of Enterococcal Isolates

The inhibitory activities of the isolates against a group of indicator strains (listed in **Table 1**) were evaluated by agar spot method (**Venema et al. 1995c**). Brain Heart Infusion broth (Oxoid, Hampshire, England) supplemented with 1.5% agar (Bacto) as well as 5 mL of BHI agar 0.7% was applied as base and top agar respectively. The top agar medium was inoculated with 20 µL of an overnight culture of indicator microorganisms. The different indicator strains used for the assessment of inhibitory activity included *Staphylococcus aureus*, *Bacillus cereus*, *Escherichia coli*, *Listeria monocytogenes*, *Enterococcus faecalis* and *E. hirea*. The strains were obtained from PTCC (Persian Type Culture Collection). A single colony of each

Enterococcus spp. clinical isolates was spotted onto a previously seeded agar plate. Subsequently, plates were incubated at 30 °C in an upright position. Isolates that showed clear zones of growth inhibition wider than 6 mm were scored positive as potential bacteriocin producers (Bac⁺) and selected for further studies. Inhibitory activity of antimicrobial substances in supernatant was measured by using a microtiter plate assay, as described previously (**Fimland et al. 2000**). *E. hirea* were applied as indicator microorganisms during the bacteriocin activity assay.

Genotypic Differentiation of Enterococcal Isolates by PCR

Total DNA was extracted by using QiaPrep MiniPrep kit (Qiagen) according to the manufacturers' protocol. The isolated DNA was used for PCR (Polymerase Chain Reaction) template in the genotypic identification. The target strains were genotyped by 16S rDNA using *Enterococcus* specific and species-specific primers (**Ke et al. 1999; Kariyama et al. 2000**) which are listed in **Table 2**. PCR amplification for genotypic identification of the isolates performed in 25 µL of reaction mixture containing 1 µL of each primer set, 5 µL of 10 × PCR buffer (Cinnagen), 2.5 mmol of MgCl₂, 1 U of *Taq* DNA polymerase 5 U/mL

(Cinnagen), and 200 μmol of each deoxyribonucleoside triphosphate (Cinnagen). Deionised sterile water and DNA extracted from known *Enterococcus* species substituted as the DNA template as the negative and positive controls in each PCR reaction. PCR amplifications were performed with the following thermal cycling profile, 4 min at 95 °C and followed by 35 cycles consisting of: a denaturation step for 45 s at 95 °C, annealing for 30 s at 60 °C (for universal), 54 °C (for *Enterococcus*-specific primers), 56 °C (for species-specific primers) and extension for 1 min at 72 °C, followed by a single 5 min final extension step at 72 °C (Eppendorf AG, Hamburg, Germany). The PCR products were analyzed by 1.5% agarose gel electrophoresis (Bio-Rad Power Pac Basic Singapore) which was set at 70 V for 45 min in Tris-Acetate-EDTA (TAE) buffer. The gel staining procedure was 15 min in 0.5 $\mu\text{g/mL}$ of ethidium bromide visualized by ultraviolet light (312 nm) with (RAPD PCR).

Detection of Bacteriocin Genes by PCR

Total DNA extracted from potential Bac⁺ isolates (as previously described) was applied as template for PCR to search the presence of bacteriocin genes previously found between enterococci. The specific primer sets of enterocin A (*entA*), enterocin B (*entB*), enterocin P (*entP*) (du Toit et al. 2000),

bacteriocin 1071 (*bac1071*), enterocin L50A/B (*entL50A/B*), enterolysin A (*enlA*), cytolysin (*cyl*) (Solheim et al. 2009), bacteriocin 31 (*bac31*), bacteriocin AS-48 (*bacAS-48*) (De Vuyst et al. 2003, Brandao et al. 2010) are shown in Table 2. PCR assay was performed using the primers (Table 2) and DNA templates in 25 μL reaction volume that contained 12.5 μL 2x PCR Master Mix (Cinnagen), 1 μL of each primer, 1 μL of template DNA and 10.5 μL water. Cycling parameters included 4 min initial denaturation at 94 °C, followed by 40 cycles of 45 s at 95 °C, 30 s at 56 °C (for *entP*, *bacAS-48*, *bac31* and *entL50A/B*), 58 °C in the case of (*entA* and *entB*), 60 °C (for *entB*, *bac1071*, *cyl* and *enlA*) as annealing temperature, and 35 s at 72 °C; this was followed by 10 min at 72 °C. Amplified PCR fragments were resolved on 1% agarose gels. Specific enterocin sequences were verified by PCR product sequencing.

Hemolytic Activity Assay

The hemolytic activity of enterococcal isolates was assessed using blood agar supplemented with 5% (v/v) horse blood. Fresh cultures of the isolates were streaked onto the plates and incubated at 37 °C for 48 h. The colonies with distinct lysis zones, and partial lysis (greenish zones) considered as β -hemolytic and α -hemolytic respectively, and no reaction produced γ -hemolysis.

PCR Screening of Virulence Genes and Assessment of Antibiotic Resistance

Strains with detectable antimicrobial activity were further screened by PCR for the presence of virulence genes: *ace* (collagen adhesion) (Dupre et al. 2003), *agg* (aggregation substance), *esp* (enterococcal surface protein) and *gelE* (gelatinase) (Eaton and Gasson 2001). PCR primers and their amplification products are listed in **Table 2**.

Also soft agar overlay disc diffusion method was used to determine antibiotic susceptibility of Bac⁺ isolates according to National Committee for Clinical Laboratory Standards (NCCLS 2003). The antibiotic-containing disk (Himedia) used was vancomycin (30 µg).

RESULTS AND DISCUSSION

Isolation and Phenotypic Identification of the Enterococcal Strains

100 dairy isolates was phenotypically classified as *Enterococcus* spp., according to the results of the identification experiments. They are shown to be Gram-positive, non-motile, catalase negative cocci. They grew in modified BHI media containing 6.5% NaCl in the temperature of 10 °C to 45 °C for up to 7 days and endured in buffered media at pH 4 and 9. All isolates were able to hydrolyze Esculin in the presence of 40% bile salts (Murray et al. 2003).

Screening of the Inhibitory Activity of Bacteriocin-like Substances

Isolates of *Enterococcus* spp. were assessed for production of antimicrobial substances. Eleventh of 100 enterococcus isolates (11%) showed antimicrobial activity by producing a clear growth inhibition zone on BHI agar against at least one of the indicator strains.

All of the detected Bac⁺ isolates had antibacterial activities against *E. coli*, *B. cereus*, *L. monocytogenes*, *E. faecalis*, with no activity against *E. hirea* (**Table 3**).

All of the detectable antimicrobial activities were produced only on the solid surfaces (agar plates) and no antimicrobial activity could be found in broth medium after growth (**Table 3**). Similar observations regarding the antimicrobial activity on solid and liquid media have also been reported in previous studies (Qi et al. 2001; Brandao et al. 2010). These conflicting findings might be explained by the effect of growth conditions such as pH, medium composition and temperature on regulation of bacteriocin production (Cintas et al. 2000; Qi et al. 2001; Rojo-Bezarez et al. 2007) as well as frequent involvement of bacteriocin-like peptides which can act as peptide pheromone in the quorum-sensing regulatory mechanism of bacteriocin gene expression (Coburn et al. 2004; Nes et al.

2007a; Sturme et al. 2007; Lebeer et al. 2008) might explain these conflicting results.

Genotypic identification of enterococcal isolates by PCR

Genus and species identification was accomplished by PCR using the universal bacterial 16S rDNA, *Enterococcus* genus and species specific primers. 6 out of 11 Bac⁺ enterococcal isolates were identified as *E. faecalis* and the rest of isolates were *E. faecium* (Figure 1). These results are in good agreement with some previous studies which show that in *Enterococcus* isolates, the bacteriocinogenic phenotype was more dominant in isolates of *E. faecalis* than *E. faecium* (del Campo et al. 2001; De Vuyst et al. 2003). However, there are other research (Solheim et al. 2009) showing that most of bacteriocin producing enterococci among healthy babies are *E. faecium*.

Screening of Structural Bacteriocin Encoding Genes in Enterococcal Isolates

The isolates with positive antibacterial activity on agar spot test were screened by PCR for the genes encoding the known bacteriocins. The results are shown in Table 4. *EntA* were found as the most frequent gene encoding bacteriocins, at an incidence of 100% among bac⁺ strains (Fig 2). Also *entL50A/B* (87%) and *cyl* (67%) were detected frequently. Interestingly, *entB*, *entP*,

bac31, *bac1071* and *bacAS-48* were not detected in any of the Bac⁺ isolates.

The PCR results (Table 4) suggest that all of Bac⁺ isolates contained multiple structural bacteriocin genes. Two different structural genes were found in seven (7 of 11) isolates while three genes were found in five isolates. Amongst the multi-bacteriocin gene isolates *entA* was the most frequent at 100% (all of the Bac⁺ isolates).

According to results of earlier studies the structural gene *entA* is widely distributed in ruminal enterococci (Morovsky et al. 2001; Nigutova et al. 2007). Our results indicate that the incidence of *entA* and also *entL50A/B* are frequently found in enterococcal isolates from dairy origin and are in line with these findings. Additionally, according to our previous study, same genes of bacteriocin have been found in human blood and fecal derived enterococci; it is rational to believe that because of the extensive distribution of enterococcal contamination in nature they are likely derived from the same environment and most probably from intestine of various animals (Hassan et al. 2012).

Interestingly, the cytolysin structural gene was detected in 45.5% and 27.2% of *E. faecalis* and *E. faecium* isolates, respectively (Table 4). Our results approve previously published studies that showed the presence of

the gene encoding cytolysin in *E. faecalis* as well as *E. faecium* (De Vuyst et al. 2003; Theppangna et al. 2007; Poeta et al. 2008). As the cytolysin structural gene was initially found in clinical isolates of *E. faecalis* (Booth et al. 1996) it is most probable that this plasmid-encoded toxin may have been moved between two strains. Although the cytolysin gene was often found in our *E. faecalis* and *E. faecium* isolates, only three of eleven isolates exhibits the β -hemolytic activity. According to recent investigations, expression of cytolysin is affected by diverse factors such as expression regulation by a quorum-sensing mechanism (Haas et al. 2002) and/or oxygen conditions (Day et al. 2003) and our results can be explained based on this evidence.

ace (collagen adhesion) (Dupre et al. 2003), *agg* (aggregation substance), *esp* (enterococcal surface protein) and *gelE* (gelatinase)

Virulence Factors and Antibiotic Resistance Pattern of Enterococcal Isolates

The presence of genes coding five virulence factors was evaluated by PCR for the Bac⁺ strains. Interestingly, aggregation substance (*agg*) and enterococcal surface protein (*esp*) genes were detected in all of the isolates except C6 (Figure 3). Only *E. faecium* M15 contains gelatinase *gelE* while (collagen adhesion) *ace*, aggregation substance (*agg*) and Cell wall adhesion genes were not detected in any of the screened isolates. *E. faecium* C6 was the only isolate not to contain the tested virulence genes.

The antibiotic resistance phenotype of all Bac⁺ strains with antibacterial activity was tested. As expected all of the candidate strains were resistant to vancomycin.

The presence of multiple virulence factors in enterococcal isolates accompanied by the antibiotic resistance is a great worry about the human health (Semedo et al. 2003; Kayaoglu and Orstavik 2004; Sood et al. 2008).

Table 1: Indicator bacteria used agar spot test

<i>Staphylococcus aureus</i> PTCC [§] 1112
<i>Listeria monocytogenes</i> PTCC 1249
<i>Bacillus cereus</i> PTCC 1015
<i>Escherichia coli</i> PTCC 1533
<i>Enterococcus faecalis</i> PTCC 1237
<i>Enterococcus hirae</i> PTCC 1239
[§] PTCC= Persian Type Culture Collection

Table 2: PCR primers for detection of bacteriocin genes used in this study

Primer	Sequence (5'-3')	Fragment size(bp)	References
Universal	f: AAYATGATIACIGGIGGICIGICARATGGA	602	Ke et al (1999)

amplification	r: AYRTTITCICCCIGGCATIACCAT		
<i>Enterococcus</i> specific	f: TACTGACAAACCATTTCATGATG r: AACTTCGTCACCAACGCGAAC	112	Ke et al (1999)
<i>E.faecalis</i>	f: ATCAAGTACAGTTAGTCTTTATTAGr:ACGATTCAAA GCTAACTGAATCAGT	941	Kariyama et al(2000)
Enterocin A	f: AAATATATGGAAATGGAGTGTAT r: GCACTCCCTGGAATTGCTC	126	Du Toit et al (2000)
Enterocin B	f: GAAAATGATCACAGAATGCCTA r: GTTGCAATTTAGAGTATACATTTG	159	Du Toit et al (2000)
Enterocin P	f: TATGGTAATGGTGTATTATTGTAA r: ATGTCCCATACCTGCCAAAC	121	Du Toit et al (2000)
Bacteriocin 31	f: CCTACGTATTACGGAAATGGT r: GCCATGTTGTACCCAACCATT	248	De Vuyst et al (2003)
Enterocin L50A/B	f: TTGGGTGGCCTATTGTTAAA r: TCTATTGTCCATCCTTGTTCCA	224	Cintas et al (1998)
Bacteriocin 1071	f: ATGCTGTAGTCCAGCTGC r: TTTCCAGGTCTCCACCAGT	210	Ben Omar et al (1996)
Bacteriocin AS-48	f: GAGGAGTATCATGGTTAAAGA r: ATATTGTTAAATTACCAA	339	De Vuyst et al (2003)
Enterolysin A	f: CGCAGCTTCTAATGAGTGGT r: CATACACACTGCCATTTCCTA	161	Nilsen et al (2003)
Cytolysin	f: TGGCGGTATTTTACTGGAG r: TGAATCGCTTCCATTCTTC	186	Gilmore et al (1994)

Table 3: The inhibitory spectra of Bac⁺ strains against selected indicator bacteria

Isolate No	Inhibition zone diameter (mm) with indicator strains					
	<i>E. faecalis</i> PTCC 1237	<i>E. hirea</i> PTCC 1239	<i>Li. mono.</i> PTCC 1249	<i>S. aureus</i> PTCC 1112	<i>E. coli</i> PTCC 1533	<i>B. cereus</i> PTCC 1015
C5	-	-	6	-	-	-
C6	-	-	7	-	-	-
C7	-	-	-	-	6	6
C8	-	-	-	-	-	8
C9	-	-	7	-	-	-
M10	7	-	-	6	-	-
M11	-	-	-	-	6	-
M12	-	-	7	-	-	6
M13	-	-	-	-	7	-
M14	9	-	8	-	-	-
M15	7	-	6	-	9	-

Table 4: Prevalence of bacteriocin structural genes and virulence factors genes in enterococcal isolates

Isolate no	Source	Enterococcus spp*	Hemolysis	Enterococcus Genes**	Virulence factor Genes***
C5	Cheese	<i>E. fs</i>	γ	A, LA	as
C6	Cheese	<i>E. fm</i>	α	A,CY	-
C7	Cheese	<i>E. fs</i>	α	A, LA, LY	as, sp
C8	Cheese	<i>E. fm</i>	β	A,CY	as
C9	Cheese	<i>E. fm</i>	α	A, LA	as, sp
M10	Milk	<i>E. fs</i>	γ	A, LA	as, sp
M11	Milk	<i>E. fs</i>	γ	A, LA	as, sp
M12	Milk	<i>E. fs</i>	α	A, LA, LY	as, sp
M13	Milk	<i>E. fs</i>	α	A, LA, LY	as, sp
M14	Milk	<i>E. fm</i>	β	A, LA, LY	as, sp
M15	Milk	<i>E. fm</i>	β	A, LA, LY	as, sp

NOTE: * *E. fm*= *E. faecium*, *E. fs*= *E. Faecalis*; ** A= *entA*, CY= cytolysin, LA= *entL50A/B*, LY= *enlA*
 *** as=aggregation substance, sp= enterococcal surface protein

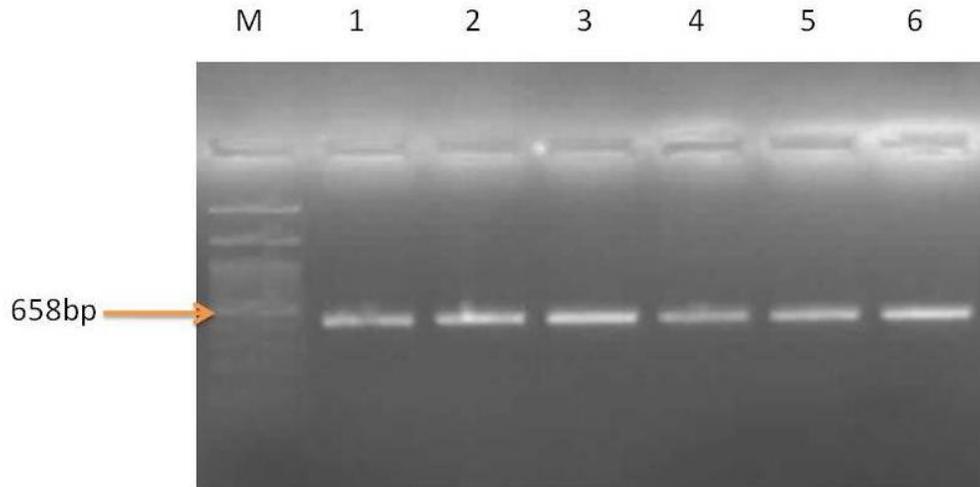


Figure 1: Agarose gel electrophoresis of PCR amplification with primers specific of specific for the *Enterococcus faecium* for 6 selected dairy isolates. (Lanes 1-6) C6, C8, C9, M14 and M15; Lane M 100-bp DNA ladder (Cinnagen).

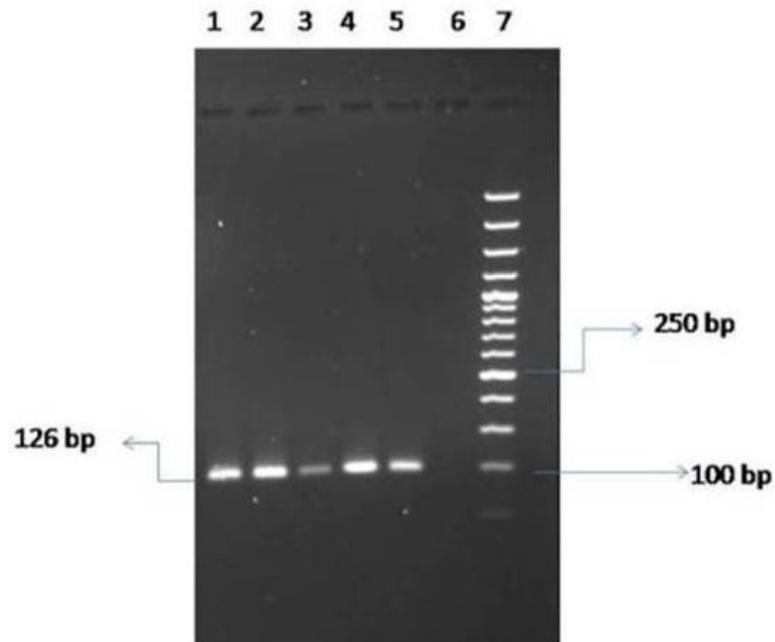


Figure 2 Agarose gel electrophoresis of PCR amplification with primers specific for enterocin A for 5 selected dairy isolates. (Lanes 1-5) C6, C8, M12, M14 and M15; Lane M 100-bp DNA ladder (Cinnagen).

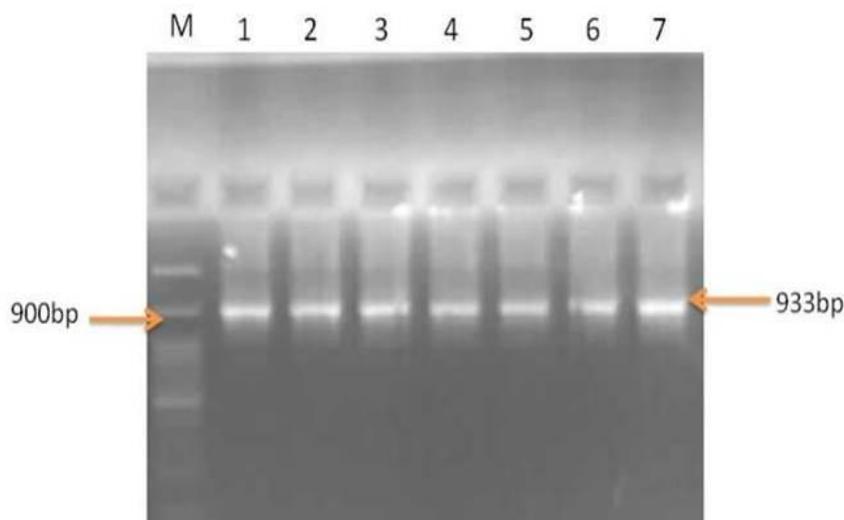


Figure 3: Agarose gel electrophoresis of PCR amplification with primers specific for enterococcal surface protein for 6 selected dairy isolates. (Lanes 1-6) C7, C9, M12, M13, M14 and M15; Lane M 100-bp DNA ladder (Cinnagen)

CONCLUSION

In conclusion, this work has shown that 11% of tested dairy isolates of enterococci displayed antimicrobial activity against closely related species and to be considered a potential probiotic strains. *EntA*, *entL50A/B* and *cyl* were detected frequently among the strains.

Further study on their safety to human showed the presence of multiple potential virulence factors and resistance to vancomycin which could make the strains pathogenic. But, C6 isolate with antibacterial activity against indicator strain) was the only isolate with absence of the virulence genes.

However, the resistance of all the tested strain to vancomycin poses alarming threat which encourage us to search for another bac⁺ strains in our future study

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