Food Control 51 (2015) 49-54



Contents lists available at ScienceDirect

Food Control



journal homepage: www.elsevier.com/locate/foodcont

Evaluation of resistance genes and virulence factors in a food isolated *Enterococcus durans* with potential probiotic effect



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ARTICLE INFO

Article history: Received 4 July 2014 Received in revised form 2 November 2014 Accepted 7 November 2014 Available online 15 November 2014

Keywords: Enterococci Resistance genes Virulence factors Biofilms Food safety

ABSTRACT

Enterococci belong to the lactic acid bacteria (LAB) group, which are often considered to provide benefit to the host organism when consumed. However, these microorganisms have a potential as infective agents, being necessary to evaluate the presence of virulence factors and resistance to antibiotics to warrant the safe use of new strains as probiotic cultures. This study aimed to detect genes of potential virulence factors related with adhesion, aggregation, biofilm formation and resistance to vancomycin, in addition to evaluate the antibiotic susceptibility and adhesion capacity of *Enterococcus durans* LA18s, a strain previously isolated from Minas Frescal cheese. The PCR reactions with specific primers to detect genes of adhesion collagen protein (*ace*), aggregation substances (*agg* and *asa*), *bopA* (putative glycosyltransferase), *bopB* (beta-phosphoglucomutase), *bopC* (aldose 1-epimerase), and *bopD* (sugar-binding transcriptional regulator) were negative for *E. durans* LAB18s. In addition, the strain did not present the resistance genes *vanA*, *vanC1* and *vanC2/3*, and exhibited sensibility to antibiotics commonly used in animal feed, such as erythromycin, tetracycline, vancomycin, gentamicin and penicillin. This strain also showed a strong capacity of biofilm formation and exhibited satisfactory auto-aggregative and hydrophobicity features. The results suggest that this strain can be safely used in animal feed.

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1. Introduction

The genus *Enterococcus* belongs to the group of lactic acid bacteria (LAB). Despite enterococci are ubiquitous bacteria, their primary habitat is the intestine of health warm-blooded animals. In this complex ecosystem, there is a delicate balance between the gut microbiota and the host. *Enterococcus faecalis*, and in a lesser extent *Enterococcus faecium*, are the predominant species in the intestine (Cebrián et al., 2012; Foulquié-Moreno, Sarantinopoulos, Tsakalidou, & de Vuyst, 2006). Enterococci may play beneficial roles in various traditional food products as they contribute to the ripening and aroma development of certain cheeses or fermented sausages (Franz, Huch, Abriouel, Holzapfel, & Gálvez, 2011; Giraffa, 2002).

Certain enterococcal strains are also successfully used as probiotics to improve human or animal health. These bacteria ingested in high numbers may achieve functional or probiotic effects especially for treatment of diseases such as irritable bowel syndrome, diarrhea or antibiotic associated diarrhea, and for health improvement such as lowering cholesterol levels or immune regulation (Franz et al., 2011). As the site of activity is the gastrointestinal system, these beneficial effects are brought about by the interaction of the enterococci with the gut microbiota. Likewise, the use of enterococci in animal feed has similar goals, i.e. either to prevent disease by influencing the gastrointestinal micropopulations or stimulation of the immune system (Gaggìa, Mattarelli, & Biavati, 2010; Kreuzer et al., 2012).

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On the other hand, other enterococcal strains are associated with nosocomial infections and cause human diseases such as endocarditis, bacteremia, and infections of the urinary tract, central nervous system, abdomen, and pelvis (Foulquié-Moreno et al., 2006). Such pathogenic strains often carry multiple antibiotic resistances and virulence factors such as adhesins and hemolysins. The role of some enterococci in human disease raises concerns for their safe use as either starters in food production or as probiotics. Studies on the incidence of virulence factors have shown that isolates from food can also present virulence factors and antibiotic resistance (Franz et al., 2001; Trivedi, Cupakova, & Karpiskova, 2011). Generally, the occurrence of virulence determinants appears to be higher in *E. faecalis* strains than in *E. faecium* strains of food origin (Cebrián et al., 2012; Leavis et al., 2004).

The *Enterococcus* strain evaluated in this study was isolated form a typical Brazilian cheese, and has being investigate for its capability for selenium bioaccumulation (Pieniz, Andreazza, Pereira, Camargo, & Brandelli, 2013), and probiotic potential for possible application as enriched inoculum in animal feed (Pieniz, Andreazza, Anghinoni, Camargo, & Brandelli, 2014). However, to guarantee the safe use of this strain as probiotic culture it is also necessary to evaluate the presence of potential virulence factors and resistance to antibiotics. Thus, the aim of this study was to detect genes involved in adhesion, aggregation, biofilm formation, resistance genes to vancomycin and susceptibility for antibiotics, as well as to evaluate the adhesion capacity of this strain.

2. Materials and methods

2.1. Microorganism

The strain *Enterococcus durans* LAB18s was isolated from Minas Frescal cheese (typical Brazilian soft cheese), and characterized as describe elsewhere (Pieniz et al., 2013). The strain was maintained in stock culture at -20 °C in Brain Heart Infusion (BHI; Oxoid) containing 20% (v/v) glycerol.

2.2. Antibiotic susceptibility test

The antibiotic susceptibility testing was performed according to standard disc diffusion method recommended by the Clinical and Laboratory Standards Institute (CLSI, 2008). The isolate was inoculated onto Mueller-Hinton (MH) agar plates and incubated at 35 $^\circ\text{C}$ for 24 h. After growth, colonies were suspended in sterile saline solution (9 g/L NaCl) and adjusted to an OD_{600} 0.150 \pm 0.02, which corresponds to 0.5 McFarland scale. Then, using swabs, plates with MH agar were inoculated with the standardized solution. Five antibiotics commonly used in animal feed were tested: erythromycin-15 (ERI), tetracycline-30 (TET), vancomycin-30 (VAN), gentamicin-120 (GEN) and penicillin-10 (PEN). The minimal inhibitory concentration (MIC) for vancomycin was determined using the E test[®] method according to the manufacturer's instructions. The diameter of inhibition zones were measured after incubation for 24 h at 35 °C. The isolate was classified according to the CLSI criteria as susceptible, intermediate or resistant to the antibiotic (CLSI, 2008). Data were expressed in millimeters (mm) of inhibition zone. The experiment was performed in triplicate in three independent experiments.

2.3. DNA extraction

The strain was grown in BHI medium at 35 °C for 24 h. Subsequently, colony forming units of bacterial cells were collected and then DNA was extracted using the kit Promega Wizard Genomic DNA Purification KitTM (Cat # A1125).

2.4. Detection of virulence and resistance genes

The strain *E. durans* LAB18s was analyzed for the presence of virulence genes *ace* (adhesion collagen protein), *agg* (aggregation), *asa* (aggregation), *bopA*, *bopB*, *bopC* and *bopD* (biofilm formation). The polymerase chain reaction (PCR) was performed in a total volume of 25 μ L containing: 2 μ L DNA template, 1.5 mM MgCl₂, 10 mM primers, 200 mM each dNTP, 1 unit (U) of DNA Taq Polymerase and 1× reaction buffer.

The strain was also evaluated for resistance genes vanA, vanC1 and vanC2/3 by PCR. The PCR reaction was performed in a total volume of 25 μ L as described above, excepting the concentration of MgCl₂ was 2 mM.

The primer sequences are described in Table 1. The PCR conditions for all genes were denaturation at 94 °C for 5 min, followed by 35 cycles of denaturation at 94 °C for 1 min, annealing extension according to Table 1, followed by final extension at 72 °C for 10 min. The PCR products were analyzed by electrophoresis with 1.5% agarose gels, stained with 5% (w/v) ethidium bromide solution and visualized under ultraviolet light.

2.5. Plasmid DNA profile

Plasmid DNA was extracted with a small-scale alkaline lysis method (Sambrook, Maniatis, & Fritsch, 1989). Extracted plasmids were electrophoresed for 2 h in a horizontal 0.7% agarose gel with pH 8.0 Tris—EDTA (TE) buffer. The gels were stained with ethidium bromide 0.5 μ g/mL for 20 min, and bands were visualized by UV transilluminator. Molecular weight marker KAPA Universal Ladder was used as the DNA standard marker. *Enterococcus mundtii* J5 isolated from feces and a commercial strain of *Escherichia coli* (NEB 10-beta competent; New England BioLabs, Ipswich, MA, USA) containing a 10 Kb plasmid were used for comparison.

2.6. Evaluation of biofilm formation capability

The isolate was analyzed for its ability of biofilm formation as described by Stepanovic, Vukovic, Dakic, Savic, and Svabic-Vlahovic

Table 1

PCR primers and the annealing temperatures used to detect the virulence genes in *Enterococcus* spp.

_					
	Primer	Sequence (5'-3')	Product (bp)	AT ^a (°C)	Reference
-	ace f	AAAGTAGAATTAGATCACAC	320	48	Duprè, Zanetti,
	ace r	TCTATCACATTCGGTTGCG			Schito, Fadda,
					& Sechi, 2003
	agg f	AAGAAAAAGTAGACCAAC	1553	48	Eaton & Gasson,
	agg r	AACGGCAAGACAAGTAAATA			2001
	asa f	GATACAAAGCCAATGTGGTTCCT	101	48	Dunny, Craig,
	asa r	TAAAGAGTCGCCACGTTTCACA			Carron, & Clewell,
					1979
	bopA f	CAGCGACATGGACAGCCTAC	108	48	Vebø, Snipen,
	bopA r	TTGCAGGACCGTCGAGTAAA			Nes, & Brede, 2009
	bopB f	ATGACAGAATCCAAAACTGC	687	48	Cassenego, 2014
	bopB r	TTACGAAGGGGTTGATTCAC			
	bopC f	TTATAGAAGGTTAAATTGAT	1010	48	Cassenego, 2014
	bopC r	ATGAAGGATAATCGTATCAC			
	bopD f	GGCTTCCTCGTTGATGGCTTC	126	48	Hufnagel et al. 2004
	bopD r	ACGGCACGGAATTTGGGTAAAC			
	vanA f	GGGAAAACGACAATTGC	732	50	Depardieu, Perichon,
	vanA r	GTACAATGCGGCCGTTA			& Courvalin, 2004
	vanC1 f	GGTATCAAGGAAACCTC	822	54	Dutka-Malen, Evers,
	vanC1 r	CTTCCGCCATCATAGCT			& Courvalin, 1995
	vanC2/3 f	CGGGGAAGATGGCAGTAT	848	54	Satake, Clark,
	vanC2/3 r	CGCAGGGACGGTGATTTT			Rimland, Nolte,
					& Tenover, 1997

^a AT = annealing temperature.

(2000). The strain was previously inoculated in a plate containing BHA and incubated at 35 °C for 24 h. Microtitration plates were filled with 180 µL of sterile BHI. After overnight growth, colonies were suspended in sterile saline and the OD₆₀₀ was adjusted to 0.150 ± 0.02 . Then, 20 μ L of this suspension were inoculated in each well containing 180 µL BHI. Staphylococcus aureus ATCC 25923 was used as a positive control, and a negative control was performed with BHI alone. The plates were covered and incubated at 35 °C for 24 h. After growth, the cultures were aspirated with a multichannel pipette and the wells were washed three times with 200 µL saline solution. The micro-plate was inverted onto absorbent paper to dry and subsequently the samples were fixed with 150 µL of methanol (CH₃OH) for 20 min. After this time, methanol was discarded and the plates were maintained inverted overnight. The samples were stained with 150 μ L crystal violet (5 g/L) for 15 min. After the plates were inverted and excess was removed under running water. Then, after a short drying period 150 μ L ethanol (95% v/v) was added. The plates were maintained for 30 min and then the absorbance was measured with microplate reader (Anthos 2010 17550 Type 4894) at 450 nm.

Based on the OD produced by bacterial films, strains were classified into the following categories: no biofilm producers (0), weak (+), moderate (++) or strong biofilm producers (+++), as previously described (Stepanovic et al., 2000). Briefly, the cut-off OD (ODc) was defined as three standard deviations above the mean OD of the negative control. Strains were classified as follows: $OD \leq ODc =$ no biofilm producer, $ODc < OD \leq (2 \times ODc) =$ weak biofilm producer, $(2 \times ODc) < OD \leq (4 \times ODc) =$ moderate biofilm producer and $(4 \times ODc) < OD =$ strong biofilm producer. All tests were carried out in triplicate.

2.7. Determination of cell surface hydrophobicity

The surface hydrophobicity was determined *in vitro* according to Rosenberg, Gutnick, and Rosenberg (1980) with some modifications. Briefly, the isolate was inoculated in BHI and incubated at 35 °C. After 24 h, the cells were collected by centrifugation at 10,000 × g for 10 min at 4 °C, washed twice and suspended in 10 mM phosphate buffered saline (PBS) pH 7.2, and the OD₆₀₀ was adjusted to 0.800 ± 0.05 (A_0). An aliquot of 0.6 mL of either xylene or chloroform was added to tubes containing 3 mL of bacterial suspension. The solution was homogenized with vortex for 2 min. The tubes were allowed to stand at 35 °C for 2 h for phase separation. After this period, the aqueous phase (A) was carefully removed and the OD₆₀₀ was measured. The cell surface hydrophobicity was calculated from three replicates using the following equation: H% = [(($A_0 - A$)/ A_0) × 100].

Two solvents were evaluated in this study. The xylene and chloroform were used as apolar and acid monopolar solvents, respectively. In terms of bacterial adhesion, only xylene reflects the cell surface hydrophobicity. The values obtained with chloroform were considered as an electron acceptor characteristic of the bacteria (Bellon-Fontaine, Rault, & Van Oss, 1996).

2.8. Auto-aggregation

The auto-aggregation was evaluated according to Juárez-Tomás, Wiese, and Nader-Macías (2005) with some modifications. The strain was grown in BHI at 35 °C for 24 h. After this, cells were sampled by centrifugation at 10,000 × g for 10 min at 4 °C, washed twice and suspended in 10 mM PBS (pH 7.2). The OD₆₀₀ was adjusted to 0.600 ± 0.05 (A_0). The cell suspension was incubated at 35 °C, and the ability to auto-aggregation was measured by OD₆₀₀ measurement after 1–24 h (At). The auto-aggregation was determined using the following equation: % AA = [(($A_0 - A_t$)/ A_0) × 100].

2.9. DNase test

DNase activity was tested as described by Bannerman (2003) using the medium DNase Test Agar with toluidine blue (Himedia, São Paulo, Brazil). A clear halo around the colonies was indicative of a positive result.

2.10. Hemolytic activity

The hemolytic activity was evaluated according Foulquié-Moreno, Callewaert, Devreese, van Beeumen, & de Vuyst (2003). The strain was tested for hemolytic activity using blood agar (7% v/v sheep blood) for 48 h incubation at 37 °C. Strains that produced green-hued zones around the colonies (α -hemolysis) or did not produce any effect on the blood plates (γ -hemolysis) are considered non hemolytic. Strains displaying blood lyses zones around the colonies are classified as hemolytic (β -hemolysis).

3. Results

3.1. Virulence genes

The presence of virulence genes was investigated by PCR. The genes for adhesion collagen protein (*ace*), and aggregation substances (*agg* and *asa*) were not detected in *E. durans* LAB18s, whereas the expected PCR products were observed for *E. faecalis* ID 2389 used as a positive control (Fig. 1). The genes *bopA* (putative glycosyltransferase), *bopB* (beta-phosphoglucomutase), *bopC* (aldose 1-epimerase), and *bopD* (sugar-binding transcriptional regulator) involved in the metabolism of maltose and biofilm formation were also evaluated. The strain *E. durans* LAB18s did not present any PCR product for the virulence factors evaluated (Fig. 1).

Likewise, *E. durans* LAB18s was evaluated for resistance genes *vanA*, *vanC1* and *vanC2/3*. It can be observed in Fig. 2 that these resistance genes were not present in *E. durans* LAB18s.

A plasmid DNA extraction was performed using standard miniprep methods and the results from the plasmid DNA profile showed the absence of plasmids in the strain LAB18s (Fig. 3).

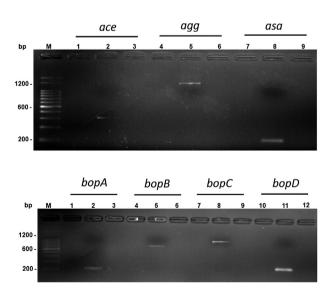


Fig. 1. Amplification of virulence-associated genes *ace*, *agg* and *asa* (upper panel), *bopA*, *bopB*, *bopC* and *bopD* (lower panel) by PCR. The letter bp indicates bases pair; the letter M indicates the molecular size marker (100 bp DNA Ladder, Invitrogen) and the numbers are the respective samples: (1, 4, 7, 10) negative controls; (2, 5, 8, 11) positive controls; (3, 6, 9, 12) the absence of the genes in *E. durans* LAB188. Vancomycin-resistant *Enterococcus faecalis* ID 2389 was used as positive control.

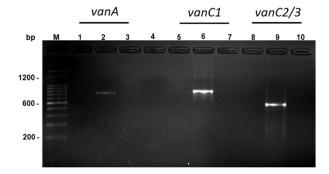


Fig. 2. Amplification of resistance-associated genes *vanA*, *vanC1* and *vanC2/3* by PCR. The letter bp indicates bases pair; the letter M indicates the molecular size marker (100 bp DNA Ladder, Invitrogen) and the numbers represent: (1, 5, 8) negative controls; (2, 6, 9) positive controls; (3, 7, 10) absence of *vanA*, *vanC1* and *vanC2/3* gene, respectively, in *E. durans* LAB18s. Vancomycin-resistant *Enterococcus faecalis* ID 2389 was used as positive control to *vanA*, and *Enterococcus faecalis* CB356 was used as positive control to *vanC2/3*.

3.2. Antibiotic susceptibility

Analysis of the results obtained for antibiotic susceptibility test showed that the isolate exhibited high sensibility for all antibiotics tested, according to CLSI standards (Table 2). When the isolate *E. durans* LAB18s was analyzed by E test[®], a MIC \leq 4 µg/mL (0.38 µg/mL) was observed indicating the susceptibility of the strain to vancomycin.

3.3. Biofilm formation, hydrophobicity and auto-aggregation

The strain showed elevated adherence to microplates and was classified as strong biofilm producer (Stepanovic et al., 2000). Interestingly, this factor was not associated with the presence of virulence-associated genes concerning biofilm formation. This capacity could be specifically related with the adhesion properties of *E. durans* LAB18s.

The hydrophobicity of *E. durans* LAB18s was analyzed using two solvents: xylene, a non-polar solvent; and chloroform, an acidic monopolar solvent. The results of hydrophobicity and acid character of the cell wall was expressed in percentage, and the values were $31.1 \pm 0.01\%$ and $66.8 \pm 0.02\%$ for xylene and chloroform, respectively. The strain showed a cell surface more acidic

Table 2

Antibiotic susceptibility of *E. durans* LAB18s and classification according to Clinical Laboratory Standards Institute (CLSI).

Antibiotic		CLSI classification			
	Inhibition zone (mm) ^a	Susceptible zone (mm)	S-I-R ^b		
Erythromycin	23.3 ± 0.35	≥23	S		
Tetracycline	20.5 ± 0.18	≥19	S		
Vancomycin	19.0 ± 0.47	≥17	S		
Gentamicin	21.5 ± 0.21	≥ 10	S		
Penicillin	26.0 ± 0.47	≥15	S		

 $^{\rm a}$ Values are expressed as mean \pm standard error of three independent experiments.

^b Standard interpretation of antimicrobial susceptibility tests of enterococci with disc diffusion method in accordance to CLSI standards (CLSI, 2008): S, susceptible; I, intermediate; R, resistant.

(chloroform) when compared with the values for hydrophobicity observed using xylene.

The percentage of auto-aggregation increased exponentially in the initial incubation period, from 27% at 1 h to 47% at 4 h, and reaching values of 79% at 24 h of incubation (Fig. 4). These data indicate that the strain has auto-aggregative and hydrophobicity features and these could be related with adherence capability.

The isolate *E. durans* LAB18s did not exhibit any hemolytic effect (γ -hemolysis, α -hemolysis and/or β -hemolysis) after 48 h incubation in blood agar plates (Fig. S1). It was also observed that the DNAse test exhibited negative results (Fig. S1).

4. Discussion

Enterococci are present in numerous food and fermented dairy products, and the species *E. faecalis, E. faecium*, and *E. durans* are commonly found in milk products (Franz et al., 2011). The presence of enterococci in foods has been known for a long time, but only recently they have been considered as potential probiotic agents (Ogier & Serror, 2008). Thus, obtaining precise information about these microorganisms, and to promote studies for possible application in food or feed is mandatory to allow their safe use. The results from this study suggest that the strain *E. durans* LAB18s may be used as a feed additive in future animal testing.

Antibiotic susceptibility of *E. durans* LAB18s was evaluated. The wide use of tetracycline in animal husbandry is frequently associated with the high levels of tetracycline resistance found among enterococci (Hayes, English, Carr, Wagner, & Joseph, 2004). In contrast, the isolate *E. durans* LAB18s was sensitive to this antibiotic.

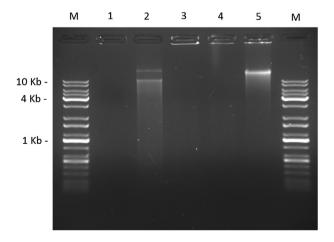


Fig. 3. Plasmid DNA profile. Plasmid DNA extracted from *E. coli* NEB 10-beta (2), *E. mundtii* J5 (3) and *E. durans* LAB18s (4) were analyzed in 0.7% agarose gels. (1) negative control, (5) chromosomal DNA of *E. durans* LAB18s, (M) molecular weight marker KAPA Universal Ladder.

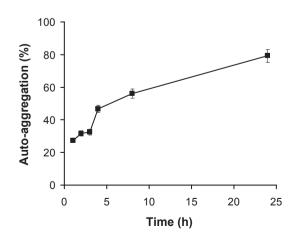


Fig. 4. Auto-aggregation of *E. durans* LAB18s after incubation at 35 °C. Data were expressed as mean percentage $(\%) \pm$ standard error of three independent experiments.

Likewise, E. durans LAB18s was susceptible to erythromycin according to CLSI classification. Resistance to erythromycin, a representative of the macrolide antibiotics, would be a matter of concern because macrolides are common substitutes for individuals with penicillin allergy (Peters, Mac, Wichmann-Schauer, Klein, & Ellerbroek, 2003). The resistance of enterococci to β-lactam antibiotics seems to be associated with clinical strains and often inaccurately generalized in the literature to the genus (Kak & Chow, 2002). However, the results obtained in the present study are not in agreement with this generalization, since the isolate was susceptible to penicillin, in agreement with results described by other authors (McGowan-Spicer, Fedorka-Cray, Frye, & Meinersmann, 2008; Peters et al., 2003). Vancomycin-resistant enterococci (VRE) have emerged in the last decade as a frequent cause of nosocomial infections, and the presence of VRE has been detected among meat isolates (Messi, Guerrieri, Niederhäusern, Sabia, & Bondi, 2006). However, the isolate E. durans LAB18s was not resistant to vancomycin, exhibiting sensitivity in both antibiogram and E-test[®].

Besides the analyses of vancomycin susceptibility, *E. durans* LAB18s was evaluated for the presence of vancomycin resistance genes. The genes *vanA*, *vanC1* and *vanC2/3* were investigated by PCR resulting in negative amplification for any of the tested genes. The assessment of resistance genes to vancomycin in strains with possible use in animal feed is of utmost importance, since this antibiotic is not metabolized by the animals and remains in the active form in the intestines (Yap et al., 2008), promoting VRE. In Europe, VRE (predominantly the *vanA* genotype) are frequently isolated in non-hospitalized patients, animals and environmental sources, and they are rare in the hospital setting (Bonten, Willems, & Weistein, 2001). This suggests that these bacteria come from a community source; they could be part of the normal animal microbiota and passed through the food chain.

Depending on the type and combination of virulence factors, they become crucial for the strain pathogenicity. In Enterococcus species, genes conferring antibiotic resistance and other virulence factors, such as aggregation substance (agg and asa) and collagen adhesins (ace), can be acquired by genetic exchange (Eaton & Gasson, 2001; Mundy, Sahm, & Gilmore, 2000). We analyzed the presence of ace, agg and asa by PCR amplification and none of these virulence genes were detected in E. durans LAB18s. Aggregation substance is a pheromone-inducible surface protein of E. faecalis that promotes mating aggregate formation during bacterial conjugation (Mundy et al., 2000). As an important component of the bacterial pheromone-responsive genetic exchange system, aggregation substance mediates efficient enterococci donor-recipient contact to facilitate plasmid transfer. Likewise, aggregation substance increases the hydrophobicity of the enterococcal surface, which may prevent or delay phagocytosis and the subsequent fate of the organism.

Creti, Koch, Fabretti, Baldassarri, and Huebner (2006) identified the operon *bopABCD* involved in biofilm formation in *E. faecalis*, which appears to be regulated by the Fsr system through quorumsensing. In this study, the virulence genes bopA, bopB, bopC and bopD were also analyzed by PCR amplification, but E. durans LAB18s did not exhibit these genes. Biofilm production plays a major role in the pathogenesis of many important microbes and the occurrence of biofilms in enterococcal infections has been frequently reported (Mohamed & Huang, 2007). Hufnagel, Koch, Creti, Baldassarri, and Huebner (2004) reported that production of biofilm may be a virulence factor in enterococci that leads to prolonged bacteremia. The ability of the strain tested to produce biofilm in vitro was correlated with its persistence in the mouse bacteremia model in vivo. In the same way, the in vitro biofilm formation capability was analyzed in this study showing that E. durans LAB18s exhibited a strong capacity of biofilm formation. However, this capacity was not associated with the virulence-associated genes. Probably this finding is related with the adhesion properties, a desirable characteristic of probiotic strains (Samot, Lebreton, & Badet, 2011).

In this study, the hydrophobicity and auto-aggregation capacity of E. durans LAB18s was also evaluated, and the strain showed satisfactory adhesion properties. Hydrophobicity and autoaggregation tests are based on the principle that attachment to the epithelial surface is a necessary first step for the colonization of probiotic microorganisms (Ocaña & Nader-Macías, 2002; Vinderola & Reinheimer, 2003). The hydrophobicity is related to the hydrophobic components present in the outer membrane of the organism and it is believed that hydrophobic interactions play an important role in the adhesion of bacteria to epithelial cells. Although the test is performed with solvents, it is possible to assess qualitatively the bacterial surface as either polar or non-polar, indicating the potential for adhesion to non-polar surfaces such as the cell surfaces (Ocaña & Nader-Macías, 2002; Rosenberg et al., 1980). Bacterial aggregation between microorganisms of the same strain (auto-aggregation) is considered important in several ecological niches (Del Re, Sgorbati, Miglioli, & Palenzona, 2000).

In summary, the strain *E. durans* LAB18s is a strain that might be considered safe for consumption, because it does not show virulence factors or vancomycin resistance genes when tested for *ace*, *agg*, *asa*, *bopA*, *bopB*, *bopC*, *bopD*, *vanA*, *vanC1* and *vanC2/3*. Furthermore, the isolate was susceptible to all antibiotics tested, and also showed adhesion capacity. In addition to its capability to bioaccumulate selenium, *E. durans* LAB18s may be used as selenium-enriched culture to be added in animal feed.

Acknowledgments

Authors thank the financial support of the Brazilian agencies CNPq and CAPES.

Appendix A. Supplementary data

Supplementary data related to this article can be found at http://dx.doi.org/10.1016/j.foodcont.2014.11.012.

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