

ANTIBIOTIC RESISTANCE IN LACTIC ACID BACTERIA ISOLATED FROM FERMENTED DAIRY PRODUCTS AND BOZA

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ARTICLE INFO	ABSTRACT
Received 14. 11. 2014 Revised 9. 3. 2015 Accepted 23. 3. 2015 Published 1. 6. 2015	In this study, the resistance of 83 strains of lactic acid bacteria isolated from Turkish cheese, yogurt, kefir and boza samples to 6 antibiotics (gentamicin, tetracycline, chloramphenicol, erythromycin, vancomycin and ciprofloxacin) was evaluated. The 83 isolates were identified by 16S rRNA gene sequencing and according to BLAST comparisons with sequences in the data banks, those strains showing the highest similarities with the isolates were <i>Enterococcus faecium</i> (10), <i>Lactococcus lactis</i> subsp. <i>Lactis</i> (10), <i>Lactobacillus</i>
Regular article Open access	<i>fermentum</i> (6), <i>Lactobacillus plantarum</i> (6), <i>Lactobacillus coryniformis</i> (7), <i>Lactobacillus casei</i> (13), <i>Leuconostoc mesenteroides</i> (14), <i>Pediococcus pentosaceus</i> (10), <i>Weisella confusa</i> (7). Antimicrobial resistance of strains to 6 antibiotics was determined using the agar dilution method. The antibiotic resistance among all the isolates was detected against chloramphenicol (31,3 % of the isolates), tetracycline (30,1 %), erythromycin (2,4 %), ciprofloxacin (2,41%), vancomycin (73,5 %, intrinsic resistance). Overall 19,3 % of the isolates showed resistance against multiple antibiotics. Antibiotic resistance genes were studied by PCR and the following genes were detected; <i>tet</i> (M) gene in <i>Lactobacillus fermentum</i> (1), <i>Lactobacillus plantarum</i> (1), <i>Pediococcus pentosaceus</i> (5), <i>Enterococcus faecium</i> (2), <i>Weisella confusa</i> (4) and the vancomycin resistance gene <i>van</i> (A) in one <i>Weisella confusa</i> strain.

Keywords: Antibiotic resistance, Lactic acid bacteria, Boza, Fermented dairy products

INTRODUCTION

Lactic acid bacteria (LAB) are a group composed of Gram positive bacteria and they excrete lactic acid into the medium as a main fermentation product (Schleifer & Ludwig 1995). Many LAB species are present as contaminants on raw agricultural materials or deliberately added as starter cultures into them (Leroy & de Vuyst, 2004; Capcarova et al., 2011; Sharma et al., 2013). LAB have a long history of safe use as fermenting natural products and probiotics intended for health benefits and have acquired the "Generally recognized as safe" (GRAS) status (Mathur & Singh, 2005) but there is a great attention to these bacteria may serve as reservoirs of antibiotic resistance (Thumu & Halami 2012). The main mechanisms of horizontal transfer in bacteria in natural environments are believed to be conjugation and transduction via bacteriophages (Kleinschmidt et al., 1993). LAB have been reported to be capable of supplying antimicrobial resistance genes to food-borne or enteric pathogens (Gevers et al., 2003). According to "qualified presumption of safety" (QPS) concept evolved by European Food Safety Authority (EFSA, 2014), the presence of transmissible antibiotic resistance markers in these bacteria has become an important safety criterion.

Fermented dairy foods and beverages like boza are extensively consumed in Turkey. Therefore investigations on antibiotic resistance profiles of LAB strains common to these products are very important for food safety. In this study antibiotic resistance of LAB strains present in fermented dairy products and boza was tested by phenotypic and genotypic methods, in an attempt to contribute to the knowledge about food associated LAB.

MATERIAL AND METHODS

Isolation and identification of strains

Bacterial strains were isolated from fermented dairy products including white cheese, sheep cheese, dry cheese, yogurt, kefir and boza samples from local markets and bazaars in Aydin (Turkey). The samples were initially homogenized and then serial dilutions between 10^{-3} - 10^{-6} were inoculated to MRS agar (Merck, Darmstadt Germany) plates supplied with 100 mg/L of cycloheximide ((Sigma-Aldrich, Taufkirchen, Germany) using spread plate method. MRS agar plates

were incubated anaerobically at 30 °C for 48 hours using the Gas Pack system (Merck, Darmstadt, Germany). Pure cultures of isolates obtained and then strains with gram positive and catalase negative reactions were finally used for further identification.

DNA was extracted from isolates according to phenol-chloroform method defined by **Ronimus** *et al* (1997). The following oligonucleotide primers were used to amplify the 16S rRNA gene from strains, forward primer 20F (5²- AGA GTT TGA TCC TGG CTC AG - 3²) and reverse primer 1390R (5²-GAC GGG CGG TGT GTA CAA-3³). PCR was utilized under the following thermocycling conditions: pre-denaturation step at 94 °C 5 min, 35 cycles of 94 °C for 30 s, 50 °C for 30 s and 72 °C for 10 s, followed by a final extension step of 72 °C for 15 min. To determine the closest relatives of the partial 16S rDNA sequences, amplified PCR products sequenced by Macrogene (South Korea). Sequences were BLAST in GenBank database (www.ncbi.nlm.nih.gov) for species assignment.

Antibiotic susceptibility testing

Minimal Inhibitory Concentrations (MIC) for 6 antibiotics was determined by agar dilution test using multipoint inoculator. Isolates were grown in MRS broth (Merck, Darmstadt, Germany) for 48 hours and then inoculated to LSM Agar (90% Iso-SensitestTM Broth (Oxoid) + 10% MRS Broth (Merck)+ 1,5% Agar (Merck) (**ISO 10932; Klare** *et al.*,2005) plates containing gentamicin, tetracycline, chloramphenicol, erythromycin and vancomycin antibiotics (Oxoid, Hampshire, UK) with the concentration range of 0.0625-128 µg/ml or 0.0625-64 µg/ml for ciprofloxacin. The MIC was defined as the lowest concentration of antibiotic giving a complete inhibiton of visible growth in comparison to an antibiotic free control point. Breakpoints were adopted from EFSA report (2008), **Ouoba** *et al.*, 2008 and **Danielsen & Wind, 2003.**

Detection of antibiotic resistance genes in LAB isolates

PCR amplification of antibiotic resistance genes was done in 50 μ L volumes that contained 30 pmol of each specific primer (BM Labrotories, Ankara, Turkey), 2 mM MgCl₂, 1X Taq DNA polymerase buffer, each dNTP at a concentration of 200 μ M, 1 U of Taq DNA polymerase (ABM, Canada) and 1 μ L DNA used as a

template. The oligonucleotide primers and annealing temperatures are listed in Table 1. DNA fragments were amplified in a Techne TC3000 thermocycler up to 40 cycles and PCR products were separated by electrophoresis on 1,2 % agarose

jel containing (0,05%, v/v) safe view solution. For tet(M), erm(C) and van(A) genes positive controls were used.

Resistance gene	Primer	T _a °C	Reference
tet(M)	5'-GGTGAACATCATAGACACGC-3' 5'-CTTGTTCGAGTTCCAATGC-3'	55 °C	(Werner et al, 2003)
tet(K)	5'-CAATACCTACGATATCTA-3' 5'-TTGAGCTGTCTTGGTTCA-3'	52 °C	(Werner et al, 2003)
van(A)	5'-TTGCTCAGAGGAGCATGACG-3' 5'-TCGGGAAGTGCAATACCTGC-3'	65 °C	(Klein et al., 2000)
van (B)	5'-TTATCTTCGGCGGTTGCTCG -3' 5'-GCCAATGTAATCAGGCTGTC-3'	62 °C	(Klein et al., 2000)
cat	5'-ATGACTTTTAATATTATTRAWTT-3' 5'-TCATYTACMYTATSAATTATAT-3'	49 °C	(Hummel et al., 2007)
erm(A)	5'-TCTAAAAAGCATGTAAAAGAA-3' 5'-CTTCGATAGTTTATTAATATTAGT-3'	52 °C	(Sutcliffe et al., 1996
erm(B)	5'-GAAAAGGTACTCAACCAAATA-3' 5'-AGTAACCGTACTTAAATTGTTTAC-3'	52 °C	(Sutcliffe et al., 1996)
erm(C)	5'-TCAAAACATAATATAGATAAA-3' 5'-GCTAATATTGTTTAAATCGTCAAT-3'	52 °C	(Sutcliffe et al., 1996)

RESULTS

Identification of bacteria

Eighty-three presumptive LAB strains isolated from Turkish cheese, yogurt, kefir and boza samples. All isolates were catalase negative and Gram positive rods, cocci or pleomorphics. Strains were identified as *Enterococcus faecium* (10), *Lactococcus lactis* subsp. *Lactis* (10), *Lactobacillus fermentum* (6), *Lactobacillus plantarum* (6), *Lactobacillus coryniformis* (7), *Lactobacillus casei* (13), *Leuconostoc mesenteroides* (14), *Pediococcus pentosaceus* (10), *Weisella confusa* (7) according to BLAST results.

Phenotypic Profile of Antibiotic Resistance

Results obtained from the MIC's of tested bacteria are presented in Table 2. None of the tested bacteria were found to be resistant to gentamicin. Only two of the eighty three strains, *Enterococcus faecium* GL-21 and *Weisella confusa* GL-33 were resistant to erythromycin. The most prevalent resistances were tetracycline and chloramphenicol (30,1 % and 31,3 respectively). Twenty five LAB strains including eight of the ten pediococci, two of the ten *E. faecium* and all of the *W. confusa*, displayed phenotypic resistance to tetracycline with MIC values of 8 µg/ml or higher. For chloramphenicol four of the thirty-two lactobacilli, eight of the ten pediococci, all *Weisella* strains, two of the ten Enterococci and five of the

thirteen *Leuc. mesenteroides* were found to be resistant with MIC values ranging between 8 and 16 µg/ml. *Weisella* and pediococci seemed like most resistant genera to tetracycline and chloramphenicol. For erythromycin, all LAB isolates displayed MIC values of 2 µg/ml or lower and evaluated as susceptible except for *E. faecium* GL-21 with MIC value of 32 µg/ µL and *W. confusa* GL-33 with of 16 µg/ml. *Lactococcus lactis* subsp. *Lactis* strains isolated in the study did not show any resistance to the tested antibiotics. Obtained LAB strains were intrinsically resistant to vancomycin except for those belonging to genera *Enterococcus* and *Lactococcus* which they were found to be susceptible to this antibiotic. *E. faecium* GLM-160 and *E. faecium* GLM-161 showed resistance to ciprofloxacin, *P.pentosaceus* strains were inherent resistant.

Detection of antibiotic resistance genes in LAB isolates

All of the isolated LAB strains were tested by PCR for the presence of the most frequently detected AR genes; *tet*(M), *tet*(K), *van*(A), *van*(B), *cat*, *erm*(A), *erm*(B) and *erm*(C) regardless of whether or not they are phenotypically resistant to antibiotics. *tet*(M) was detected in twelve of the tetracycline resistant LAB strains, while *van*(A) detected in one of the seven vancomycin resistant *Weisella* isolates. *Lb. fermentum* GL-9 and *Lb. plantarum* which are phenotypically susceptible to tetracycline, were found to carry the *tet*(M) gene (Table 3).

Table 2 LAB species is	olated in the study.	, numbers and MIC ranges
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Isolated LAB species	Gentamicin	Tetracycline	Chloramphenicol	Erythromycin	Vancomyci n	Ciprofloxacin
<i>Lb. fermentum</i> (n=6)	0.25-8	4-16	2-8	≤0,0625-0,25	128-≥128	4-16
Lb. plantarum (n=6)	≤0,0625-4	2-32	1-8	≤0,0625-0,125	≥128	1-16
Lb. coryniformis (n=7)	1-4	4-32	≤0,0625-4	≤0,0625-0,5	≤0,0625- ≥128	0,5-8
Lb. casei (n=13)	0,25-8	0,125-8	1-16	≤0,0625-0,5	≥128	0,25-2
P. pentosaceus (n=8)	0,5-4	4-32	8-32	≤0,0625-0,125	≥128	16-32
P. parvulus (n=2)	0,25	8-16 r	2-4	≤0,0625	≥128	1-2
E. faecium (n=10)	8-32	0,125-16	4-16	0,125-32	0,25-1	≤0,0625-4
<i>L. lactis</i> subsp. <i>lactis</i> (n=10)	0,25-4	≤0,0625-0,5	1-4	≤0,0625-0,125	0,125-0,25	0,5-2
W. confusa (n=7)	0,5-8	8-32	16	0,125-16	≥128	0,25-0,5
Leuc. mesenteroides (n=14)	0,125-2	0.0,5-4	2-4	≤0,0625-0,125	≥128	0,5-4

Table 3 PCR	positive LAB	strains and	their MIC values
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LAB strain	Gene	MIC value (µg/mL)	
Lb. fermentum GL-9	Tet (M)	8	
Lb. plantarum GLM-209	Tet (M)	32	
P. pentosaceus GL-20	Tet (M)	16	
P. pentosaceus GL-62	Tet (M)	32	
P. pentosaceus GL-20	Tet (M)	16	
P. pentosaceus GL-63	Tet (M)	32	
E. faecium GL-83	Tet (M)	16	
E. faecium GL-89	Tet (M)	16	
W.confusa GL-31	Tet (M)	8	
W.confusa GL-55	Tet (M)	8	
W.confusa GL-74	Tet (M)	8	
W.confusa GL-56	Van (A)	≥128	
W.confusa GL-76	Tet (M)	8	

DISCUSSION

In the present study, 83 LAB isolates from Turkish fermented foods and boza were isolated and identified by 16S rRNA gene sequencing. After bacterial identification, the strains were evaluated by phenotypic and genotypic methods for their antibiotic resistance profiles.

The resistance of the studied Lactobacillus spp. to antibiotics was variable according to species and antibiotic tested. While none of the lactobacilli were resistant to gentamicin, erythromycin or ciprofloxacin, some Lb. fermentum and Lb. coryniformis strains were detected as resistant to tetracyclin and tet(M) gene was found in Lb. fermentum GL-9 as a silence resistance gene. Chloramphenicol resistance was more common in Lb. casei strains (GL-72, GLM-210, GLM-212) than other lactobacilli, only one Lb. fermentum was resistant to chloramphenicol. It has been shown that Lactobacillus spp. are generally susceptible to chloramphenicol, erythromycin and tetracycline (Zhou et al., 2005; Rojo-Bezares et al., 2006; D'Aimo et al., 2007, Bujnakova et al., 2014). However, resistant strains to these agents, and several genes providing resistance have also been identified. For example a chloramphenicol resistance cat gene has been found in Lactobacillus plantarum (Ahn et al., 2002), tet(M) gene in Lactobacillus fermentum isolates (Gfeller et al., 2003). Cataloluk and Gogebakan (2004) reported that six isolates of Lactobacillus casei from dairy products and human origin carried tet(M) genes. A previous study conducted with home-made Spanish cheese reported that L. plantarum, L. acidophilus, L. brevis and L. casei strains were resistant to tetracycline and chloramphenicol (Herrero et al., 1996).

Lactobacillus spp, P.pentosaceus, W. confusa and L. mesenteroides isolates showed very high MIC values (128 µg/ml or higher) for vancomycin. Leuconostoc, Weissella, Pediococcus, Lactobacillus, and Erysipelothrix are involved in clinically relevant, non-enterococcal intrinsic glycopeptide resistant Gram positive organisms (Klein et al. 2000; Lahtinen et al., 2012). Many strains of Lb. plantarum, Lb. casei, Lb. salivarius, Lb. leichmannii, Lb. acidophilus carry intrinsic resistance towards vancomycin which is due to the presence of Dalanine: D-alanine ligase-related enzymes (Elisha and Courvalin 1995). Intrinsic vancomycin resistance of Lactobacillus, Leuconostoc and Pediococcus species has been used to separate them from other Gram-positive bacteria on vancomycin supplemented selective media (Simpson et al. 1995).

Among the Pediococci isolates, only two were susceptible to tetracycline and tet(M) gene was detected in four resistant *Pediococcus pentosaceus* strains. As indicated in the literature, data on the antibiotic susceptibility of *Pediococcus* spp. isolated from food are very scarce (Ammor *et al.*, 2007). Hummel *et al.* (2007) investigated antibiotic resistances of 45 lactic acid bacteria those belong to the genera *Lactobacillus, Streptococcus, Lactococcus, Pediococcus* and *Leuconostoc*. One of the *Pediococcus* strain *P. pentosaceus* strain BFE 7436 was found to show low resistance to tetracycline. However, it was reported that neither of the genes those encode the ribosomal protection proteins [*tet*(M), *tet*(Q), *tet*(S) or *tet*(W)] nor the genes those encode the tetracycline efflux pumps [*tet*(K) or *tet*(L)] were found.

While chloramphenicol resistance seems to be common in *P. pentosaceus* strains isolated in our study, cat gene could not be detected in any of these resistant strains. It has been reported chloramphenicol usually active against *Pediococcus pentosaceus* isolates [Gevers *et al.*, 2000; Sabir *et al.*, 2010) and susceptibility levels are thought to be species-dependent (Ammor *et al.*, 2007). The ciprofloxacin MICs were 16-32 μ g/ml for *P. pentosaceus*. Danielsen et al., (2005) reported that ciprofloxacin resistance in *Pediococcus pentosaceus* was likely to be an intrinsic property of the species.

Enterococcus faecium strains isolated in our study were found to be resistant to different antibiotics. *E. faecium* GL-21 showed high level of resistance to erythromycin ($32 \mu g/ml$), and also chloramphenicol resistant which was isolated from boza, but none of the *erm*(A), *erm*(B), *erm*(C) or cat genes could be detected. Two of the four *E. faecium* strains, GL-83 and GL-89 were resistant to tetracycline and carried *tet*(M) gene.

In a study undertaken by **Temmerman** *et al.* (2003), a total of 29 *E. faecium* strains were isolated from different European probiotic products and antibiotic resistance was detected against tetracycline (24% of the isolates), erythromycin (97% of the isolates) and chloramphenicol (34% of the isolates). The resistance of *Enterococcus* species isolated from Turkish white cheese samples to 13 antibiotics is studied by Citak and coworkers (2004) and 96% of *E.faecium* isolates were found to be resistant to erythromycin, whereas 76% and 44% were resistant to chloramphenicol and tetracycline respectively. Huys and coworkers (2004) have found that 24% of *Enterococcus* isolates from European cheeses displayed phenotypic resistance to tetracycline with MIC ranges of 16 to 256 μ g/ml. *E. faecium* isolates from different food sources at varying degrees.(Franz *et al.*, 2001; Drahovska *et al.*, 2004; Johnston and Jaykus, 2004; Belicova *et al.*, 2007; Valenzuela *et al.*, 2008)

W. confusa is present in some fermented vegetables and milk (**Bjorkroth** et al., **2002**), as well as in human faeces of healthy individuals (**Walter** et al., **2001**) or in some bacteremia cases (**Kumar** et al., **2011**; **Harlan** et al., 2011), In Weisella confusa strains from KoKo (fermented millet porridge) of Africa origin, one of these strains was found to be resistant to tetracycline (**Ouoba** et al., **2008**). All the strains belonging to Weisella confusa species in our study showed multiresistant to tetracycline and chloramphenicol. Strain GL-33 which has the highest MIC value for tetracycline was also eryrthromycin resistant.

Ayeni *et al.*, (2011) reported that *Weisella confusa* isolates obtained from Nigerian dairy products and cow's intestine are chloramphenicol resistant and authors argued that their results could indicate the presence of specific chloramphenicol resistance genes in *Weisella*.

While the most *Leuconostoc* species those have been investigated previously were reported to be susceptible to chloramphenicol, like to rifampicin, erythromycin, clindamycin and tetracycline (Swenson *et al.*; 1990; Florez *et al.*, 2005) *Leuc. mesenteroides* strains isolated in our study were found to be resistant to chloramphenicol.

CONCLUSION

Knowledge on the antibiotic resistance of LAB is still limited and it is hard to evaluate the resistance profiles because of the heterogeneity of this group. Our findings suggest that the LAB strains belonging to the genera *Pediococcus*, *Leuconostoc*, *Weisella*, *Enterococcus* are generally resistant to clinically relevant antibiotics such as tetracycline and chloramphenicol. The authors concluded that prevalence of antibiotic resistant LAB in traditionally fermented dairy products and boza is high and these kinds of foods should be monitored carefully.

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