INTRODUCTION

The present evidences emphasize the health benefits of some microorganisms. In this regard, probiotics are currently among the most studied beneficial microorganisms (Cassani, Gomez-Zavaglia, & Simal-Gandara, 2020). Lactic acid bacteria (LAB) are a diverse group of microorganisms, having the ability to produce lactic acid as the main product, which prevents the proliferation of food spoilage bacteria and pathogens. They are Gram-positive, nonspore forming, coccis or rods, with the ability to secrete a variety of antimicrobial compounds, for example, organic acids, bacteriocins, etc. (Quigley et al., 2013). LAB are normal inhabitants of the healthy gut microbiota in animals and can be found in the milk and dairy products such as cheese.

Lactic acid bacteria are the most commonly used probiotics in the food. Nowadays, the development of novel probiotic-based foods has gained more attention. Probiotics display several health benefits by affecting the intestinal flora and permeability, modulating the immunological parameters in the body, and producing bioactive or regulatory metabolites (George et al., 2018). Nowadays,
there is a global interest to isolate LAB from food commodities for application in functional food and dietary supplement (Chiang & Pan, 2012). LAB isolated from different food sources draw a lot of attention in combating food-associated pathogens and spoilers, biodegradation of chemical contaminants, and development of unique food with special interests for the consumers (Koohestani, Moradi, Tajik, & Badali, 2018; Lim, Yeu, Hong, & Kang, 2018). LAB secrete diverse bioactive metabolites such as organic acids, short-chain fatty acids, carbohydrates, antimicrobial peptides, enzymes, vitamins, cofactors, immune-signaling compounds, and complex agents, and most of them, for example, organic acids, hydrogen peroxide, bacteriocins, etc. exhibit different antibacterial activity in individual and synergistic forms on foodborne pathogens (Moradi et al., 2020). The bactericidal effects of such agents on a wide range of pathogens such as Listeria monocytogenes, Escherichia coli, and Staphylococcus aureus have been studied (De Vuyst & Leroy, 2007; Hassanzadazar, Ehsani, & Mardani, 2014).

To date, various food sources, for example, human and animal milk, cheese, meat products, etc. have been investigated for isolation and identification of new LAB strains with novel functional properties (Al-Gamal et al., 2019; Awaishesh & Ibrahim, 2009; Hassanzadazar et al., 2014). This has resulted in the acquisition of new strains. However, researchers are still trying to isolate and identify new isolates with unique properties from different sources. Koopeh, Shal, and Shoor are three popular traditional cheese varieties consumed in the North-West of Iran. Koopeh cheese is one of the most popular fermented dairy food not only in Iran but also in some parts of Turkey and Iraq (Amirbozorgi, Samadlouie, & Shahidi, 2016). It is a semisoft type cheese made mainly from raw ewe’s milk and less commonly from cow milk or a mixture of both kinds of milk without using any starter in clay jugs (Hassanzadazar et al., 2014). Shoor is a salty cheese that traditionally is produced from boiled buttermilk with a reasonable amount of salt, and Shal cheese is another popular milk product in the west of Iran which is freshly prepared in large casts.

In the present study, we attempted to isolate and discriminate LAB from three traditional cheese varieties consumed in West Azerbaijan province, Iran, using biochemical and molecular methods. The phylogenetic tree of the isolated LABs was generated based on the partial sequences of the 23s rRNA gene. Additionally, the antibacterial performance of LAB isolates was investigated on L. monocytogenes.

2 | MATERIAL AND METHODS

2.1 | Cheese collection

Sixty traditional cheese samples (200 g) composed of Koopeh (n = 20), Shal (n = 20), and Shoor (n = 20) were collected from markets from three different geographical locations in West Azerbaijan province, Iran. The samples were aseptically transferred to the Faculty of Veterinary Medicine, Urmia University, under cold and aseptic conditions.

2.2 | Bacteria isolation and biochemical characterization

First, an amount of 25 g of each cheese sample was added to 225 ml 0.1% w/v peptone water (Merck, Darmstadt, Germany) and homogenized using a stomacher (Seward Medical Ltd., London, U.K) at 280 rpm for three min. The cheese suspension was diluted in 2% w/v sodium citrate (Merck) and cultured on two De Man, Rogosa and Sharpe (MRS) agar (Quelab, Montréal, Canada) plates and incubated under anaerobic (anaerobic jar) and aerobic conditions for 1-2 days at 37°C. The 3-4 different single colonies were randomly selected from each cultured plate. The selected colonies were Gram stained, examined microscopically, and catalase test was also performed. Gram-positive and catalase-negative bacilli/cocci were chosen and stored in cryotube containing 15% (v/v) glycerol (Merck) at −20°C for further molecular and antibacterial characterization.

2.3 | Molecular characterization

2.3.1 | Extraction of bacterial genomic DNA

Genomic DNA from previously cultivated LAB in MRS broth (Quelab) for 12-18 hr at 37°C was used. The DNA was extracted using DNA extraction kit (SinaClon, Tehran, Iran) according to the kit’s manufacturer instruction. The quality and amount of extracted DNA were evaluated by Nano-Drop 2000c (Termo Scientific, Massachusetts, USA). Then, extracted DNA samples were kept at −20°C for subsequent application.

2.3.2 | Amplification of 23s rDNA

A pair of primers EGE1 (5’-AGAGTTTGATCCTGGCTCAG-3′) and EGE2 (5’-CTACGGCTACCTTGTTACGA-3′) described by Sharifpour, Mardani, and Ownagh (2016) was used for the amplification of a fragment on 1,540 bp in size. Polymerase chain reaction (PCR) was performed in 25 μl reaction volume, containing 0.5 μl Taq DNA polymerase (5 U per μl), 1 μl MgCl₂ (50 mM), 0.5 μl of each primer, 4 μl of dNTP (1.25 mM), 2.5 μl of 10X PCR buffer, and 4 μl (50-100 ng) of genomic DNA. Thermal conditions for PCR were as follow: Initial denaturation at 94°C for 5 min, followed by 32 cycles of denaturation at 94°C for 45 s, annealing at 55°C for 45 s, and elongation at 72°C for 1.25 min, and a 5 min final elongation at 72°C. PCR products were electrophoresed in 1.5% w/v agarose gel and visualized by Ultraviolet (UV) transilluminator (Synoptics, Cambridge, UK) after staining with Safe Stain (Sharifpour et al., 2016).
2.3.3 | Purification and restriction endonuclease digestion of PCR products

All amplified PCR products were subjected to purification using Combo GP Kit (GeneALL, Seoul, Korea) following the kit’s manufacturer instruction. For restriction endonuclease digestion of purified PCR products, HinfI endonuclease (Jena Biosciense, Germany) was used. Digestion reaction was performed in 15 µl reaction volume, containing 1 µl FastDigest HinfI enzyme, 1.5 µl universal buffer, 4.5 µl dH2O, and 8 µl of the purified PCR product. The reaction mixture was incubated at 37°C for 5 min. The digested PCR products were electrophoresed, stained with Safe Stain, and visualized using a UV transilluminator.

2.3.4 | DNA sequencing and phylogenetic analysis

Purified PCR products of eight bacterial isolates with different restriction fragment length polymorphism (RFLP) patterns were selected for further nucleotide sequencing. Purified PCR products from the gel were sequenced (Bioneer Company, Daejeon, Korea). The obtained nucleotide sequences of 16S rRNA were BLAST searched in GenBank (National Centre for Biotechnology Information, Rockville Pike, Bethesda, USA) using the advanced BLAST similarity search option and compared to the 16S rRNA sequences of Lactococcus, Lactobacillus, and Enterococcus subsp. from GenBank (Table 1). Nucleotide sequences were aligned and compared to other nucleotide sequences retrieved from GenBank using Clustal W, and the phylogenetic tree was generated using the neighbor-joining method in MEGA software (version 6.0; Biodesign Institute, Tempe, USA) (Kumar, Stecher, Li, Knyaz, & Tamura, 2018).

2.4 | Antibacterial activity of LAB isolates

To determine the antibacterial performance of 8 LAB isolates with different RFLP patterns, spot-on-the-lawn method was applied (Koohestani et al., 2018). For this, bacterial suspension was prepared by inoculation of each isolate in MRS broth under anaerobic or aerobic conditions at 37 ± 1°C and then 10 µl of each bacterial suspension was carefully dropped on a plate containing MRS agar. After 48 hr incubation, 7 ml of soft (0.8% w/v agar) trypticase soy broth that previously standardized approximately 6 log10 cfu/ml of L. monocytogenes ATCC 19,115, by visible-ultraviolet spectrophotometer at 600 nm, was poured on the palate and inoculated at 37 ± 1°C for 24 hr. Zone of inhibition (ZOI), as a clear area around each spotted bacterial suspension, was checked by a caliper in triplicate. Lb. casei 431 was used as a control strain with antibacterial activity.

3 | RESULTS

3.1 | Screening and phenotypic characterization of lactic acid bacteria

After incubating each cheese suspension on MRS agar for 24–48 hr at 37°C, various types of bacterial colonies appeared on the surface of MRS agar. A total of 60 MRS agar plates were screened for small,
round, matte, and white colonies, of which 70 bacterial colonies showed biochemical properties of LAB including cocci or rods in the shape, Gram-positive and catalase-negative.

### PCR and RFLP

A DNA fragment of 1,540 bp in size was amplified for all isolates from 70 bacterial isolates (Figure 1a). RFLP analysis of the PCR products revealed three different digestion patterns (patterns I-III) (Figure 1b). Of 70 isolates, amplified fragments of 16s rRNA from 63 (90%) isolates showed RFLP pattern I. RFLP patterns II and III each with two and five isolates were all the RFLP patterns identified using Hinf I endonuclease enzyme.

### 3.2 | Phylogenetic analysis

Phylogenetic tree constructed based on neighbor-joining analysis of 16s rRNA clustered eight examined isolates in four different clusters (Figure 2). Isolates with different RFLP patterns were clustered differently except for isolates 22 and 44 which clustered in two different clusters in the phylogenetic tree. Based on the generated phylogenetic tree, LAB isolates from traditional cheese samples were identified as *Enterococcus* subsp., *Lb. lactis*, *Lb. farcininis*, and *Lb. paracasei*. The most of LAB isolates (90%) from examined cheese samples showing RFLP pattern I (isolates 7, 76, 90, 91) belonged to *Enterococcus* subsp. Isolates 14 and 32 showings RFLP pattern II were clustered together. Two isolates 22 and 44 had the same RFLP pattern III; however, based on the phylogenetic tree, these two isolates were clustered in two distinct clusters. *Enterococcus* subsp. were the most prevalent LAB which were identified in the traditional cheeses in the present study.

### 3.3 | Antibacterial activity

The ZOI (Figure 3) of selected LAB isolates were shown in Table 2. Results showed that antimicrobial performances of all investigated isolates with ZOI were ranged from 6.72 to 14.00 mm, while *Lb. casei* 431 as control strain had 21.00 ± 0.40 mm ZOI. *Lb. paracasei*, which belongs to RFLP pattern III, had the highest ZOI (14.00 mm) among different isolates.

### 4 | DISCUSSIONS

Lactic acid bacteria are a group of beneficial microorganisms that are widely distributed in the nature. They are well known owing to their probiotic potential for food and nutrition application. Probiotic bacteria can confer health benefits to the human gastrointestinal tract. Therefore, nowadays isolation and characterization of LAB strains from different sources is one of the interesting fields of research in the food industry (Alkalbani, Turner, & Ayyash, 2019; Bartkiene et al., 2020). In the present study, the PCR-RFLP method and phylogenetic analysis based on 16s rRNA gene were used for molecular characterization of LAB isolated from traditional cheese at the species level.

The application of molecular techniques in food microbiology improves our understanding of the ecology and diversity of microbial populations (Hassanzadazar, Mardani, Yousefi, & Ehsani, 2017). Our results confirm the suitability of PCR-RFLP and phylogenetic analysis for the identification of LAB in food samples at the species level, from which we have obtained useful information on the composition of the microbiota in the traditional cheese. The identification of microbiota of traditional dairy products will help to improve and standardize these products and thus enhance consumer acceptability in broader regions (Yu et al., 2015).

*Enterococcus* subsp. was the most prevalent LAB genus identified in the examined traditional cheese in the present study. The genus *Enterococcus* comprises many species, in which only a few have been studied to be used as probiotics, for example, *Ent. faecalis*, *Ent. faecium*, *Ent. lactis*, and more recently *Ent. hirae* (Adnan, Patel, & Hadi, 2017) and *Ent. durans* (Li et al., 2018). These strains have the ability to produce a variety of antimicrobial compounds, such as organic acids and bacteriocins (Hassanzadazar et al., 2014).
In a study by Silva et al. (2015), about 50% of identified LAB isolated from Brazilian water buffalo mozzarella cheese belonged to Enterococcus subsp. It was also reported that four strains out of six identified LAB isolates from traditionally fermented Xinjiang cheese were Ent. hirae (Azat et al., 2016). Ghahremani, Mardani, and Rezapour (2015) reported that 81% of LAB isolated from traditional cheese in Khorramabad city of Iran belonged to Enterococcus subsp. All these studies demonstrated that the majority of LAB isolated from different traditional cheese from various regions have belonged to Enterococcus genus. In Russia, seven Lactobacillus and Bifidobacterium species were identified in the traditional fermented dairy products sampled from different regions (Yu et al., 2015). All these mentioned reports and other works from different countries demonstrating that traditional dairy products have complex compositions of LAB species (Campagnollo et al., 2018; Parsaeimehr, Khazaei, Jebellijavan, & Staji, 2019).

Two strains, Lb. farcininis and Lb. paracasei, were identified in the examined cheese samples. Lb. farcininis is a probiotic strain commercialized by Dupont–Danisco for animal nutrition as a feed additive (Tareb, Bernardeau, Amiel, & Vernoux, 2017). It was shown that Lb. farcininis as a feed additive would help to improve ruminal fermentation digestibility without any adverse effect on the pH of rumen and enhance ruminant productivity through manipulation of the rumen microbial ecosystem (Elghandour et al., 2019). Lb. paracasei and Lac. lactis were the next LAB strains which were identified in the examined cheese in the present study.

Antibacterial potential of LAB is one of the most promising specifications that influence the application of LAB in the food industry.
(Moradi, Mardani, & Tajik, 2019). Antibacterial agents such as bacteriocins, organic acids, enzymes, alcohols, and low molecular mass substances are among the most studied antimicrobial agents responsible for the antimicrobial action of LAB (Moradi et al., 2020). As reported in this study (Table 2), this activity is species- and strain-dependent. For example, isolates with RFLP pattern of II and III that belong mainly to Lactococcus subsp. and Lactobacillus subsp. revealed strong antibacterial activity than isolates with RFLP pattern I that consist of Enterococcus subsp. Similar results were reported on antibacterial activity of LAB isolated from raw camel milk (Rahmeh et al., 2019), Genestoso cheese (González et al., 2007) and Brazilian artisanal cheeses (Margalho et al., 2020). Organic acids production, as the main antibacterial agents, by LAB is mainly a genus-specific phenomenon and partially specie-specific. In this regard, lactic acid production by LAB strains is significantly higher than acetic acid production (Thierry et al., 2015). There is a relationship between organic acid production, type of culture media, and antibacterial activity of LAB. For example, LAB at fish broth and MRS produce succinic and acetic acids at the highest and lowest contents (Özçelik, Kuley, & Özoğul, 2016). However, the EPS derived from LAB represent moderate to strong antibacterial activity on some foodborne microorganisms (i.e., pathogens and spoilage groups), depending on bacterial species and EPS source and characterization (Moradi et al., 2020).

### 5 | CONCLUSIONS

In conclusion, traditional cheeses examined in the present study were identified as sources of LAB especially Enterococcus subsp. It was revealed that PCR-RFLP combined with 16s rRNA gene sequencing will be a valuable tool for the identification and molecular characterization of LAB in the food commodities especially dairy products. It seems that the observed antibacterial activity appears to be strain-dependent.

### ACKNOWLEDGMENTS

The authors would like to thank the Dean of Research of the Ferdowsi University of Mashhad for funding this project and the Faculty of Veterinary Medicine, Urmia University for the technical support.

### REFERENCES

Adnan, M., Patel, M., & Hadi, S. (2017). Functional and health promoting inherent attributes of Enterococcus hirae F2 as a novel probiotic isolated from the digestive tract of the freshwater fish Catla catla. Peer Journal, 5, e3085.

Al-Gamal, M. S., Ibrahim, G. A., Sharaf, O. M., Radwan, A. A., Dabiza, N. M., Youssef, A. M., & El-sayad, M. F. (2019). The protective potential of selected lactic acid bacteria against the most common contaminants in various types of cheese in Egypt. Heliyon, 5, e01362. https://doi.org/10.1016/j.heliyon.2019.e01362

Alkalbani, N. S., Turner, M. S., & Ayyash, M. M. (2019). Isolation, identification, and potential probiotic characterization of isolated lactic acid bacteria and in vitro investigation of the cytotoxicity, antioxidant, and anti-diabetic activities in fermented sausage. Microbial Cell Factories, 18, 188. https://doi.org/10.1186/s12934-019-1239-1

Amirbozorgi, G., Samadlouie, H., & Shahidi, A. (2016). Identification and characterization of lactic acid bacteria isolated from Iranian traditional dairy products. International Biological and Biomedical Journal, 2, 47–52.

Awaïsheh, S. S., & Ibrahim, S. A. (2009). Screening of antibacterial activity of lactic acid bacteria against different pathogens found in vacuum-packaged meat products. Foodborne Pathogens and Disease, 6, 1125–1132. https://doi.org/10.1089/fpd.2009.0272

Azat, R., Liu, Y., Li, W., Kayir, A., Lin, D. B., Zhou, W. W., & Zheng, X. D. (2016). Probiotic properties of lactic acid bacteria isolated from traditionally fermented Xinjiang cheese. Journal of Zhejiang University, Science B, 17, 597–609.

Bartkiene, E., Lelem, V., Ružauskas, M., Domig, J. K., Starkute, V., Zavistanaviciute, P., & Rocha, M. J. (2020). Lactic acid bacteria isolation from selected cheeses and their antibacterial activity against some foodborne pathogens. Heliyon, 6, e05568. https://doi.org/10.1016/j.heliyon.2020.e05568

Bartkiene, E., Lelem, V., Ružauskas, M., Domig, J. K., Starkute, V., Zavistanaviciute, P., & Rocha, M. J. (2020). Lactic acid bacteria isolation from selected cheeses and their antibacterial activity against some foodborne pathogens. Heliyon, 6, e05568. https://doi.org/10.1016/j.heliyon.2020.e05568

### DATA AVAILABILITY STATEMENT

All data are available upon request.

### ORCID

Mehran Moradi https://orcid.org/0000-0002-6004-6874

Abdollahlam Jamshidi https://orcid.org/0000-0001-9935-4666

### CONFLICT OF INTEREST

The technical assistance of Ms. E. Divsal and Dr. P. Khademi is greatly appreciated.

### ETHICAL STATEMENTS

The authors declare no conflict of interest.

### ACKNOWLEDGMENTS

The authors would like to thank the Dean of Research of the Ferdowsi University of Mashhad for funding this project and the Faculty of Veterinary Medicine, Urmia University for the technical support.

### TABLE 2 Antibacterial activity of some LAB isolates with different RFLP patterns on L. monocytogenes according to spot-on-the-lawn method

| Isolate | Species | Identity % | Type of cheese | Incubation condition | RFLP pattern | Antimicrobial activity (ZOI) |
|---------|---------|------------|----------------|----------------------|--------------|-----------------------------|
| AC7     | Ent. faecium | 98.00 | Koopah | Aerobic | I | 9.10 ± 0.30 |
| AC14    | Lb. farciminis | 98.30 | Koopah | Aerobic | II | 11.00 ± 0.10 |
| AC22    | Lct. lactis | 99.00 | Shoor | Aerobic | III | 10.00 ± 0.10 |
| AC32    | Lb. farciminis | 98.00 | Shal | Anaerobic | II | 11.30 ± 0.10 |
| AC44    | Lb. paracasei | 98.00 | Shal | Anaerobic | III | 14.00 ± 0.60 |
| AC76    | Ent. faealci | 98.22 | Koopah | Aerobic | I | 6.70 ± 0.30 |
| AC90    | Ent. faecium | 93.25 | Shoor | Anaerobic | I | 9.40 ± 0.20 |
| AC91    | Ent. durans | 98.00 | Koopah | Anaerobic | I | 9.20 ± 0.40 |

*Zone of inhibition.*
from spontaneous sourdough and their characterization excluding antimicrobial and antifungal properties revaluation. Microorganisms, 8, 64.

Campagnollo, F. B., Margalho, L. P., Kamimura, B. A., Feliciano, M. D., Freire, L., Lopes, L. S., ... Sant’Ana, A. S. (2018). Selection of indigenous lactic acid bacteria presenting anti-listerial activity, and their role in reducing the maturation period and assuring the safety of traditional Brazilian cheeses. Food Microbiology, 73, 288–297. https://doi.org/10.1016/j.fm.2018.02.006

Cassani, L., Gomez-Zavaglia, A., & Simal-Gandara, J. (2020). Technological strategies ensuring the safe arrival of beneficial microorganisms to the gut: From food processing and storage to their passage through the gastrointestinal tract. Food Research International, 129, 108852. https://doi.org/10.1016/j.foodres.2019.108852

Chiang, S. S., & Pan, T. M. (2012). Beneficial effects of Lactobacillus paracasei subsp. paracasei NTU 101 and its fermented products. Applied Microbiology and Biotechnology, 93, 903–916.

De Vuyst, L., & Leroy, F. (2007). Bacteriocins from lactic acid bacteria: Production, purification, and food applications. Journal of Molecular Microbiology and Biotechnology, 13, 194–199. https://doi.org/10.1159/000104752

Elghandour, M. M. Y., Adegbeye, M. J., Vallejo, L. H., Elahi, M. Y., Barbabosa-Pliego, A., Recillas Morales, S., & Salem, A. Z. M. (2019). Role of dose-dependent Lactobacillus farcinimnis on ruminal microflora biogases and fermentation activities of three silage-based rations. Journal of Applied Microbiology, 127, 1627–1634.

George, F., Daniel, C., Thomas, M., Singer, E., Guibaud, A., Tessier, F. J., ... Foligné, B. (2018). Occurrence and dynamism of lactic acid bacteria in distinct ecological niches: A multifaceted functional health perspective. Frontiers in Microbiology, 9, 2899. https://doi.org/10.3389/fmicb.2018.02899

Gahremani, E., Mardani, M., & Rezapour, S. (2015). Phenotypic and genotypic characterization of lactic acid bacteria from traditional cheese in Khorramabad city of Iran with probiotic potential. Applied Biochemistry and Biotechnology, 175, 2516–2527. https://doi.org/10.1007/s12010-014-1434-9

González, L., Sandoval, H., Sacristán, N., Castro, J. M., Fresno, J. M., & Tornadizo, M. E. (2007). Identification of lactic acid bacteria isolated from Genestoso cheese throughout ripening and study of their antimicrobial activity. Food Control, 18, 716–722. https://doi.org/10.1016/j.foodcont.2006.03.008

Hassanzadazar, H., Ehsani, A., & Mardani, K. (2014). Antibacterial activity of Enterococcus faecium derived from Koopeh cheese against Listeria monocytogenes in probiotic ultra-filtered cheese. Veterinary Research Forum, 5, 169–175.

Hassanzadazar, H., Mardani, K., Yousefi, M., & Ehsani, A. (2017). Identification and molecular characterisation of lactobacilli isolated from traditional Koopeh cheese. International Journal of Dairy Technology, 70, 556–561. https://doi.org/10.1111/1471-0307.12396

Koohestani, M., Moradi, M., Tajik, H., & Badali, A. (2018). Effects of cell-free supernatant of Lactobacillus acidophilus LA5 and Lactobacillus casei 431 against planktonic form and biofilm of Staphylococcus aureus. Veterinary Research Forum, 5, 301–306.

Kumar, S., Stecher, G., Li, M., Knypsy, C., & Tamura, K. (2018). MEGA X: Molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution, 35, 1547–1549. https://doi.org/10.1093/molbev/msy096

Li, B., Zhan, M., Evivie, S. E., Jin, D. A., Zhao, L. I., Chowdhury, S., ... Liu, F. (2018). Evaluating the safety of potential probiotic Enterococcus durans KLD56.0930 using whole genome sequencing and oral toxicity study. Frontiers in Microbiology, 9, 1943. https://doi.org/10.3389/fmicb.2018.01943

Lim, H. S., Yeu, J. E., Hong, S. P., & Kang, M. S. (2018). Characterization of antibacterial cell-free supernatant from oral care probiotic Weissella cibaria, CMU. Molecules, 23, 1–13. https://doi.org/10.3390/molecules23081984

Margalho, L. P., Feliciano, M. D., Silva, C. E., Abreu, J. S., Piran, M. V. F., & Sant’Ana, A. S. (2020). Brazilian artisanal cheeses are rich and diverse sources of nonstarter lactic acid bacteria regarding technological, biopreservative, and safety properties—Insights through multivariate analysis. Journal of Dairy Science, 103, 7908–7926. https://doi.org/10.3168/jds.2020-18194

Moradi, M., Kousheh, S. A., Almasi, H., Alizadeh, A., Guimarães, J. T., Yilmaz, N., & Lotfi, A. (2020). Postbiotics produced by lactic acid bacteria: The next frontier in food safety. Comprehensive Reviews in Food Science and Food Safety. In Press, https://doi.org/10.1111/1541-4337.12613

Moradi, M., Mardani, K., & Tajik, H. (2019). Characterization and application of postbiotics of Lactobacillus spp. on Listeria monocytogenes in vitro and in food models. LWT - Food Science and Technology, 111, 457–464. https://doi.org/10.1016/j.lwt.2019.05.072

Özçelik, S., Kuley, E., & Özgul, F. (2016). Formation of lactic, acetic, succinic, propionic, formic and butyric acid by lactic acid bacteria. LWT - Food Science and Technology, 73, 536–542. https://doi.org/10.1016/j.lwt.2016.06.066

Parsaeimehr, M., Khazaei, M., Jebelliavan, A., & Staji, H. (2019). The isolation and identification of dominant lactic acid bacteria by the sequencing of the 16S rRNA in traditional cheese (Khiki) in semnan, Iran. Journal of Human Environment and Health Promotion, 5, 15–20. https://doi.org/10.29225/jhehp.5.1.3

Quigley, L., O’Sullivan, O., Stanton, C., Beresford, T. P., Ross, R. P., Fitzgerald, G. F., & Cotter, P. D. (2013). The complex microbiota of raw milk. FEMS Microbiology Reviews, 37, 664–698. https://doi.org/10.1111/1574-6976.12030

Rahmeh, R., Akbar, A., Kishk, M., Al-Onaizi, T., Al-Azmi, A., Al-Shatti, A., ... Akbar, B. (2019). Distribution and antimicrobial activity of lactic acid bacteria from raw camel milk. New Microbes and New Infections, 30, 100560. https://doi.org/10.1016/j.nmni.2019.100560

Sharifpour, M. F., Mardani, K., & Ownagh, A. (2016). Molecular identification and phylogenetic analysis of Lactobacillus and Bifidobacterium spp. isolated from gut of honeybees (Apis mellifera) from West Azerbaijan, Iran. Veterinary Research Forum, 7, 287–294.

Silva, L. F., Casella, T., Gomes, E. S., Nogueira, M. C. L., De Dea Lindner, J., & Penna, A. L. B. (2015). Diversity of lactic acid bacteria isolated from Brazilian water buffalo Mozzarella cheese. Journal of Food Science, 80, M411–M417. https://doi.org/10.1111/1750-3841.12771

Tareb, R., Bernardau, M., Amiel, C., & Vernoux, J. P. (2017). Usefulness of FTIR spectroscopy to distinguish rough and smooth variants of Lactobacillus farcinimnis CNCM-I-3699. FEMS Microbiology Letters, 364(2), 1–8.

Thierry, A., Valence, V., Deutsch, S.-M., Even, S., Falentin, H., Le Loir, Y., ... Gagnaire, V. (2015). Strain-to-strain differences within lactic and propionic acid bacteria species strongly impact the properties of cheese—A review. Dairy Science & Technology, 95, 895–918. https://doi.org/10.1007/s13954-015-0267-9

Yu, J., Wang, H. M., Zha, M. S., Qing, Y. T., Bai, N., Ren, Y., ... Zhang, H. P. (2015). Molecular identification and quantification of lactic acid bacteria in traditional fermented dairy foods of Russia. Journal of Dairy Science, 98, 5143–5154. https://doi.org/10.3168/jds.2015-9460

How to cite this article: Hajigholizadeh M, Mardani K, Moradi M, Jamshidi A. Molecular detection, phylogenetic analysis, and antibacterial performance of lactic acid bacteria isolated from traditional cheeses, North-West Iran. Food Sci Nutr. 2020;8:6007–6013. https://doi.org/10.1002/fsn3.1887