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Korrespondenzadresse:
didemkankaya@isparta.edu.tr

Summary

¹⁾ Department of Food Processing, Gelendost Vocational School, Isparta University of Applied Sciences, 32900, Isparta, Turkey; ²⁾ Faculty of Engineering, Department of Food Engineering, Süleyman Demirel University, 32260, Isparta, Turkey

Safety assessment of Lactobacilli isolated from foods of animal origin

Sicherheitsbewertung von aus Lebensmitteln tierischen Ursprungs isolierten Laktobazillen

Didem Akpınar Kankaya¹⁾, Banu Özden Tuncer²⁾, Yasin Tuncer²⁾

In this study, lactobacilli strains that were isolated from different foods of animal origin were identified at the species level and investigated for antibiotic resistance, virulence factors, biofilm, and biogenic amine production characteristics. According to the results of the 16S rDNA sequence analysis, thirty isolates were identified as 22 *Lactiplantibacillus plantarum*, three *Lacticaseibacillus paracasei* subsp. *tolerans*, two *Lactilactobacillus sakei* subsp. *sakei*, one *Lacticaseibacillus rhamnosus*, one *Limosilactobacillus fermentum*, and one *Lactilactobacillus curvatus*. By disk diffusion test, all strains were found to be resistant to at least one antibiotic. Most of the strains were found resistant to vancomycin (90%), followed by ceftiofur (86.67%) and norfloxacin (66.67%). The only *vanX* gene (93.33%, 28/30) was detected in strains, but no other antibiotic resistance genes were detected in any of the strains. PCR findings revealed the presence of the *acm* (3/30, 10%) and *efaA₁₅* (1/30, 3.33%) genes in strains, but other virulence factor genes were not detected in any of the strains. The biofilm production genes were not found in any of the isolates. Only the tyrosine decarboxylase gene *tdc* was found in *Lactilactobacillus curvatus* DYB17, which decarboxylates tyrosine.

Keywords: Lactobacilli, antibiotic resistance, virulence factor, biofilm, biogenic amine

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Introduction

Lactic acid bacteria (LAB) are industrially important bacteria known for their fermentative properties as well as their positive effects on nutrition and health (Badr et al., 2005). Certain lactobacilli belonging to the LAB family are used as starters or beneficial cultures in traditional applications and are employed as probiotics to help human health. The nomenclature of the genus *Lactobacillus* was revised in 2020 and *Lactobacillus plantarum*, *Lactobacillus paracasei* subsp. *tolerans*, *Lactobacillus sakei* subsp. *sakei*, *Lactobacillus rhamnosus*, *Lactobacillus fermentum* and *Lactobacillus curvatus* were renamed as *Lactiplantibacillus plantarum*, *Lacticaseibacillus paracasei* subsp. *tolerans*, *Latilactobacillus sakei* subsp. *sakei*, *Lacticaseibacillus rhamnosus*, *Limosilactobacillus fermentum*, *Latilactobacillus curvatus* respectively (Zheng et al., 2020). However, in the article, the term *Lactobacillus* in the old nomenclature was used for convenience in specifying the strains. Several *Lactobacillus* species have been given ‘generally recognized as safe’ (GRAS) status and are considered safe for human and animal consumption (Todorov et al., 2017). However, lactobacilli can also cause some infections such as endocarditis, bacteremia, and abscesses (Slover and Danziger, 2008). Moreover, there is a risk that these bacteria may act as reservoirs for the spread of antibiotic resistance genes to other bacteria (Mathur and Singh, 2005; Bernardeau et al., 2006; Courvalin, 2006a). Bacteria can show intrinsic or acquired resistance to the main groups of antibiotics used clinically (Davies and Davies, 2010; Fraqueza, 2015). In addition to medical treatment, antibiotics are also used in livestock and agricultural production (Nisha, 2008; Dugassa and Shukuri, 2017). This has led to an increase in the incidence of resistant strains (Ammor et al., 2007). Previous studies show that beneficial and common bacterial populations play a role in the transfer of antibiotic resistance to pathogenic and opportunistic pathogenic bacteria (Levy and Marshall, 2004; Salyers et al., 2004). Glycopeptide group antibiotics, which act by modifying the antibiotic target, are mainly used in the treatment of infections caused by Gram-positive bacteria (Kristich et al., 2014). Lactobacilli are inherently resistant to vancomycin, which works by interfering with the production of peptidoglycan precursors, which are necessary for the formation of the bacterial cell wall (Eliopoulos and Gold, 2001; Courvalin, 2006b; Goldstein et al., 2015). Compared to enterococci, although lactobacilli lack *vanA*, *vanB*, and *vanC* genes (Klein et al., 2000), some strains of lactobacilli have the *vanX* gene encoding D-alanyl-D-alanine dipeptidase, which is essential for cell wall synthesis (Liu et al., 2009). For this reason, their survival even with the use of antibiotics strengthens the use of these bacteria for probiotic purposes (Das et al., 2020). However, there is a risk that probiotic bacteria with transferable antibiotic resistance genes may act as reservoirs for transferring these resistance genes to other bacteria. The emergence of vancomycin-resistant strains has been a cause for concern, especially since vancomycin is used as a last resort in the treatment of infections caused by multi-resistant Gram-positive bacteria (Garcia-Migura et al., 2007; Fisher and Philips, 2009).

The presence of virulence factors increases the likelihood that bacteria will cause disease. The virulence factors of LAB, especially of enterococci, have been well researched. However, the long history of safe use of non-enterococcal LAB and their low virulence potential

make it difficult to find virulence factors for these bacteria (Franz et al., 2010). Even if the presence of virulence factors does not necessarily result in clinical infections, commensal bacteria that contain virulence factors may mediate the spread of virulence genes to other bacteria (Eaton and Gasson, 2001; Comerlato et al., 2013; Jimenez et al., 2013). Despite the fact that lactobacilli are generally recognized as safe, it is important to investigate the virulence factors they have due to their potential applications in food products (Eaton and Gasson, 2001).

Biofilm formation is a dynamic process that is affected by various environmental parameters such as bacterial strain, surface properties, pH, nutrient concentration, and temperature (Donlan, 2002). Biofilm production allows bacteria to adapt to harsh environmental conditions (Zhang et al., 2013) and also protects them from antibiotics and enzymes (Lewis, 2001). Biofilm formation is seen as a positive feature for probiotic microorganisms to adhere to surfaces and create various health effects (Lepargneur and Rousseau, 2002). On the other hand, biofilm production is accepted as a potential danger in the food industry, as it enables bacteria to be resistant to adverse conditions and causes bacterial contamination in foods (Kumar and Anand, 1998). Biogenic amines are naturally produced by plants, animals, and microorganisms (Shalaby, 1996) and play a role in the fulfillment of various activities of the cell (Medina et al., 2003). However, consumption of foods containing high amounts of biogenic amines leads to toxic results (Shalaby, 1996). The presence of biogenic amines in foods is an indicator of undesirable microbial activity. High biogenic amine levels in foods are considered an indication of faulty production or food spoilage (Linares et al., 2011).

The European Food Safety Authority (EFSA) has adopted a general approach to the safety assessment of microorganisms used in food and feed and has included a group of microorganisms in the “Qualified Presumption of Safety” (QPS) application (EFSA, 2005). In order to prevent the transmission of antibiotic resistance genes to pathogenic or other commensal bacteria, it is not desirable to have antibiotic resistance genes in starter or protective cultures, according to QPS conditions (EFSA, 2012). It is also desirable that these strains do not have other virulence factors and biogenic amine production characteristics (EFSA, 2011). For this reason, in this study, antibiotic resistance profiles, antibiotic resistance genes, virulence factors, biofilm and biogenic amine production properties of lactobacilli strains isolated from foods of animal origin were investigated.

Material and methods

Bacteria and growth conditions

A total of 30 isolates obtained from the Süleyman Demirel University Bacterial Genetic Laboratory culture collection were used in this study. These isolates were previously isolated from different foods of animal origin such as traditional Turkish cheeses, raw red meat, red meat products (sucuk and pastırma), raw chicken meat and sea fish. Isolates were randomly picked from vancomycin-containing (4 µg/mL) enterococcosel agar (BBL, Becton Dickinson and Company, Spark, USA) during the isolation of vancomycin-resistant enterococci from food samples of animal origin according to Robredo et al. (2000). Thirty isolates were identified as Gram-positive bacilli were stored at

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–32°C by adding 20% sterile glycerol. Isolates were grown in de Man Rogosa Sharpe (MRS, Biokar, France) broth at 37°C for 18 h before analysis.

Identification of isolates

Genomic DNA samples were extracted from isolates using a combination of the methods of Cancilla et al. (1992) and Abed (2013). Briefly, 0.5 mL of overnight cultures were centrifuged (15394 xg for 5 min) in 2 mL Eppendorf tubes, and cell pellets were dissolved in 0.5 mL of lysis buffer. Tubes were incubated in a water bath at 37°C for 60 min. Then, 2 µL of proteinase K (50 mg/mL) was added to the tubes and incubated at 37°C for 15 min. Following incubation, 30 µL of 10% (w/v) sodium dodecyl sulfate was added to the tubes and incubated for 5 minutes at 80°C. Then 0.7 mL of phenol-chloroform (1:10, v/v) was added to the cell suspensions and the tubes were centrifuged (15394 xg for 5 min) and this step was repeated two times. The upper phase was taken into new sterile tubes, 0.7 mL of 2-propanol was added, and the tubes were centrifuged (15394 xg for 5 min). The nucleic acid pellet was also extracted using 1 mL of 70% ethanol and centrifuged (15394 xg for 5 min). The precipitates were dissolved in 50 µL of Tris-EDTA buffer (pH 8.0) and stored at –20°C. The presence of the obtained genomic DNA samples was checked in gels prepared with a 0.7% (w/v) agarose ratio.

The universal bacterial primers pA and pE⁺ were used in the amplification of the 16S rDNA region of the isolates by PCR (Edwards et al., 1989). Amplified products were analyzed in a 1% (w/v) agarose gel. DNA sequence analysis of PCR products was carried out by BM Labosis (Ankara, Turkey). The 16S rDNA sequence similarity of the samples was determined using the BLAST program of the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) algorithm.

Antibiotic susceptibility

The antibiotic susceptibility of isolates was determined using the disk diffusion test. The test was performed on Mueller Hinton agar (LAB M, Lancashire, United Kingdom) plates using 18 commercial antibiotic disks: ampicillin (10 µg), erythromycin (15 µg), gentamicin (10 µg and 120 µg), kanamycin (30 µg), clindamycin (2 µg), chloramphenicol (30 µg), norfloxacin (10 µg), ofloxacin (5 µg), penicillin G (10 U), rifampin (5 µg), cephalothin (30 µg), cefoxitin (30 µg), ciprofloxacin (5 µg), streptomycin (10 µg and 300 µg), tetracycline (30 µg), vancomycin (30 µg) (Oxoid Ltd., UK). Strains were classified as resistant, intermediary, or susceptible according to Charteris et al. (1998) and CLSI (2016) guidelines.

Minimum inhibitory concentration (MIC)

The minimum inhibitory concentration (MIC) of isolates against vancomycin was tested using E-test strips (Liofilchem, Italy) according to the method recommended by the manufacturer. *Enterococcus faecalis* ATCC 29212 (*van*[–]) and *E. faecium* ATCC 51559 (*vanA*⁺) strains were used as controls in the MIC test.

Antibiotic resistance genes

Erythromycin (*ermA*, *ermB*, *ermC*), tetracycline (*tetK*, *tetL*, *tetM*, *tetO*, *tetS*), vancomycin (*vanA*, *vanB*, *vanCI*, *vanC2*, *vanC3*, *vanD*, *vanE*, *vanG*, *vanX*) and aminoglycoside (*aph(3')-IIIa*, *ant(4')-Ia*, *ant(6')-Ia*, *aac(6')-Ie-aph(2'')-Ia*, *aph(2'')-Ib*, *aph(2'')-Ic*, *aph(2'')-Id*) resistance genes in isolates were investigated by PCR using

specific primer pairs and protocols indicated by previous researchers (Dutka Malen et al., 1995; Lemcke and Bülte, 2000; Vakulenko et al., 2003; Depardieu et al., 2004; Ouoba et al., 2008; Liu et al. 2009; Niu et al., 2016). *E. faecium* ATCC 51559 (*vanA*⁺), *E. faecalis* ATCC 51299 (*aph(3')-IIIa*⁺, *aac(6')-Ie-aph(2'')-Ia*⁺, *ant(6')-Ia*⁺, *vanB*⁺), *E. gallinarum* DYE45 (*ermA*⁺, *ermB*⁺), *E. casseliflavus* DYE26 (*tetS*⁺, *vanC2*⁺, *vanC3*⁺), *E. gallinarum* DYE22 (*vanCI*⁺, *vanD*⁺) (Akpınar Kankaya and Tuncer, 2020), *E. faecium* FYE41 (*ermC*⁺, *tetM*⁺, *tetL*⁺) (Demirgöl and Tuncer, 2017), *E. faecium* MSE53.1 (*ant(4')-Ia*⁺, *aph(2'')-Ib*⁺, *aph(2'')-Ic*⁺) (Yalçın et al., 2023) were used as positive controls in the experiments.

Hemolytic and gelatinase activities

For the detection of hemolytic activity, the overnight cultures grown in MRS broth were transferred to blood agar (5% v/v) medium (Liofilchem) with the sterile loop and plates kept at 37°C for 48 hours of incubation. At the end of the incubation period, the formation of a clear zone around the colonies was evaluated as beta (β) hemolytic, the formation of a fuzzy greenish zone was considered alpha (α) hemolytic, and the absence of a zone was considered a gamma (γ) hemolytic reaction (Cariolato et al., 2008). In the hemolytic activity test, β-hemolytic *Staphylococcus aureus* ATCC 25923 was used as a control strain.

For the detection of gelatinase activity, overnight cultures were spread on Todd-Hewitt agar medium (Liofilchem) containing 3% gelatine (Merck, Germany) and incubated at 37°C for 24 hours. After the incubation period, the Petri dishes were kept in a refrigerator at 4°C for 5 hours. At the end of the period, the formation of an opaque zone around the colonies was accepted as a positive result (Eaton and Gasson, 2001). The *E. faecalis* NYE7 strain was used as a positive control in the gelatinase test (Inoğlu and Tuncer, 2013).

Detection of virulence factors

For the detection of virulence genes in isolates, gelatinase (*gelE*), cell wall adhesins (*efaA_{fm}*, *efaA_{fs}*), sex pheromones (*cpd*, *cob*, *ccf*, *cad*), collagen binding protein (*ace*, *acm*), aggregation protein (*agg*), cytolysin (*cylM*, *cylB*, *cylA*) and hyaluronidase (*hyl*) encoding genes were investigated by PCR (Eaton and Gasson, 2001; Vankerckhoven et al., 2004; Reviriego et al., 2005; Camargo et al., 2006; Belgacem et al., 2010). The *E. faecalis* ATCC 29212 (*gelE*⁺, *efaA_{fs}*⁺, *cpd*⁺, *cob*⁺, *ccf*⁺, *cad*⁺, *ace*⁺, *acm*⁺, *cylB*⁺, *cylA*⁺) was used as a positive control strain (Kasap and Tuncer, 2019).

Detection of biofilm production genes

The existence of genes involved in the production of extracellular surface protein (*esp_{fm}*, *esp_{fs}*), endocarditis and biofilm-associated pili (*ebpA*, *ebpB*, *ebpC*), and D-alanine lipotaichoic acid (*dltA*) in isolates was investigated according to Reviriego et al. (2005), Nallapareddy et al. (2006), and Fabretti et al. (2006).

Detection of biogenic amine production and amino acid decarboxylase genes

For the detection of the biogenic amine production of the isolates, basal medium containing lysine, tyrosine, ornithine, or histidine (Merck) precursor amino acids with a final concentration of 1% was used (Bover-Cid and Holzappel 1999). The presence of histidine (*hdc*), lysine (*ldc*), ornithine (*odc*) and tyrosine (*tdc*) decarboxylase genes in isolates was investigated using the primers given by De Las Rivas et al. (2006).

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Results and discussion

Identification of isolates

According to 16S rDNA gene sequence analysis, 30 isolates were identified to be *Lactiplantibacillus plantarum* (22), *Lacticaseibacillus paracasei* subsp. *tolerans* (3), *Lactilactobacillus sakei* subsp. *sakei* (2), *Lacticaseibacillus rhamnosus* (1), *Limosilactobacillus fermentum* (1), and *Lactilactobacillus curvatus* (1). LAB are used as starter cultures in the production of many fermented foods due to their fermentation abilities.

The metabolites produced by LAB not only provide the desired taste, aroma, and textural properties to fermented products, but also contribute to extending the shelf life of the products (Rattanachaikunsopon and Phumkhachorn, 2010). Previous studies have shown that lactobacilli can be isolated in many fermented foods (Liu et al., 2009; Nawaz et al., 2011; Kumar and Kumar, 2015; Yüceer and Özden Tuncer, 2015; Eid et al., 2016; Sharma et al., 2016; Kakelar et al., 2019). Similar to our results, Dos Santos et al. (2015) reported that vancomycin-resistant *L. rhamnosus* and *L. plantarum* strains were isolated from Coalho cheese in Brazil. Pavli et al. (2016) found

that lactobacilli isolated from traditional dairy products in Greece also include vancomycin-resistant *L. plantarum*, *L. pentosus*, *L. paraplantarum*, *L. sakei*, and *L. brevis*. Sharma et al. (2016) identified vancomycin-resistant *L. rhamnosus*, *L. acidophilus*, *L. fermentum*, and *L. plantarum* strains from commercial probiotic and pharmaceutical products.

Antibiotic susceptibility

The antibiotic resistance profiles of the isolates are given in Table 1. It was found that 90% (27/30) of the isolates had multidrug resistance. Similar to our results previous studies indicated that multidrug resistance was observed in *Lactobacillus* isolates (Kumar and Kumar, 2015; Anisimova and Yarullina, 2019). Considering that the examined isolates are food isolates, this situation may pose a serious threat to public health. Resistance to vancomycin (90.0%, 27/30), cefoxitin (86.67%, 26/30) and norfloxacin (66.67%, 20/30) was found to be most common among the isolates. Isolates were found to be resistant to other antibiotics used in this study at different rates. Antibiotic susceptibility and resistance rates of isolates were given in Table 2.

TABLE 1: Antibiotic resistance profile, antibiotic resistance genes, hemolytic and gelatinase activities, virulence genes, biofilm formation genes, biogenic amine production and decarboxylase genes in isolates.

Strain	Isolation material	Antibiotic resistance profile ^a	Antibiotic resistance genes	Hemolytic / gelatinase activities	Virulence genes	Biofilm formation genes	Biogenic amine production/ decarboxylase genes
<i>Lactiplantibacillus plantarum</i> DYB1	Lamb meat	AMP, RD, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB2	Goat meat	NOR, KF, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB3	Lamb meat	NOR, RD, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB5	Butter	NOR, OFX, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB6	Tulum cheese	NOR, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB7	White cheese	NOR, KF, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB8	Yoruk cheese	NOR, KF, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB9	Tulum cheese	NOR, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB10	Tulum cheese	NOR, OFX, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB12	Çökelek cheese	NOR, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB15	Lamb meat	OFX	vanX	α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB16	Chicken breast meat	NOR, P, KF, FOX, CIP, VA	vanX	γ / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB18	Tulum cheese	NOR, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB19	Tulum cheese	NOR, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB20	Tulum cheese	NOR, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB23	Otlu (herby) cheese	NOR, OFX, P, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB24	Tulum cheese	NOR, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB25	Tulum cheese	NOR, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB26	Sucuk	FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB27	Sucuk	NOR, OFX, P, KF, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB28	Sucuk	NOR, OFX, P, FOX, VA	vanX	weak α / -	-	-	-
<i>Lactiplantibacillus plantarum</i> DYB30	Sucuk	VA	vanX	weak α / -	-	-	-
<i>Lacticaseibacillus rhamnosus</i> DYB4	Kasar cheese	CN, K, FOX, S, VA	vanX	weak α / -	acm	-	-
<i>Limosilactobacillus fermentum</i> DYB11	Pastrma	K, NOR, FOX, CIP, S, VA	-	weak α / -	-	-	-
<i>Lacticaseibacillus paracasei</i> subsp. <i>tolerans</i> DYB13	Çökelek cheese	FOX, VA	vanX	weak α / -	-	-	-
<i>Lacticaseibacillus paracasei</i> subsp. <i>tolerans</i> DYB14	Ezine cheese	FOX, VA	vanX	weak α / -	acm, efaA ₅	-	-
<i>Lacticaseibacillus paracasei</i> subsp. <i>tolerans</i> DYB29	Ezine cheese	K, FOX, VA	-	weak α / -	-	-	-
<i>Lactilactobacillus curvatus</i> DYB17	Red mullet (<i>Mullus barbatus</i>)	CN, K, NOR, OFX, RD, CIP, S, VA	vanX	weak α / -	acm	-	Tyramine / tdc
<i>Lactilactobacillus sakei</i> subsp. <i>sakei</i> DYB21	Chicken breast meat	FOX	vanX	α / -	-	-	-
<i>Lactilactobacillus sakei</i> subsp. <i>sakei</i> DYB22	Chicken breast meat	OFX, FOX	vanX	weak α / -	-	-	-

^aAMP: Ampicillin, CN: Gentamicin (10 µg), K: Kanamycin, NOR: Norfloxacin, OFX: Ofloxacin, P: Penicillin, RD: Rifampin, KF: Cephalothin, FOX: Cefoxitin, CIP: Ciprofloxacin, S: Streptomycin (10 µg), VA: Vancomycin

TABLE 2: Antibiotic susceptibility and resistance (%) of vancomycin-resistant lactobacilli isolates.

Antibiotic	Concentration µg/disk	Sensitive	Intermediary	Resistance	Interpretative zone diameters (mm) ^d		
					R	I	S
Ampicillin ^a	10	96.67	0	3.33	≤12	13-15	≥16
Cefoxitin ^a	30	6.67	6.67	86.67	≤14	15-17	≥18
Cephalothin ^a	30	73.33	10	16.67	≤14	15-17	≥18
Chloramphenicol ^a	30	100.0	0	0	≤13	14-17	≥18
Ciprofloxacin ^a	5	40	50	10	≤13	14-18	≥19
Clindamycin ^a	2	100.0	0	0	≤8	9-11	≥12
Erythromycin ^a	15	96.67	3.33	0	≤13	14-17	≥18
Gentamicin (low-level) ^a	10	93.33	0	6.67	≤12	-	≥13
Gentamicin (high-level) ^b	120	100.0	0	0	6	7-9	≥10
Kanamycin ^a	30	73.33	13.33	13.33	≤13	14-17	≥18
Norfloxacin ^a	10	13.33	20	66.67	≤13	14-18	≥19
Ofloxacin ^a	5	16.67	56.67	26.67	≤13	14-18	≥19
Penicillin G ^a	10 ^c	46.67	40	13.33	≤19	20-27	≥28
Rifampin ^a	5	90	0	10	≤14	15-17	≥18
Streptomycin (low-level) ^a	10	80	10	10	≤11	12-14	≥15
Streptomycin (high-level) ^b	300	100.0	0	0	6	7-9	≥10
Tetracycline ^a	30	100.0	0	0	≤14	15-18	≥19
Vancomycin ^a	30	10	0	90	≤14	15-16	≥17

^aCharteris et al. (1998); ^bCLSI (2016) Performance Standards for Antimicrobial Susceptibility Testing 26th Information Supplement. ^cPenicillin G 10 U/disk; ^dR: resistant, I: intermediary, S: susceptible

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The glycopeptide antibiotic vancomycin acts by inhibiting the synthesis of peptidoglycan, which provides mechanical stability to the cell wall. Vancomycin is used in the treatment of infections caused by Gram-positive bacteria with multiple antibiotic resistance and is very important in clinical applications (Kristich et al., 2014). For this reason, the presence of transferrable vancomycin resistance genes in lactobacilli used for commercial purposes is the main concern due to the possibility of transferring antibiotic resistance genes to pathogenic bacteria (Bernardeau et al. 2008). On the other hand, it has been reported that some *Lactobacillus* species are naturally resistant to vancomycin (Gueimonde et al., 2013). Different researchers stated that the *Lactobacillus* isolates they examined were highly resistant to vancomycin (Yüceer and Özden Tuncer, 2015; Sharma et al., 2016; Anisimova and Yarullina, 2019; Saif and Sakr, 2020). The data that 90% of the lactobacilli isolates examined in this study were resistant to vancomycin is similar to the previous data. The MIC values of all isolates were found to be > 256 µg/mL for vancomycin. The data obtained in this study shows similarities with the studies conducted by different researchers (Dos Santos et al., 2015; Georgieva et al., 2015; Pavli et al., 2016). In a study examining the antimicrobial activity and antibiotic susceptibility of *Lactobacillus* isolates collected from different ecological niches, it was reported that 10 of 23 *Lactobacillus* isolates were resistant to vancomycin (> 256 µg/mL) (Georgieva et al., 2015). Dos Santos et al. (2015) reported that *L. plantarum* and *L. rhamnosus* isolates (except *L. plantarum* EM270), which they examined, showed high resistance to vancomycin (MIC >256 µg/mL). Pavli et al. (2016) found that the vancomycin MIC values of *Lactobacillus* isolates that they isolated from traditional fermented products of Greece were >256 µg/mL (except *L. lactis* T4 with an MIC of 32 µg/mL and *L. brevis* T47 with an MIC of 64 µg/mL). Although all isolates were found to be resistant to vancomycin according to the MIC results, *Lactiplantibacillus plantarum* DYB15, *Latilactobacillus sakei* subsp. *sakei* DYB21, and *Latilactobacillus sakei* subsp. *sakei* DYB22 strains were determined sensitive to vancomycin by the antibiotic disk diffusion test. A 10% very major error was found when disk diffusion results and MIC values of the isolates were compared. This means that these three strains were found to be false-susceptible in the disk diffusion test. The very major error rate of isolates was found to be higher than acceptable error rates (3%) according to CLSI guidelines (CLSI, 2016). The results of antibiotic susceptibility tests showed that the vancomycin susceptibility of lactobacilli isolates should be examined according to the MIC method. Similarly, very major errors were reported for the antibiotic disk diffusion test for vancomycin (Akpınar Kankaya and Tuncer, 2020) and high-level of gentamicin and streptomycin (Özdemir and Tuncer, 2020).

Another peptidoglycan inhibitor is β-lactam group of antibiotics (Pandey and Cascella, 2021). In this study, 46.67% and 96.67% of the isolates were found to be susceptible to penicillin G and ampicillin, respectively. Similar to our results, previous studies have shown that lactobacilli are sensitive to penicillin G (Bacha et al., 2010; Yüceer and Özden Tuncer, 2015; Talib et al., 2019) and ampicillin (Sharma et al., 2016; Anisimova and Yarullina, 2019; Talib et al., 2019). Beta-lactams are broad-spectrum antibiotics used for clinical purposes. Compared to other classes, beta-lactam antibiotics are generally safe and well tolerated (Chiriac et al., 2017). For this reason, resistance to this group of antibiotics is a concern for public health.

Since the ribosome is responsible for the synthesis of all cell proteins, it is an important target for antibiotics. Many antibacterial agents prevent cell development by affecting ribosome functions (Wilson, 2014; Lin et al., 2018). Due to the low permeability of the cell surface to aminoglycosides, lactobacilli are usually intrinsically resistant to low-level aminoglycosides, which act by disrupting the protein synthesis of the cell (Liu et al., 2009; Sharma et al., 2016; Anisimova and Yarullina, 2019). Disk diffusion test results showed that a low rate of isolates were found to be resistant to kanamycin (13.33%), low-level streptomycin (10%), and low-level gentamicin (6.67%). Contrary to our results, high rates of aminoglycoside resistance have been reported in previous studies (Yüceer and Özden Tuncer, 2015; Sharma et al., 2016; Anisimova and Yarullina, 2019). However, all (100%) of the isolates examined in our study were found to be susceptible to high-level gentamicin and streptomycin, as well as 73.33% of isolates were found to be sensitive to kanamycin. Lactobacilli do not usually cause infections. However, they can cause various infections in immunocompromised individuals. Because of the synergistic effect, the use of aminoglycosides together with β-lactams is generally recommended in the treatment of these infections (Slover and Danziger, 2008; Grazioli-Gauthier et al., 2022). Moreover, aminoglycosides have an important role in the treatment of infections caused by pathogenic bacteria that threaten human life. Therefore, the spread of high-level aminoglycoside resistance in bacteria leads to difficulties in the treatment of bacterial infections (Jaimee and Halami, 2016; Sparo et al., 2018). The fact that a high-level aminoglycoside resistance can be encoded on mobile genetic elements raises concerns due to the possibility of transmission of resistance genes from commensal bacteria to pathogenic bacteria (Özdemir and Tuncer, 2020; Yalçın et al., 2023). The use of clinically important antibiotics for growth-promoting purposes in animals is prohibited in most countries (Jaimee and Halami, 2016; Sparo et al., 2018). However, aminoglycoside antibiotics are recommended for use as therapeutic and protective agents in farm animals due to their effects against Gram-positive and Gram-negative bacteria (Jaimee and Halami, 2016). High-level aminoglycoside resistance is associated with transferable aminoglycoside-modifying enzymes (AMEs) genes (Niu et al., 2016; Özdemir and Tuncer, 2020). Therefore, the sensitivity of isolates to high-level aminoglycosides is important for the safety of the strains.

Antibiotics, members of the macrolide group, target the bacterial ribosome and also inhibit protein synthesis (Vázquez-Laslop and Mankin, 2018). It was determined that 96.67% of the isolates were susceptible to the macrolide group antibiotic erythromycin. Similar to our results, lactobacilli from fermented milk products and traditional fermented foods were found to be sensitive to erythromycin in previous studies (Liu et al., 2009; Turchi et al., 2013; Yadav et al., 2016; Saif and Sakr, 2020).

Quinolones inhibit DNA replication by binding to type II topoisomerases (DNA gyrase and DNA topoisomerase IV), which are responsible for DNA supercoiling (Kristich et al., 2014). In this study, 66.67% (30), 26.67% (30) and 10% (3/30) of isolates were found to be resistant to norfloxacin, ofloxacin and ciprofloxacin, respectively. Similarly, the presence of lactobacilli resistant to norfloxacin, ofloxacin, and ciprofloxacin has been reported by Sharma et al. (2016) and Anisimova and Yarullina (2019). Yüceer and Özden Tuncer (2015) reported that all of the lactobacilli isolated from fermented Turkish sausages were resistant to ofloxacin and 83.33% to norfloxacin.

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All isolates tested in the study were found susceptible to chloramphenicol, which is in agreement with the results obtained in previous studies (Liu et al., 2009; Turchi et al., 2013; Sharma et al., 2016; Anisimova and Yarullina, 2019). All of the strains examined in this study were found to be sensitive to tetracycline and clindamycin, and 90% to rifampin. Previous studies have shown that lactobacilli are generally sensitive to tetracycline and clindamycin, which act by inhibiting protein synthesis (Sharma et al., 2016; Anisimova and Yarullina, 2019; Talib et al., 2019). Cefoxitin is another antimicrobial to which lactobacilli are generally considered resistant. Cell wall impermeability is probably the main mechanism of resistance to cefoxitin (Delgado et al. 2007). The lactobacilli examined were generally resistant (86.67%) against cefoxitin. At the same time, 73.33% of the isolates were found to be susceptible to cephalothin. Similarly, Sharma et al. (2016) stated that 90% of the isolates they examined were susceptible to cephalothin.

Antibiotic resistance genes

Today, the spread of antibiotic resistance among pathogenic bacteria poses a global risk to public health. The use of antibiotics outside of clinical practice not only promotes the development of antibiotic resistance in bacteria, but may also lead to the spread of resistant pathogenic bacteria, which may compromise the efficacy of antibiotic therapy. The high intake of LAB, which contain transferable antibiotic resistance genes, into the body through foods raises the risk that these bacteria could act as a reservoir for the spread of resistance genes to other bacteria (Rozman et al., 2020). Of the resistance genes tested in this study, only *vanX* could be detected among the isolates (Table 1). The presence of the *vanX* gene was detected in all isolates, except *Limosilactobacillus fermentum* DYB11 and *Lacticaseibacillus paracasei* subsp. *tolerans* DYB29. Similar to our results, previous studies indicated that the *vanX* gene is commonly observed among *Lactobacillus* isolates (Guo et al., 2017; Anisimova and Yarullina, 2019). It is thought that vancomycin resistance is provided by a different mechanism in *Limosilactobacillus fermentum* DYB11 and *Lacticaseibacillus paracasei* subsp. *tolerans* DYB29 strains with phenotypically vancomycin-resistant detected but no *vanX* gene found. Similarly, Toomey et al. (2010), Zhang et al. (2013), and Shao et al. (2015) did not detect the presence of vancomycin resistance genes in phenotypically vancomycin-resistant *Lactobacillus* isolates. Even if the isolates are resistant to antibiotics, they may not contain antibiotic resistance genes. This may be due to the presence of natural antibiotic resistance in isolates, biofilm formation, mutations or changes in membrane structure, or the presence of resistance genes in isolates that could not be detected by the methods used in the study (Zhang et al., 2013).

Erythromycin, tetracycline, gentamicin, and streptomycin resistance genes were not detected in any of the isolates by PCR. These results confirm the disk diffusion test results. According to antibiotic disk diffusion results, all of the isolates were found to be sensitive to erythromycin (except for intermediate resistant *Lactiplantibacillus plantarum* DYB7), tetracycline, high-level gentamicin, and high-level streptomycin. Conversely to our results, it was reported that erythromycin (Ammor et al., 2008; Comunian et al., 2010; Mayrhofer et al., 2010; Nawaz et al., 2011; Gueimonde et al., 2013; De Souza et al., 2019; Arellano et al., 2020), tetracycline (Comunian et al., 2010; Mayrhofer

et al., 2010; Nawaz et al., 2011; Gueimonde et al., 2013; Arellano et al., 2020), gentamicin (Shao et al., 2015; De Souza et al., 2019; Arellano et al., 2020) and streptomycin (Shao et al., 2015; De Souza et al., 2019; Arellano et al., 2020) resistance genes were previously detected in *Lactobacillus* isolates. It is important for the safety of isolates that they do not include antibiotic resistance genes that may be transferred to other organisms.

Hemolytic and gelatinase activities

As a result of the hemolytic activity test, it was determined that 27 (90%) of the isolates showed weak α -hemolytic activity, two (6.67%) showed α -hemolytic activity and one (3.33%) γ -hemolytic activity. β -hemolytic activity was not detected in any of our isolates (Table 1). *Lactobacillus* isolates were shown to be absent of β -hemolytic activity in a number of investigations (Saelim et al., 2017; Abouloifa et al., 2020; Banwo et al., 2021), which is in agreement with our results. Since hemolytic activity is an important virulence factor that threatens human health, isolates to be used as starter cultures or for probiotic purposes should not show beta-hemolytic activity (Semedo et al., 2003).

Gelatinase activity was not detected in any of the isolates (Table 1). This result is consistent with the findings for *Lactobacillus* isolates of other researchers (Aarti and Khusro et al., 2019; Mami et al., 2019; Abouloifa et al., 2020; Saif and Sakr, 2020; Banwo et al., 2021). As stated by the Food and Agriculture Organization (FAO) and EFSA, no strains with hemolytic/gelatinase activity are allowed to be used in food production (FAO, 2006; EFSA, 2012).

Detection of virulence factors

Virulence factors are effector molecules that increase the disease-causing effect of microorganisms. Except for some *L. rhamnosus* strains, which are opportunistic pathogens, *Lactobacillus* species are not considered pathogenic for humans (EFSA, 2007). Despite the general acceptance of lactobacilli as safe, it is important to investigate the virulence factors of lactobacilli due to their potential applications in food products because these genes are usually plasmid encoded and there is a risk of transmission to intestinal pathogens (Eaton and Gasson, 2001). In this study, the *acm* gene was detected in three (10%) and *efaA_{fs}* in one (3.33%) of the isolates. The gelatinase (*gelE*), cell wall adhesion (*efaA_{fm}*), sex pheromones (*cpd*, *cob*, *ccf*, *cad*), collagen-binding protein (*ace*), aggregation protein (*agg*), cytolysin (*cylM*, *cylB*, *cylA*), hyaluronidase (*hyl*) genes were found in none of the isolates (Table 1). Previous study on the virulence factor genes in *Lactobacillus* has found that isolates either do not have any virulence factor genes or have a low rate of them, which is consistent with our findings (Dos Santos et al. 2015; Sanchart et al., 2016; Li et al., 2017; Saelim et al., 2017; Arellano et al., 2020). The collagen-binding proteins Ace and Acn are encoded by the *ace* and *acm* genes, respectively (Rich et al., 1999; Nallapareddy et al., 2008). Collagen-binding proteins, which play an important role in colonization, are effective on endocarditis in previous studies (Nallapareddy et al., 2008; Singh et al., 2010). It has also been reported that ace proteins facilitate binding to collagen during infections (Girish and Kemparaju, 2007). Efa is an important colonization factor (Kafil et al., 2016), and it also plays an important role in biofilm formation (Kafil et al., 2016; Beomidehagh et al., 2018; Narenji et al., 2020). In particular, *efaA_{fs}* has been reported to play a pathological role in animal models (Eaton and Gasson, 2001). Similar to our results, the

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presence of the *ace* gene in one *L. rhamnosus* and three *L. plantarum* strains isolated from artisanal Coalho cheeses was reported by Dos Santos et al. (2015). De Moraes et al. (2017) detected the *efaA* in the *L. mucosae* CNPC009 strain isolated from goat milk. Furthermore, Motahari et al. (2017) indicated that both the *ace* and *efaA_{fs}* genes were found in the *L. pentosus* 22C strain isolated from Iranian traditional yogurt. According to the results of this study, gelatinase activity was not found in any of the isolates. This was in line with the fact that the *gelE* gene was not found in the isolates. In the same way, the lack of *cylA*, *cylB*, and *cylM* genes in isolates and the absence of hemolytic activity in isolates support one another.

Detection of biofilm production genes

The presence of biofilm production associated genes encoding extracellular surface protein (*esp_{fm}*, *esp_{fs}*), endocarditis and biofilm-associated pili (*ebpA*, *ebpB*, *ebpC*), and D-alanine lipoteichoic acid (*dltA*) was not detected in isolates (Table 1). Similar to the data obtained in our study, some researchers reported that the *Lactobacillus* isolates did not have the *esp* gene (Jeronymo-Ceneviva et al., 2014; Todorov et al., 2017; De Souza et al., 2019). Biofilm-associated pili (Ebp) are among the virulence factors that play an important role in biofilm formation and endocarditis development in *E. faecalis* (Nallapareddy et al., 2006). Similar to the data obtained in our study, Landeta et al. (2013) reported that the *ebpA* gene was not found in *L. paracasei*, *L. plantarum*, and *L. sakei* strains, isolated from dry-cured sausages. Teichoic acids are molecules found in the cell-wall of Gram-positive bacteria. Commonly, it consists of variable-length polyglycerol phosphate or polyribitol phosphate chains substituted by glycosyl residues, D-alanyl esters, or both. Studies on *dlt* mutants show that D-alanyl ester reduction of teichoic acid affects various phenotypes in Gram-positive bacteria, especially biofilm production (Walter et al., 2007). The *dlt* operon has been extensively studied in enterococci isolates (Fabretti et al., 2006; Wang et al., 2015). However, there are limited studies on the presence and effects of the *dltA* gene in *Lactobacillus* isolates. Along with that, it has been reported that d-alanylation of teichoic acid is an important cell function for the survival of *L. reuteri* in acidic environments and other adverse stomach conditions (Walter et al., 2007). The biofilm formed by lactobacilli has been mostly studied in terms of the survival of probiotic bacteria and interaction with the host. Some researchers state that biofilm formation of starter cultures is a positive feature, as it will prevent the adhesion of pathogens and spoilage bacteria by providing colonization of starter cultures (Leriche and Carpentier, 2000; Lebeer et al., 2007). However, biofilm formation is undesirable because of the potential problems it creates in the food industry, and biofilm-forming isolates are more resistant to antimicrobials (Radovanovic et al., 2020). In studies conducted by different researchers, biofilm production has been reported in lactobacilli (Landeta et al., 2013; Zhang et al., 2013; Sun et al., 2020).

Detection of biogenic amine production and amino acid decarboxylase genes

Phenotypic decarboxylase activity tests indicated that only the *Lactilactobacillus curvatus* DYB17 strain decarboxylated tyrosine, but other strains did not decarboxylate any of the precursor amino acids used in this study. These results showed 100% correlation with the PCR results (Table 1). The tyrosine decarboxylase gene *tdc* was detected

only in the *Lactilactobacillus curvatus* DYB17 strain. The amino acid decarboxylase genes *tdc*, *hdc*, *odc*, or *ldc* were not detected in any of the other strains. Similar to our results, De Moraes et al. (2017) reported that the *tdc* gene was detected only in the *L. mucosae* CNPC009 strain among three *L. mucosae* isolates. Previously, biogenic amine production was not detected in *Lactobacillus* species isolated from food samples (Lee et al., 2011; Zhang et al., 2012; Yüceer and Özden Tuncer, 2015; Sanchart et al., 2016; Arellano et al., 2020). On the other hand, the presence of biogenic amine producer *Lactobacillus* strains was detected in wine (Bonnin-Jusserand et al., 2012), sausage (Pircher et al., 2007; Moracanian et al., 2015) and cheese (Pircher et al., 2007; Diaz et al., 2016). Biogenic amine production is associated with food fermentation (Shiling et al., 2015) and causes serious health problems if consumed in high amounts (Arellano et al., 2020). Except for *Lactilactobacillus curvatus* DYB17, all isolates were found to be safe in terms of biogenic amine production.

Conclusion

The isolates were found to be susceptible to most of the clinically important antibiotics. Only the *vanX* gene was detected in isolates, and none of the isolates contained transferrable antibiotic resistance genes examined in this study. When disk diffusion results and MIC values of the isolates were compared, a 10% very major error was found. The results of this study showed that the disk diffusion test should be supported by the MIC test in the investigation of vancomycin resistance in lactobacilli. As a result of the analysis in which the safety evaluation of isolates was performed, it was determined that they had a generally low-risk profile. These results are an advantage in terms of consumer health. Isolates that are shown to be safe for human consumption in future research may then be studied for their technological and probiotic capabilities to assess their use in the food industry.

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Conflict of interest

The authors declare no conflicts of interest.

ORCID

Didem Akpınar Kankaya: 0000-0002-1091-6210

Banu Özden Tuncer: 0000-0001-9678-4441

Yasin Tuncer: 0000-0002-2075-5027

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Address of corresponding author:

Didem Akpınar Kankaya
 Department of Food Processing
 Gelendost Vocational School
 Isparta University of Applied Sciences
 32900, Isparta
 Turkey
 didemkankaya@isparta.edu.tr

Kontakte

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Ravenstraße 45 · 31061 Alfeld (Leine)
 Postfach 16 42 · 31046 Alfeld (Leine)
 Telefon (0 51 81) 80 02-0
 Telefax (0 51 81) 80 02-55
 E-Mail info@p-d-ges.de