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Investigation of a new *Lactobacillus delbrueckii* **strain from human milk as a probiotic candidate**

Untersuchung eines neuen Lactobacillus delbrueckii-Stammes aus menschlicher Milch als probiotischer Kandidat

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Summary In this study, the safety evaluation, health-beneficial potential, probiotic and functional properties of *Lactobacillus delbrueckii* MA-9 strain originating from human breast milk were investigated in vitro. MA-9 strain showed very high resistance to simulated in vitro gastrointestinal conditions and food preservatives. The strain demonstrated nonhemolytic activity, inhibitory action on different indicator pathogen microorganisms (twelve clinical or human food-borne bacteria, two yeast and seven bacterial fish pathogens), high levels of aggregation, strong cholesterol removal ability and 2,2-Diphenyl-1 picrylhydrazyl (DPPH) radical scavenging activity (43.40%). Moreover, the strain showed positive α -amylase and lichenase (β -1,3-1,4-glucanase) enzyme activities. The results demonstrated that the *L. delbrueckii* MA-9 strain can be a good probiotic candidate and natural food additive to promote health.

Keywords: Human milk, enzyme activity, anti-cholesterol ability, aggregation

Introduction

The upper respiratory system, gastrointestinal tract and urogenital system of all vertebrate organisms, including humans, have a very large microbial population. The majority of these microbial populations are bacteria and these are most commonly localized in the intestinal and immune system $(10^{10} - 10^{12} \text{ CFU/g})$ (Kerry et al., 2018; Parker et al., 2020). The beneficial-harmful microorganisms in the gastrointestinal tract of a healthy host are in equilibrium and the metabolites of useful microorganisms have many beneficial/positive effects on host health. For example, probiotic microorganisms can support the maintenance and repair of the epithelial barrier by producing various metabolic byproducts (such as polysaccharides, short-chain fatty acids) that induce mucus secretion of intestinal cells and the synthesis of tight junction proteins (Silva et al., 2020; Song et al., 2021). However, metabolite output of the intestinal microflora can influence not only intestinal health but also the function of many other distal organs and systems through some axis such as; gutbrain, gut-lung, gut-liver, gut-kidney, gut-bone, gut-muscle (Schroeder and Bäckhed, 2016; Cianci et al., 2018; Feng et al., 2018; Grosicki et al., 2018; Yang et al., 2018). In the case of impaired gut microbiota (dysbiosis), there is a decrease in the number-diversity of the beneficial microorganisms and their metabolites. In dysbiosis, the intestinal epithelial cells are destroyed and consequently, the flow of undigested food and toxic substances into the bloodstream takes place (Parker et al., 2020). In such a case, re-modulation of health and the regulation of intestinal-associated multiple host metabolic pathways can be achieved by consuming probiotic-supplemented foods.

Probiotics have been currently defined as "live microorganisms which when administered in adequate amounts confer a health benefit on the host" (Hill et al., 2014). It has been determined that probiotic microorganisms have important therapeutic effects on host health such as feeding other intestinal microbial communities, providing energy homeostasis and affecting the functions of various organs and systems (Wang et al., 2017). Most of the strains identified as probiotic cultures are found in the lactic acid bacteria (LAB) group and these microorganisms are widely used in the fields of medicine, food and feed production.

Lactobacillus delbrueckii group members are obligately homofermentative lactobacilli and the G + C ratio in their DNA is in the range of 49–51% mole (Rizzello and De Angelis, 2011; Hammes and Hertel, 2006). *L. delbrueckii* strain has been genetically identified in many studies in the past to determine the bacterial diversity of breast milk (Collado et al., 2009; Xu et al., 2018; Ding et al., 2019). However, studies focusing on the determination of probiotic properties mostly cover *L. delbrueckii* subsp. *bulgaricus* strains from yogurt and fermented food (Nwamaioha and Ibrahim, 2018). Studies on *L. delbrueckii* strains of human milk origin are very limited and it is always desirable to identify new strains with probiotic potential. Because generally, the probiotic properties of these microorganisms are specific for strain. Therefore, in this study, susceptibility of *L. delbrueckii* MA-9 strain to the gastrointestinal system, food preservatives and various antibiotics was tested in an *in vitro* experiment. In addition, some properties that can modulate health such as antimicrobial, antioxidant and anti-cholesterol activities and aggregation abilities have been investigated.

Material and methods

Strain

L. delbrueckii MA-9 was isolated from breast milk collected from volunteer mothers in Aksaray University Scientific and Technological Application and Research Center (ASUBTAM) as part of a project we have previously carried out.

2.2. Safety screening

The susceptibility of MA-9 strain to antibiotics was performed using the disc diffusion method on MRS medium (Anisimova and Yarullina, 2019). Ten commercial antibiotic discs (Oxoid) were used in the study. The antibiotic discs used and their concentrations were as follows: amikacin, (10 µg), gentamycin (10 µg), kanamycin (30 µg), amoxicillin (30 µg), ampicillin (10 µg), penicillin G (10 µg), chloramphenicol (30 µg), erythromycin (15 µg), nalidixic acid (30 µg), ofloxacin (5 µg). The active culture of *L.* delbrueckii MA-9 strain (McFarland $0.5 = 5.1 \times 10^8$ CFU/ mL, 100 µl) was spread on MRS agar plates. The antibiotic discs were placed on the surface of the inoculated plates. Petri dishes were placed in an anaerobic jar containing Anaerocult® (Merck) moistened with approximately 5 mL of distilled water and incubated at 37°C for 24 h. The inhibition zone diameters were measured and the results were presented as resistance (R), moderate susceptibility (MS), or susceptibility (S) according to interpretative standards described previously (Charteris et al., 1998).

Screening for hemolytic activity was performed using Columbia sheep blood agar (Çağdaş 06 Sağlık Hizmetleri Ltd.Şti, OR-BAK, Lot number: 1602472). Briefly, streak plate method was used for inoculation of MA-9 strain on the growth media surface. After incubation at 37°C for 24 h, the plates were examined for the formation of blood lysis zones (α , β or γ -hemolysis) around MA-9 colonies.

Resistance to Simulated Gastrointestinal Conditions

Tolerance to simulated gastrointestinal conditions (low pH, bile, gastric and small intestinal fluids) was tested by viable colony count. For this purpose, MRS broth and agar medium were prepared separately to simulate the different conditions mentioned. In order to detect the low pH resistance of the strain, media with pH 2 and 3 were prepared, while media containing 0.3% and 1.0% (Thermo Scientific™ Oxoid™ Bile) bile were prepared to determine their viability at different bile concentrations (Reuben et al., 2019). In order to determine the simulated gastric juice tolerance of the strain, media containing 3 g/L (Sigma-Aldrich) pepsin adjusted to pH 2 and 3 were prepared. Finally, MRS broth and agar media containing 1 g/L pancreatin (Sigma-Aldrich)-0.03 g/L bile salt (Oxoid) were prepared to determine the tolerance of the strain to the small intestinal fluid (Asan-Ozusaglam and Gunyakti, 2019; Kaur et al., 2020). Free cell concentrations of *L. delbrueckii* MA-9 strains were adjusted based on the Mc Farland 0.5 (\approx 5.1 \times 108 cfu/mL) system in saline solution (Bin Masalam et al., 2018; Sharafi and Nateghi, 2020). Concentration-adjusted cell suspension, sterile control group and test group were inoculated separately at 1% in MRS broth. After inoculation, control and test groups were incubated for 0, 1 and 3 hours for low pH tolerance, 0 and 4 hours for bile tolerance, 0 and 3 hours for stomach and 0 and 4 hours for small intestine solutions. These incubation times used in the experiments were chosen based on the exposure times of the foods to the gastrointestinal tract. At the end of the

incubation periods, serial dilutions were made in SF solutions for all groups. From the prepared dilution sets, 1% inoculation was performed on MRS agar media and petri plates were incubated at 37°C for 24 hours under anaerobic conditions. At the end of the incubation period, viable cell counts were performed and the obtained values were presented based on Log10. The experiments were performed with three replicates.

Determination of Aggregation Abilities

The aggregation assays were assayed according to Behbahani et al. (2019) with slight modifications. The coaggregation ability of *L. delbrueckii* MA-9 strain with various pathogen microorganisms such as *L. monocytogenes* ATCC 7644, *E. coli* ATCC 35218, *E. coli* O157:H7 ATCC 43895, *S. enteritidis* ATCC 13076, *S. enteritidis* RSKK 171, *S. agalactiae* and *V. alginolyticus* was tested. For both experiments, the cell densities of MA-9 strain and pathogenic test bacteria were adjusted to a density of 0.6 ± 0.02 at 600 nm ($\approx 12x$ 10⁸ CFU/mL) with a spectrophotometer (Beckman Coulter DU 730) in phosphate-buffered saline (PBS). For the auto-aggregation assay, *L. delbrueckii* MA-9 strain was incubated at 37 ºC for 4 h without agitation in three replicates. For the co-aggregation assay, equal volumes (2 mL) aliquots of *L. delbrueckii* MA-9 strain and pathogenic microorganisms were mixed and then incubated at 37 ºC for 4 h. After the incubation period, the sample (0.1 mL) was suspended in PBS buffer (3.9 mL) and read at $OD₆₀₀$ nm for auto-aggregation and co-aggregation assays.

The percentage of auto-aggregation was expressed as follows:

$$
Auto-aggregation \% = \frac{OD1 - OD2}{OD1} \times 100
$$

OD1: pre-incubation absorbance, OD2: after incubation absorbance

The percentage of co-aggregation was calculated as follows:

$$
Co-aggregation \% = \frac{(OD strain+OD pathogen right) - 2(OD mix)}{(OD strain+OD pathogen)} \times 100
$$

ODstrain: absorbance of *L. delbrueckii* MA-9 (pre-incubation), ODpathogen: absorbance of pathogen strain (pre-incubation), ODmix: absorbance of mixed strains (after 4 h)

Determination of tolerance to food preservative substances

The tolerance of *L. delbrueckii* MA-9 to sodium benzoate (Sigma Aldrich Saint Louis, USA, CAS number: 532- 32-1) and nisin (Sigma Aldrich Saint Louis, USA, CAS number: 1414-45-5) which are used as food preservatives was investigated. The sodium benzoate resistance of the strain (McFarland $0.5 \cong 10^8$ CFU/mL) was tested spectrophotometrically OD_{600} nm) in MRS broth medium prepared in seven different concentrations (0.015–1%) and acid production capabilities were determined at the same concentrations. The viability of the strain was also assayed at 0.1% sodium benzoate on solid agar after 24 h incubation at 37°C. The tolerance of the strain to various concentrations of nisin (1.25-150 µg/mL) was tested using the well diffusion method (Tsai and Sandine, 1987). The inhibition zones were recorded after incubation at 37 ºC for 24 h.

Determination of Enzymatic Activities

Amylase and lichenase (ß-1,3-1,4-glucanase) enzyme activities of *L. delbrueckii* MA-9 were qualitatively determined by spot-dropping free-cell supernatants on agar media. Nutrient agar media containing soluble starch (0.5% w/v) was used for amylase enzyme activity while medium containing Lichenan (0.1% w/v) was used for lichenase enzyme activity. The free cell supernatant $(50 \mu L)$ was dropped onto agar and incubated for 30 min at 37 °C. Then, the plates were stained with iodine and Congo Red to determine amylase and lichenase enzyme activities. The forming of clear zone around the spot-dropping areas on the agar medium was considered positive for the enzyme activity (Aşan and Ozcan, 2007).

Antimicrobial Activity

The antimicrobial effect of sterile cell-free supernatant (CFS) of 18–24 hours of active *L. delbreuckii* MA-9 culture against the fourteen clinical human-food borne bacteria, two yeast and seven bacterial fish pathogens were investigated using the agar well diffusion method described by Prabhurajeshwar and Chandrakanth (2017) with slight modifications. Active MA-9 culture was centrifuged at 5000 rpm for 15 minutes and bacterial cell-free supernatant (CFS) was separated from the pellets. CFS was filtered with the help of 0.2 µm micro filters, taken into sterile glass tubes and stored at +4°C for use in the experiment. The indicator strains (Mc Farland 0.5 standard turbidity, 100 μ L) were inoculated to the appropriate agar media. The sterile CFS (100 µL) was placed into the wells (7 mm in diameter). Following inoculation, the plates were incubated at the appropriate temperature for the development of indicator microorganisms for 24 h. Suitable media and incubation temperatures used for culturing pathogenic strains are as follows; Tryptic Soy Broth (TSB) medium containing 2% NaCl and 25ºC for Vibrio species, TSB medium/25ºC for *L. garvieae, Y. ruckeri* strains, TSB medium/37 ºC for *S. agalactiae* strain, Nutrient medium/30ºC for *A. hydrophila* ATCC 1970 strain, Yeast Extract-Peptone-Dextrose (YPD) medium/30ºC for Candida species, TSB medium/37ºC for *E. faecalis* ATCC 29212, *L. monocytogenes* ATCC 7644 strains, and Nutrient medium/37ºC for all other indicator pathogen microorganisms. Antimicrobial activity experiments were performed in triplicate and at the end of the incubation period the inhibition zone diameter values were measured using automatic caliper. The results were given as mean ± standard deviation.

Antioxidant Activity

Antioxidant activity of *L. delbreuckii* MA-9 strain was performed by DPPH (2,2-diphenyl-1-picrylhydrazyl; Sigma-Aldrich, Cas no:1898-66-4) radical scavenging and ferrous-ion chelating activity methods according to Chenet al. (2014) and Parrella et al. (2012) with minor modifications. For the DPPH radical reduction activity, 0.2 mM methanolic DPPH solution and of MA-9 strain (Mc Farland 0.5 standard turbidity, 0.8 mL) were mixed and then kept in the dark at room temperature for 30 min. After the incubation period, the absorbance of the mixed solution was read with the spectrophotometer at OD_{517} nm. For ferrousion chelating activity (FCA), ferrozine solution (5 mM, 2 mL), FeCl₂ (2 mM , 0.05 mL) solution and MA-9 strain (Mc Farland 0.5 standard turbidity, 1 mL) were mixed and then the absorbance was measured by using the spectrophotometer at OD_{562} nm. The DPPH radical scavenging and

ferrous ion chelating activities were estimated using the following formulas:

DPPH radical scavenging activity (%) =
$$
1 - \frac{OD2}{OD1} x 100
$$

Ferrous ion chelating activity (%) = $1 - \frac{OD1 - OD2}{OD1} x 100$

OD1= the absorbance of the control and OD2= the absorbance of the sample.

Determination of Cholesterol Assimilation Ability

The cholesterol assimilation ability of *L. delbrueckii* MA-9 strain was determined by using the "o-phthalaldehyde" descripted assay as we previously reported (Gunyakti and Asan-Ozusaglam, 2018). Briefly, strain MA-9 in MRS broth containing 1% Cholesterol (Sigma-Aldrich, Saint Louis, USA) (100 μ g/mL) and bile (0.3% vs 1%) (Oxoid, Hampshire, UK) were inoculated and incubated at 37 °C for 24 hours. At the end of the incubation period, the strain was centrifuged to obtain supernatant and pellets. The pellets were suspended in distilled water equal volume to the previous original media. Then, 3 mL of 99% ethanol was added into 0.5 mL of supernatant or pellet and vortex-mixed. 2 mL of 50% KOH (Sigma-Aldrich, Saint Louis, USA) was added to the samples and heated in a water bath (60 °C) for 10 min and then cooled at room temperature. 5 mL of hexane was added to the samples and the mixture was stirred for 20 s. Distilled water (3 mL) was added to each sample and gently mixed. The samples were kept at room temperature for 15 min. 2.5 mL of the hexane layer was taken and completely evaporated in a water bath at 60 °C. 4 mL of o-phthalaldehyde reagent (Sigma-Aldrich, Saint Louis, USA) was added to each tube. After 10 min, 2 mL of pure sulfuric acid (Merck, Darmstadt, Germany) was added to the samples. The samples were mixed and then incubated at room temperature for 10 min. Absorbance was read using a spectrophotometer at 550 nm. Cholesterol assimilation was calculated using the equation:

$A = 100 - [(B/C) \times 100]$

where A is cholesterol assimilation (%), B is cholesterol content in the culture medium (μg) , C is cholesterol content in the non-inoculated (control) medium (μg) .

Result and discussion

Safety aspects

The hemolytic and antibiotic resistance activities of the *L. delbrueckii* MA-9 strain were determined for the in vitro safety assessment. The resistance of MA-9 strain to various group antibiotics was evaluated and inhibition zone diameter values around antibiotic discs are given in millimeter (Table 1). Inhibition zone values obtained as a result of the antibiogram test were determined in the range of 7.44–29.61 mm. It was determined that the MA-9 strain was resistant (Resistant≤14) to all aminoglycoside (amikacin, gentamicin, kanamycin) and Quinolone (nalidixic acid, ofloxacin) group antibiotics. Conversely, the strain showed sensitivity against Beta-lactam (amoxicillin, ampicillin, penicillin G), Chloramphenicol (chloramphenicol) and Macrolide (erythromycin) groups (Susceptible>20). *L. delbrueckii* MA-9 strain showed the highest sensitivity with an inhibition zone value of 29.61 mm against penicillin G.

The resistance to antibiotic of probiotic microorganisms is regarded as a safety concern due to the risk of gene transfer. However, it has been reported that if a strain shows intrinsic resistance to any antibiotic, these resistance traits are not transferrable by horizontal gene transfer to other microorganisms in the intestinal microbiota (de Melo Pereira et al., 2018). In the literature, it has been determined that some Lactobacillus species such as *L. delbrueckii, L. rhamnosus, L. helveticus* and, *L. acidophilus* have intrinsic resistance to aminoglycoside and quinolone group antibiotics (Hummelet al., 2007; Sharma et al., 2017; Tang et al., 2018; Botthoulath et al., 2018). Considering the literature findings, a similar antibiotic resistance pattern was obtained for the *L. delbrueckii* MA-9 strain in our study. This may indicate that the MA-9 strain has intrinsic/innate resistance to aminoglycoside and quinolone group antibiotics, but further confirmation is still needed. The ability of the MA-9 strain to resist aminoglycoside and quinolone group antibiotics may be beneficial for the restoration of intestinal microflora destroyed during or after antibiotic treatment. One of the important selection criteria is a hemolytic activity for probiotic microorganisms. Lactic acid bacteria showing alpha-hemolytic activity were evaluated as nonhemolytic in the previous literature reports (Aryantiniet al., 2017; García et al., 2017; Peres et al., 2014). Similarly, in this study, it was determined that *L. delbrueckii* MA-9 showed α -hemolytic activity and based on this result, it was a non-hemolytic strain. On the basis of these results, it is considered that the MA-9 strain does not carry any risk factors for host health.

Cell survival in simulated gastrointestinal conditions

The tolerance of *L. delbrueckii* MA-9 to the simulated gastrointestinal tract conditions was assayed by counting viable cell and the results are given in log_{10} CFU/mL (Figure 1). In the viability of the strain, an increase was observed in the first hour of incubation in culture medium at

TABLE 1: *Antibiotic susceptibility of L. delbrueckii MA-9 strain.*

^a: Indicates no inhibition zone. ^b: Diameter of the inhibition zone including disc diameter. Values are reported as means ± SD of three separate replicates. **AK:** Amikacin, **AMC:** Amoxicillin, **AM:** Ampicillin, **C:** Chloramphenicol, **E:** Erythromycin, **CN:** Gentamycin, **K:** Kanamycin, **NA:** Nalidixic Acid, **OFX:** Ofloxacin, P: Penicillin G, c: R (resistant), MS (moderately susceptible), S (susceptible)

FIGURE 1: Survival in simulated gastrointestinal conditions of L. delbrueckii MA-9 (log₁₀ CFU/ *mL). a: Resistance to low pH values. b: Resistance to different concentrations of bile. c: Pepsin tolerance of L. delbrueckii MA-9. d: Pancreatin tolerance of L. delbrueckii MA-9.*

pH 3 and 2, but a decrease was observed in the 3rd hour. At the last hour of incubation, there was more live cell loss at the pH 2 than pH 3, but *L. delbrueckii* MA-9 still maintained its cell viability (Figure 1a). The viability of the MA-9 strain decreased by 0.24 CFU/mL after the incubation period in the culture medium containing bile at a concentration of 0.3%, while an interesting increase by 0.66 CFU/ mL was observed for 1% bile. The protection and survival of *L. delbrueckii* MA-9 from the toxic effect of bile suggest that this strain has protein expression, possibly related to bile resistance (bile salt hydrolase (BSH)). However, this assessment needs further validation (Figure 1b). Similarly, the strain has been able to preserve its vitality in culture media including pepsin and pancreatin (Figure 1c, d). It was determined that MA-9 strain tolerated different stress conditions of the gastrointestinal tract when all these results were obtained from the assays performed in the simulated medium.

Assessment of auto and co-aggregation

The aggregation ability of the *L. delbrueckii* MA-9 strain was tested spectrophotometrically. The auto-aggregation activity of MA-9 was recorded as 95%. The co-aggregation abilities of various group pathogen test microorganisms varied from 43 to 56% (Table 2). For human origin test bacteria, the highest coaggregation value was determined for E. coli O157:H7 ATCC 43895, while the lowest value was recorded for *S. enteritidis* RSKK 171. For both *S. agalactiae* and *V. alginolyticus* fish pathogen bacteria, coaggregation value was determined as 49%. The aggregation abilities of LAB are considered an important probiotic feature that supports the host defense mechanism (Abushelaibiet al., 2017; Śliżewska, et al., 2021). Aggregation ability of MA-9 strain indicated that the strain can colonize on host epithelial surfaces and can also prevent pathogenic microorganisms from adhering to these surfaces.

Tolerance to food preservative substances

The susceptibility properties of *L. delbrueckii* MA-9 strain against sodium benzoate and nisin food additives were tested (Figure 2 (a, b, c, and d)). When the spectrophotometric data of the strain for sodium benzoate were examined, it was observed that there was some decrease in vitality as the concentration of sodium benzoate increased (Figure 2a). When the acid production data at the same concentrations were

examined, an increase in the pH of the media was determined as the concentration of sodium benzoate increased (Figure 2b). The increase in pH of the media indicates a slight decrease in the strain viability. According to both methods, the strain was determined to maintain its viability even at high concentrations of sodium benzoate. For the 0.1% concentration of sodium benzoate, determined as the general limit of use in foods, live cell counting was performed. According to the obtained data, the viability of the strain decreased by 0.14 log/CFU compared to the control group (Figure 2c). The nisin susceptibility data showed that MA-9 strain growth was only inhibited at the highest concentration of nisin (150 µg/mL) with an inhibition zone of 3.14 ± 0.13 mm (Figure 2d). The strain showed resistance to the other eight concentrations of nisin. The results indicated that the strain was tolerant to the legal limits used in foods and even to the upper concentrations of both additives. Therefore, it can be thought that more viable strains will have an advantage in the digestive system and exceed the gastrointestinal tract barrier.

Screening of strain for enzymatic activities

The enzyme activities of the MA-9 strain were assayed by spot-dropping on agar media. In both media containing starch and lichenan, clear zone formation was observed in the spot-dropping regions. Therefore, the amylase and lichenase enzyme activities of the strain was evaluated as positive. After molecular characterization and purification of amylase and lichenase enzymes by further studies, it may be possible to use MA-9 strain in various fields such as foodstuff, alcoholic beverages, textile industry.

TABLE 2: *Co-aggregation ability of the L. delbrueckii MA-9.*

| Auto- | Coaggregation % | | | | | | | |
|--------------------|--|---------|---------------------------------------|-------------------------------------|-----------------------------------|---------------------------|------------------------------|--|
| aggre- gation % | L. monocyto- genes ATCC 7644 ATCC 35218 | E. coli | E. coli 0157: H7 ATCC 43895 | S. enteritidis ATCC 13076 | S. enteritidis RSKK 171 | S. aga- lactiae | V. algino- lyticus | |
| 95 | | | ካh | | | | 49 | |

FIGURE 2: *Sodium benzoate and nisin resistance of L. delbrueckii MA-9 strain. a: spectrophotometric data for seven different (0.075–1%) concentrations of sodium benzoate resistance of L. delbrueckii MA-9. b: acid production data of the strain in media containing sodium benzoate. c: Viability of L. delbrueckii MA-9. d: Nisin resistance of L. delbrueckii MA-9 (1.25–150 μg/mL).*

Antimicrobial activity

The inhibitory activity of cell free culture supernatants of MA-9 strain against different group indicator microorganisms was determined using well diffusion method and the results were presented in Table 3. The antibacterial activities of *L. delbrueckii* MA-9 against some human-originated bacteria varied from 2.91 to 10.95 mm. The anti-candidal activity of the strain was determined as 2.73 ± 0.57 mm and 3.22 ± 0.07 mm for *C. albicans* ATCC 10231 and *C. glabrata* RSKK 04019. The inhibitory activity of the strain against various fish pathogens varied from 3.61 to 10.49 mm. The highest inhibitory activity among all different group indicator microorganisms was determined for *S. epidermidis* ATCC 11228 (10.95±0.71), *L. monocytogenes* ATCC 7644 (10.63±0.38) and *A. hydrophila* ATCC 19570 (10.49±1.60), respectively. In our study, no inhibitory activity against only two clinical human-foodborne bacteria (*E. coli* O157:H7 ATCC 43895 and *M. luteus* NRRL B 4375) was recorded among twenty-three test microorganisms. The detailed listing of used twentythree pathogen test microorganisms has been provided in Table 3.

Zhang et al. (2019) reported a significant increase in growth performance of *Cyprinus carpio* fed with dietary supplementation of *L. delbrueckii.* Also, Zhang et al. (2017) indicated that the same fish species fed with dietary supplementation of *L. delbrueckii* had a 40% reduction in diseases caused by the *A. hydrophila* pathogen bacteria compared to the control group. In our study, *L. delbrueckii* MA-9 strain showed inhibitory activity against all indicator fish pathogens. Therefore, the use of the strain as a feed supplement in aquaculture can be suggested.

TABLE 3: *Antibiotic susceptibility of L. delbrueckii MA-9 strain.*

a : Diameter of the inhibition zone including disc diameter. Values are reported as means ± SD of three separate experiments. ^b : Indicates no antimicrobial activity. No inhibition (–), inhibition zone diameter value <8 mm (±), inhibition zone diameter value 8–10 mm (+), inhibition zone diameter value > 10 mm (++).

Antioxidant activity

Lactic acid bacteria contribute to the preservation of colonic epithelial cell integrity and tissue hemostasis by modulating the redox state in the intestine, mucosal surface and mucosa (Sun, et al., 2010). Therefore, in this study, the antioxidant properties of *L. delbrueckii* MA-9 strain were investigated in order to determine its possible therapeutic effect on the host gastrointestinal redox potential. The antioxidant properties of *L. delbrueckii* MA-9 strain were determined using DPPH radical scavenging and ferrous-ion chelating assays. DPPH radical scavenging activity tests the hydrogen donor ability of the strain whose antioxidant properties were investigated. Ferrousion chelating activity, on the other hand, is the situation where $Fe²⁺$ ions, which can be a source of hydroxyl radicals, are partially converted into ferric state (Fe^{3}) by lactic acid bacteria and rendered unusable in the Fenton reaction region. In this study, it was determined that DPPH free radical scavenging activity of *L. delbrueckii* MA-9 strain was determined as 43.40%, while iron ion chelating activity was not found. It is thought that this result may be due to the differences in the working mechanisms of these methods used. In some recent studies, it has been reported that the DPPH radical scavenging activities of *L. delbrueckii* strains isolated from different sources (fermented yak milk, fermented foods, milk) are in the range of 17.20–35% (Ding, et al., 2017; Cheon et al., 2020; Riane et al., 2021). The per cent DPPH scavenging value we obtained was similar to the literature data, but higher activity was recorded. Although studies on the iron ion chelating activity of various foods or exopolysaccharides obtained by using *L. delbrueckii* strains have been reported in the literature (Jhan et al., 2015; Adebayo-Tayo and Fashogbon, 2020) as far as we know, there is no study on the activity of the strain directly. The data obtained show that the strain has good antiradical activity. Therefore, it is thought that the MA-9 strain may exert therapeutic effects on the host health by modulating the redox state in the gastrointestinal system.

Assimilation of cholesterol

The anti-cholesterol activities of the pellet and supernatant were tested in different bile concentrations and the results were presented in Figure 3. The supernatant of the MA-9 strain had the higher cholesterol assimilation ability at both bile concentrations than the pellet. The highest assimilation value for the supernatants was determined at

FIGURE 3: *lus.* Turk J Vet Anim Sci 31: 319–324. *Cholesterol removal ability of L. delbrueckii MA-9.*

a concentration of 0.3% bile (82.30%), followed by 1% bile (71.24%) concentration. For the pellets, the anti-cholesterol activity values were 38.05% and 54.65% for 0.3 and 1% bile. Based on the positive *in vitro* results, we may assume that the *L. delbrueckii* MA-9 strain can assimilate dietary cholesterol and stabilize serum cholesterol level by showing a similar activity in the gastrointestinal tract of the host. However, these inferences need to be confirmed by in vivo experiments in future studies.

Conclusions

In the present study, the non-hemolytic *L. delbrueckii* MA-9 strain was found to be resistant to simulated gastrointestinal system conditions and various food preservatives. This is important in terms of reaching more intestinal cultures and producing various mediators. The strain also showed antimicrobial activity against various clinical human food-borne bacteria, yeast and fish pathogen microorganisms, reduction of the DPHH radical, high levels of cholesterol assimilation activity and aggregation ability. It is thought that the host health can be modulated by using *L. delbrueckii* MA-9 strain as a dietary supplement.

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Conflict of Interest

The authors declare none conflict of interest.

References

Abushelaibi A, Al-Mahadin S, El-Tarabily K, Shah NP, Ayyash M (2017): Characterization of potential probiotic lactic acid bacteria isolated from camel milk. LWT-Food Science and Technology 79: 316–325. doi: http://dx.doi.org/10.1016/j.lwt.2017.01.041 **Adebayo-Tayo, B., Fashogbon, R. (2020):** In vitro antioxidant, an-

tibacterial, in vivo immunomodulatory, antitumor and hematological potential of exopolysaccharide produced by wild type and mutant *Lactobacillus delbureckii* subsp. *bulgaricus.* Heliyon, 6(2), e03268. doi: https://doi. org/10.1016/j.heliyon.2020.e03268

> **Anisimova EA, Yarullina DR (2019):** Antibiotic resistance of *Lactobacillus* strains. Current microbiology, 76(12), 1407–1416. doi: https://doi.org/10.1007/s00284-019- 01769-7

> **Aryantini NPD, Yamasaki E, Hisao K, Nengah S, Tadasu U, Fukuda K (2017):** In vitro safety assessments and antimicrobial activities of *Lactobacillus rhamnosus* strains isolated from a fermented mare's milk. Animal Science Journal 88: 517–525. doi: https://doi.org/10.1111/asj.12668

Aşan M, Ozcan N (2007): Expression of the beta-(1, 3-1, 4)-Glucanase Gene in *Streptococcus salivarius* subsp. *thermophi-*

- **Asan-Ozusaglam M, Gunyakti A (2019):** *Lactobacillus fermentum* strains from human breast milk with probiotic properties and cholesterol-lowering effects. Food science and biotechnology, 28(2), 501–509.doi: https://doi.org/10.1007/s10068-018-0494-y
- **Bao Y, Zhang Y, Zhang Y, Liu Y, Wang S, Dong X, Wang Y, Zhang H (2010):** Screening of potential probiotic properties of *Lactobacillus fermentum* isolated from traditional dairy products. Food Control 21: 695–701. doi: 10.1016/j.foodcont.2009.10.010
- **Behbahani BA, Noshad M, Falah F (2019):** Inhibition of *Escherichia coli* adhesion to human intestinal Caco-2 cells by probiotic candidate *Lactobacillus plantarum* strain L15. Microb Pathogenesis 136: 103677. doi: https://doi.org/10.1016/j.micpath.2019.103677
- **Bin Masalam MS, Bahieldin A, Alharbi MG, Al-Masaudi S, Al-Jaouni SK, Harakeh SM, Al-Hindi RR (2018):** Isolation, molecular characterization and probiotic potential of lactic acid bacteria in Saudi raw and fermented milk. Evidence-Based Complementary and Alternative Medicine, 2018. doi: https:// doi.org/10.1155/2018/7970463
- **Botthoulath V, Upaichit A, Thumarat U (2018):** Identification and in vitro assessment of potential probiotic characteristics and antibacterial effects of *Lactobacillus plantarum* subsp. *plantarum* SKI19, a bacteriocinogenic strain isolated from Thai fermented pork sausage. JFST 55: 2774-2785. doi: 10.1007/s13197- 018-3201-3
- **Charteris WP, Kelly PM, Morelli L, Collins JK (1998):** Antibiotic susceptibility of potentially probiotic *Lactobacillus* species. J Food Prot 61: 1636–1643.
- **Chen P, Zhang Q, Dang H, Liu X, Tian F, Zhao J, Chen Y, Zhang H, Chen W (2014):** Screening for potential new probiotic based on probiotic properties and α -glucosidase inhibitory activity. Food Control 35: 65–72. doi:10.1016/j.foodcont.2013.06.027
- **Cheon MJ, Lim SM, Lee NK, Paik HD (2020):** Probiotic properties and neuroprotective effects of *Lactobacillus buchneri* KU200793 isolated from Korean fermented foods. International journal of molecular sciences, 21(4), 1227. doi: https://doi. org/10.3390/ijms21041227
- **Cianci R, Pagliari D, Piccirillo CA, Fritz JH, Gambassi G (2018):** The microbiota and immune system crosstalk in health and disease. Volume 2018:|Article ID 2912539. doi: https://doi. org/10.1155/2018/2912539
- **Collado MC, Delgado S, Maldonado A, Rodríguez JM (2009):** Assessment of the bacterial diversity of breast milk of healthy women by quantitative real-time PCR. Letters in applied microbiology, 48(5), 523–528.
- **De Melo Pereira GV, De Oliveira Coelho B, Júnior AIM, Thomaz-Soccol V, Soccol CR (2018):** How to select a probiotic? A review and update of methods and criteria. Biotechnol Adv 36: 2060–2076. doi: 10.1016/j.biotechadv.2018.09.003
- **Ding M, Qi C, Yang Z, Jiang S, Bi Y, Lai Sun J (2019):** Geographical location specific composition of cultured microbiota and *Lactobacillus* occurrence in human breast milk in China. Food & function, 10(2), 554–564.
- **Ding W, Wang L, Zhang J, Ke W, Zhou J, Zhu J, Long R (2017):** Characterization of antioxidant properties of lactic acid bacteria isolated from spontaneously fermented yak milk in the Tibetan Plateau. Journal of Functional Foods, 35, 481–488. doi: https://doi.org/10.1016/j.jff.2017.06.008
- **Feng Q, Chen WD, Wang YD (2018):** Gut microbiota: an integral moderator in health and disease. Frontiers in microbiology, 9, 151.doi: https://doi.org/10.3389/fmicb.2018.00151
- **García A, Navarro K, Sanhueza E, Pineda S, Pastene E, Quezada M, Henríquez K, Karlyshev A, Villena J, González C (2017):** Characterization of *Lactobacillus fermentum* UCO-979C, a probiotic strain with a potent anti-*Helicobacter pylori* activity. Electron J Biotechn 25: 75–83. doi: https://doi.org/10.1016/j. ejbt.2016.11.008
- **Grosicki GJ, Fielding RA, Lustgarten MS (2018):** Gut microbiota contribute to age-related changes in skeletal muscle size, composition, and function: biological basis for a gut-muscle axis. Calcified tissue international, 102(4), 433–442. doi: https://doi. org/10.1007/s00223-017-0345-5
- **Gunyakti A, Asan-Ozusaglam M (2018):** Investigation of the potential use of *Lactobacillus gasseri* originated from human bre-

ast milk as food additive. LWT Food Science and Technology 93: 613–619. doi: https://doi.org/10.1016/j.lwt.2018.04.020

- **Hammes WP, Hertel C (2006):** The genera *lactobacillus* and *carnobacterium.* In: The Prokaryotes, Bacteria: Firmicutes, Cyanobacteria, Springer-Verlang, New York, 4: 320–403.
- **Hill C, Guarner F, Reid G, Gibson GR, Merenstein DJ, Pot B, Sanders ME (2014):** Expert consensus document: The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. Nature reviews Gastroenterology & hepatology, 11, 506–514. doi: http://www.nature.com/doifinder/10.1038/ nrgastro.2014.66
- **Hills RD, Pontefract BA, Mishcon HR, Black CA, Sutton SC, Theberge CR (2019):** Gut microbiome: Profound implications for diet and disease. Nutrients 11: 1613. doi: 10.3390/nu11071613
- **Hummel AS, Hertel C, Holzapfel WH, Franz CM (2007):** Antibiotic resistances of starter and probiotic strains of lactic acid bacteria. Appl Environ Microbiol 73: 730–739.doi: 10.1128/ AEM.02105-06
- **Jhan JK, Chang WF, Wang PM, Chou ST, Chung YC (2015):** Production of fermented red beans with multiple bioactivities using co-cultures of *Bacillus subtilis* and *Lactobacillus delbrueckii* subsp. *bulgaricus.* LWT-food science and technology, 63(2), 1281–1287. doi: https://doi.org/10.1016/j.lwt.2015.03.107
- **Kaur Sidhu M, Lyu F, Sharkie TP, Ajlouni S, Ranadheera CS (2020):** Probiotic Yogurt Fortified with Chickpea Flour: Physico-Chemical Properties and Probiotic Survival during Storage and Simulated Gastrointestinal Transit. Foods, 9(9), 1144. doi: https://doi.org/10.3390/foods9091144
- **Kerry RG, Patra JK, Gouda S, Park Y, Shin HS, Das G (2018):** Benefaction of probiotics for human health: A review. Journal of food and drug analysis, 26(3), 927–939. doi: https://doi. org/10.1016/j.jfda.2018.01.002
- **Li P, Zhou Q, Gu Q (2016):** Complete genome sequence of *Lactobacillus plantarum* LZ227, a potential probiotic strain producing B-group vitamins. J Biotechnol 234: 66–70. doi: 10.1016/j. jbiotec.2016.07.020
- **Nwamaioha NO, Ibrahim SA (2018):** A selective medium for the enumeration and differentiation of *Lactobacillus delbrueckii* ssp. *bulgaricus.* J Dairy Sci 101: 4953–4961. doi: https://doi. org/10.3168/jds.2017-14155
- **Parker A, Fonseca S, Carding SR (2020):** Gut microbes and metabolites as modulators of blood-brain barrier integrity and brain health. Gut Microbes, 11(2), 135–157. doi: https://doi.org/10.10 80/19490976.2019.1638722
- **Parrella A, Caterino E, Cangiano M, Criscuolo E, Russo C, Lavorgna M, Isidori M (2012):** Antioxidant properties of different milk fermented with lactic acid bacteria and yeast. Int J Food Sci Tech 47:2493-2502. doi: https://doi.org/10.1111/j.1365- 2621.2012.03127.x
- **Peres CM, Alves M, Hernandez-Mendoza A, Moreira L, Silva S, Bronze MR, Vilas-Boas L, Peres C, Malcata FX (2014):** Novel isolates of *lactobacilli* from fermented Portuguese olive as potential probiotics. LWT-Food Science and Technology 59: 234–246. doi: http://dx.doi.org/10.1016/j.lwt.2014.03.003
- **Prabhurajeshwar C, Chandrakanth RK (2017):** Probiotic potential of *Lactobacilli* with antagonistic activity against pathogenic strains: An in vitro validation for the production of inhibitory substances. Biomed J 40: 270–283. doi: 10.1016/j.bj.2017.06.008
- **Reuben RC, Roy PC, Sarkar SL, Alam RU, Jahid IK (2019):** Isolation, characterization, and assessment of lactic acid bacteria toward their selection as poultry probiotics. BMC microbiology, 19(1), 1–20.doi: https://doi.org/10.1186/s12866-019-1626-0
- **Riane K, Sifour M, Ouled-Haddar H, Idoui T, Bounar S, Boussebt S (2021):** Probiotic properties and antioxidant efficiency of *Lactobacillus plantarum* 15 isolated from milk. Journal of Microbiology, Biotechnology and Food Sciences, 516–520. doi: https://doi.org/10.15414/jmbfs.2019/20.9.3.516-520
- **Rizzello CG, De Angelis M (2011):** Lactic Acid Bacteria | *Lactobacillus* spp.: *Lactobacillus delbrueckii* Group. In: Fuquay JW, editor. Encyclopedia of Dairy Sciences (Second Edition). San Diego: Academic Press; 119-24.: https://doi.org/10.1038/ nm.4185

- **Sharafi S, Nateghi L (2020):** Optimization of gamma-aminobutyric acid production by probiotic bacteria through response surface methodology. Iranian Journal of Microbiology, 12(6), 584. doi: https://dx.doi.org/10.18502%2Fijm.v12i6.5033
- **Shryock TR (2002):** Performance standards for antimicrobial disk and dilution susceptibility tests for bacteria isolated from animals: approved standard. Clinical & Laboratory Standards Institute.
- **Silva YP, Bernardi A, Frozza RL (2020):** The role of short-chain fatty acids from gut microbiota in gut-brain communication. Frontiers in endocrinology, 11, 25. doi: https://doi.org/10.3389/ fendo.2020.00025
- **Song Q, Wang Y, Huang L, Shen M, Yu Y, Yu Q, Xie J (2021):** Review of the relationships among polysaccharides, gut microbiota, and human health. Food Research International, 140, 109858. doi: https://doi.org/10.1016/j.foodres.2020.109858
- Śliżewska K, Chlebicz-Wójcik A, Nowak A (2021): Probiotic properties of new *Lactobacillus* strains intended to be used as feed additives for monogastric animals. Probiotics and Antimicrobial Proteins, 13(1), 146–162. doi: https://doi.org/10.1007/s12602- 020-09674-3
- **Sun J, Hu XL, Le GW, Shi YH (2010):** *Lactobacilli* prevent hydroxy radical production and inhibit *Escherichia coli* and *Enterococcus* growth in system mimicking colon fermentation. Letters in applied microbiology, 50(3), 264–269.doi: https://doi. org/10.1111/j.1472-765X.2009.02786.x
- **Tang H, Qian B, Xia B, Zhuan Y, Yao Y, Gan R, Zhang J (2018):** Screening of lactic acid bacteria isolated from fermented *Cornus officinalis* fruits for probiotic potential. J Food Saf 38: e12565. doi: https://doi.org/10.1111/jfs.12565
- **Tsai HJ, Sandine W (1987):** Conjugal transfer of nisin plasmid genes from *Streptococcus lactis* 7962 to *Leuconostoc dextranicum* 181. Appl Environ Microbiol 53: 352–357.
- **Wang B, Yao M, Lv L, Ling Z, Li L (2017):** The human microbiota in health and disease. Engineering 3: 71–82. doi: https://doi. org/10.1016/J.ENG.2017.01.008
- **Xu H, Liu Y, Jin H, Wang J, Yu Z, Liu W, Sun Z (2018):** Diversity and composition of lactic acid bacteria and *Bifidobacterium*

in breast milk form mothers living in Inner Mongolia. Chinese Science Bulletin, 64(3), 348–359.

- **Yang T, Richards EM, Pepine CJ, Raizada MK (2018):** The gut microbiota and the brain-gut-kidney axis in hypertension and chronic kidney disease. Nature Reviews Nephrology, 14(7), 442–456. doi: https://doi.org/10.1038/s41581-018-0018-2
- **Yürümez E (2011):** Probiotics properties of some lactic acid bacteria isolated from faeces samples. MSc thesis, University of Ankara, Ankara, Turkey.
- **Zhang C, Zhang J, Fan W, Huang M, Liu M (2019):** Effects of dietary *Lactobacillus delbrueckii* on growth performance, body composition, digestive and absorptive capacity, and gene expression of common carp (*Cyprinus carpio Huanghe* var). Aquac Nutr 25: 166–175. doi: https://doi.org/10.1111/anu.12840
- **Zhang CN, Zhang JL, Guan WC, Zhang XF, Guan SH, Zeng QH, Cheng GF, Cui W (2017):** Effects of *Lactobacillus delbrueckii* on immune response, disease resistance against *Aeromonas hydrophila,* antioxidant capability and growth performance of *Cyprinus carpio Huanghe* var. Fish Shellfish Immunol 68: 84–91. doi: 10.1016/j.fsi.2017.07.012

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