

# Molecular Epidemiology Of Mycobacterium Avium Subspecies Paratuberculosis In The Milk Of Animal Species

<sup>1</sup>Rasoul Shirvani, <sup>2</sup>Ebrahim Rahimi, <sup>3</sup>Amir Shakerian, <sup>4</sup>Hassan Momtaz

<sup>13</sup>Department of Food Hygiene, Faculty of Veterinary Medicine, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran.

<sup>2</sup>Department of Food Hygiene, Faculty of Veterinary Medicine, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran, Ebrahimrahimi55@yahoo.com.

<sup>4</sup>Department of Microbiology, Faculty of Basic Sciences, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran

## Abstract

Mycobacterium subspecies paratuberculosis is an important zoonotic pathogen responsible for Johne's and Crohn's diseases in animals and humans population, respectively. Foods with animal origins may act as reservoirs of *M. avium* subsp. paratuberculosis. The present survey was done to assess the molecular distribution of *M. avium* subspecies paratuberculosis in the milk of cow, sheep, goat, donkey, buffalo, and camel species. In this study, a total of 300 raw milk samples were collected from Chaharmahal Va Bakhtiary and Isfahan province, Iran. Samples were subjected to DNA extraction. Extracted DNA was assessed for the *M. avium* subspecies paratuberculosis genome using the Polymerase Chain Reaction. Thirty out of 300 (10%) raw milk samples were positive with *M. avium* subsp. paratuberculosis. Raw buffalo milk samples harbored the highest contamination rate of *M. avium* subsp. paratuberculosis (17.50%), while raw donkey milk samples harbored the lowest (5%). Total prevalence of *M. avium* subspecies paratuberculosis amongst the raw milk samples collected from Isfahan and Chaharmahal Va Bakhtiary province were 66.66% and 33.33%, respectively. Statistically significant differences were obtained between types of samples and bacterial distribution ( $P < 0.05$ ) and also geographic area of sampling and bacterial distribution ( $P < 0.05$ ). Role of raw milk, particularly raw buffalo milk samples as reservoir of *M. avium* subsp. paratuberculosis have been determined. Using pasteurized and sterilized milk will decrease the risk of *M. avium* subsp. paratuberculosis.

**Keywords:** Mycobacterium avium subspecies paratuberculosis, Molecular epidemiology, Prevalence, Raw milk, Iran.

## Introduction

Milk of animal species is a rich source of proteins, minerals, fats, vitamins and several supplementary and essential materials for the human health (1-5). Its consumption has diverse health benefits in human, especially in neonate and elder people (6). In some parts of the world, raw milk is consumed routinely (7). They mainly didn't consume pasteurized or setrilized milk. In these cases, there is a risk of the occurrence of foodborne diseases due to the consumption of raw milk and meat (8-17).

Mycobacterium avium subspecies paratuberculosis (*M. avium* subsp. paratuberculosis) is the causative agents of Johne's disease (JD), which is a chronic gut infection progressively developed to complicated diseases, including prolonged diarrhea, poor digestion, and excessive weight loss (18). JD is mainly occurred in ruminants animals that provide milk and/or meat for human consumption, particularly cow, sheep, deer, goat, llamas, bison, and elk (19). Ruminants infected with *M. avium* subsp. paratuberculosis

excrete the bacterium in their feces and milk. In fact, *M. avium* subsp. *paratuberculosis* is excreted into the milk within the udder and also through fecal contamination during milking (20).

*M. avium* subsp. *paratuberculosis* also may be involved in Crohn's disease and type 1 diabetes in humans. However, the *M. avium* subsp. *paratuberculosis* role in human diseases has not been determined well, minimizing the exposure of humans to the organism is considered desirable as a precautionary measure (21). In this regard, the role of foods with animal origins, particularly milk as a reservoirs of *M. avium* subsp. *paratuberculosis* have been estimated (22). Infected ruminants may shed *M. avium* subsp. *paratuberculosis* in milk, and the bacterium can become disseminated (23). As a result, *M. avium* subsp. *paratuberculosis* presence in raw milk and in natural waters is probable, but the *M. avium* subsp. *paratuberculosis* numbers in milk and waters should be decreased by bioling. Thus, the highest risk of infection through milk consumption is in communities that consume raw milk.

According to the high importance of *M. avium* subsp. *paratuberculosis* and high consumption rate of raw milk in some parts of the world, the present survey was done to assess the molecular epidemiology of *M. avium* subsp. *paratuberculosis* in raw milk samples of cow, sheep, goat, buffalo, camel, and donkey species in Iran.

## Materials and methods

### Samples

A total of three-hundred raw milk samples, including cow (n= 80), goat (n= 60), sheep (n= 50), buffalo (n= 40), donkey (n= 30), and camel (n= 40) samples were collected from Chaharmahal va Bakhtiary and Isfahan province, Iran. Animal species were clinically healthy and their milk samples showed normal properties. Fifty milliliters per each animal case were collected using a sterile tubes. Initial droplets of raw milk samples were thrown away and the samples were taken from the middle stream part of the milk. Samples were transferred to laboratory at 4 °C.

### DNA extraction and analysis

Genomic DNA was extracted from the raw milk of animal species using the DNA extraction kit (Dneasy tissue kit, Qiagen, Hilden, Germany). Before DNA extraction, raw milk samples were centrifuged (1000 g, 15 min) and the supernatant discarded. The resultant pellet was washed using phosphate buffer saline (PBS, pH 7.3, Merck, Germany) and centrifuged again (500 g, 15 min). The pellet was suspended in 1 mL of PBS, centrifuged and resuspended in 100 mL of 0.2 N NaOH. In the initial procedure, the enzymatic digestion was done. For this purpose, lysozyme buffer (lysozyme (18 mg/ml), Tris-HCl pH 8.0 (15 mM), EDTA (1 mM), and Triton X100 (1%)) and proteinase K (Qiagen, Hilden, Germany) were applied. According to the manufacture's instruction, the procedure of the DNA extraction was done.

### Quality assessment of DNA samples

The purity (A260/A280) and concentration of the extracted DNA were then checked (NanoDrop, Thermo Scientific, Waltham, MA, USA) (24-28). Furthermore, the DNA's quality was assessed on a 2% agarose gel stained with ethidium bromide (0.5 µg/mL) (Thermo Fisher Scientific, St. Leon-Rot, Germany) (29-33).

### Polymerase Chain Reaction (PCR)

To identify the presence of *M. avium* subspecies *paratuberculosis* amongst the DNA extracted from raw milk samples, the PCR was used. For this purpose, a set of primer (F: 5'-GTTCCGGGGCCGTCGCTTAGG-3' and R:5'-GAGGTTCGATCGCCACGTGA-3' (400 bp)) was used (34). The reaction was done using 50 µl volume containing 2.0 mM MgCl<sub>2</sub>, 60 mM Tris-HCl buffer (pH 8.8), 10 pmol of each of the primers, 0.2 mM of each of the four dNTPs (Thermo Fisher Scientific, St. Leon-Rot, Germany), 0.5 U Taq DNA polymerase, and 5 mL DNA. A positive control (Positive DNA of *M. avium* subsp. *paratuberculosis*, 250 fg), and a negative control (PCR-garde water) (Thermo Fisher Scientific, St. Leon-Rot, Germany), were also used in each reaction. A programmable DNA thermocycler (Eppendorf Mastercycler 5330, Eppendorf-Nethel-Hinz GmbH, Hamburg, Germany) was used in all PCR reactions. Amplication of products were done at 1 cycle of 94°C for 3 min, 35 cycles of 94°C for 1 min, 63°C for 1 min, and 72°C for 1 min, and a final 1 cycle of 72°C for 5 min.

## Gel electrophoresis

Amplified samples were analyzed by electrophoresis (120 V/208 mA) in a 2.5% agarose gel stained with 0.1% ethidium bromide (0.4 µg/ml) (35, 36). Besides, UVI doc gel documentation systems (Grade GB004, Jencons PLC, London, UK) were used to analyze images (37, 38).

## Statistical analysis

Data analysis was performed by SPSS Statistics 21.0 (SPSS Inc., Chicago, IL, USA) (39). Chi-square and Fisher's exact two-tailed tests were performed to assess any significant relationship between the *M. avium* subspecies paratuberculosis prevalence amongst the examined samples (40). Besides, P-value < 0.05 was considered statistically significant (41).

## Results

The present survey was done to assess the molecular distribution of *M. avium* subspecies paratuberculosis in the milk of cow, sheep, goat, donkey, buffalo, and camel species. Figure 1 shows the PCR amplification gel electrophoresis of *M. avium* subspecies paratuberculosis.

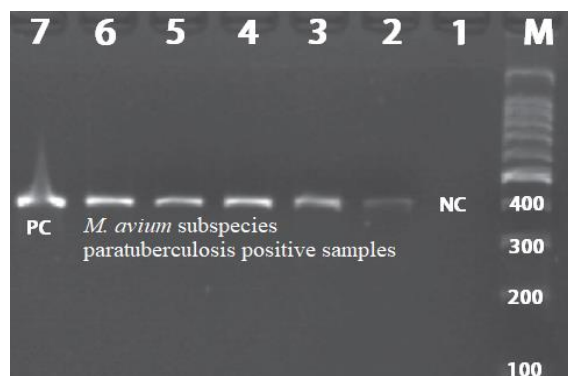


Figure 1. *M. avium* subspecies paratuberculosis prevalence amongst the collected raw milk samples. M: Ladder 100 bp, 1: Negative control, 2-6: Positive samples of the bacteria, and 7: Positive control.

Table 1 shows the *M. avium* subspecies paratuberculosis prevalence amongst the collected raw milk samples. Thirty out of 300 (10%) raw milk samples were contaminated with *M. avium* subspecies paratuberculosis. Raw buffalo milk samples harbored the highest rate of contamination with *M. avium* subspecies paratuberculosis (17.50%), while raw donkey

milk samples harbored the lowest (5%). Statistically, significant differences were obtained between type of raw milk samples and *M. avium* subspecies paratuberculosis distribution ( $P < 0.05$ ).

Table 1. *M. avium* subspecies paratuberculosis prevalence amongst the collected raw milk samples.

Types of raw milk samples	N. collected	N. positive for <i>M. avium</i> subspecies paratuberculosis (%)
Cow	80	8 (10)
Sheep	50	6 (12)
Goat	60	4 (6.66)
Donkey	30	1 (5)
Buffalo	40	7 (17.50)
Camel	40	4 (10)
Total	300	30 (10)

Figure 2 shows the *M. avium* subspecies paratuberculosis prevalence based on the geographical area of sampling procedure. According to obtained data, total prevalence of *M. avium* subspecies paratuberculosis amongst the raw milk samples collected from Isfahan and Chaharmahal Va Bakhtiary province were 66.66% and 33.33%, respectively. Statistically, significant differences were obtained between geographical area of sampling and *M. avium* subspecies paratuberculosis distribution ( $P < 0.05$ ).

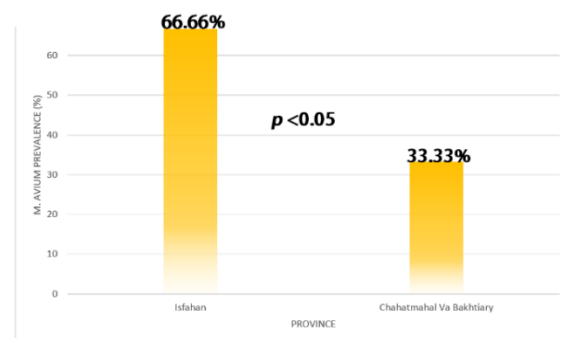


Figure 2. *M. avium* subsp. paratuberculosis prevalence based on the geographical area of sampling procedure.

## Discussion

The present survey was aimed to assess the PCR-based prevalence of *M. avium* subsp. paratuberculosis amongst the raw milk samples of animal species. Findings showed that the *M. avium* subsp. paratuberculosis prevalence amongst the raw cow, sheep, goat, donkey,

buffalo and camel milk samples were 10%, 12%, 6.66%, 5%, 17.50%, and 10%, respectively. Geographical distribution was also recorded with the high prevalence in Isfahan province.

As diverse kinds of animal species, particularly cow, sheep, goat, deer, and other ruminants may be the source of *M. avium* subsp. paratuberculosis dissemination in the nature, close contact of other species such as buffalo, donkey and camel with them may be the main reason for the presence of bacteria in their milk samples. Additionally, some kinds of wild ruminants, such as deer, llamas, bison, and elk may also be reservoirs of *M. avium* subsp. paratuberculosis. Thus, contact of domestic animals with wild ruminants or even their infected samples, such as feces and milk, may disseminate the infection in the environment. According to the high prevalence of *M. avium* subsp. paratuberculosis in examined raw milk samples, consumption of these types of milk may cause severe Crohn's disease in human population. Thus, well boiling of raw milk samples before consumption and also consumption of pasteurized and sterilized milk may decrease the risk of *M. avium* subsp. paratuberculosis in the community.

Scarce studies have been focused on the detection of *M. avium* subsp. paratuberculosis in raw milk of animal species. Shirvani et al. (2019) (42) reported that the *M. avium* subsp. paratuberculosis prevalence amongst the raw bovine, ovine, caprine, camel, buffalo and donkey milk samples were 15.83, 10, 8.18, 9.41, 25, and 6.66%, respectively. According to previous meta-analysis review, the *M. avium* subsp. paratuberculosis amongst the dairy farms of Iran, USA, Australia, Mexico, Czech Republic, Cyprus, Argentina, Denmark, Brazil, Switzerland, and Germany ranged between 0.0% to 0.80% (43). In Colombia (44), an apparent *M. avium* subsp. paratuberculosis herd-level prevalence was 4.1% (12/292; 95% CI: 1.8–6.4). In Canada (45), an apparent *M. avium* subsp. paratuberculosis cow level prevalence was 1.7% and 2.6% on the milk and serum ELISA, respectively. In Italy (46), 155 out of 780 dairy herds (19.9%) were found positive by ELISA and/or real time PCR. The estimated prevalence of *M. avium* subsp. paratuberculosis amongst the milk samples varies from region to region between 2.8 and 5.5%. In Switzerland (47), 4.2% of the raw milk

cheese samples tested positive for *M. avium* subsp. paratuberculosis with the F57-based real-time PCR. Another survey in Canada (48) showed that 8.1, 1.2 and 2.0% of cattle were positive for *M. avium* subsp. paratuberculosis using IS900 qPCR, F57 qPCR and bacterial culture, respectively. Furthermore, 14% of collected environmental samples, but no dust samples, were test-positive for *M. avium* subsp. paratuberculosis.

Such a large variation across countries in *M. avium* subsp. paratuberculosis prevalence rate from meat and animal carcasses may show real regional differences or may be affected by the use of various detection techniques. Additional developments in the *M. avium* subsp. paratuberculosis detection techniques in foods are desirable.

## Conclusion

Role of raw milk of animal species, particularly raw cow, sheep, goat, donkey, buffalo and camel milk samples were determined as reservoirs of *M. avium* subsp. paratuberculosis. This matter will be an important public health threat regarding the consumption of raw milk of animal species. Increase knowledge about the epidemiology of *M. avium* subsp. paratuberculosis in foods with animal origins will decrease the risk of *M. avium* subsp. paratuberculosis expansion in the community.

## References

- [1] Momtaz H, Safarpour Dehkordi F, Taktaz T, Rezvani A, Yarali S. Shiga toxin-producing *Escherichia coli* isolated from bovine mastitic milk: serogroups, virulence factors, and antibiotic resistance properties. *The Scientific World Journal*. 2012 Oct;2012.
- [2] Ranjbar R, Safarpour Dehkordi F, Sakhaei Shahreza MH, Rahimi E. Prevalence, identification of virulence factors, O-serogroups and antibiotic resistance properties of Shiga-toxin producing *Escherichia coli* strains isolated from raw milk and traditional dairy products. *Antimicrobial Resistance & Infection Control*. 2018 Dec; 7(1):1-1.

- [3] Momtaz H, Farzan R, Rahimi E, Safarpour Dehkordi F, Souod N. Molecular characterization of Shiga toxin-producing *Escherichia coli* isolated from ruminant and donkey raw milk samples and traditional dairy products in Iran. *The Scientific World Journal*. 2012 Oct; 2012.
- [4] Dehkordi FS, Barati S, Momtaz H, Ahari SN, Dehkordi SN. Comparison of shedding, and antibiotic resistance properties of *Listeria monocytogenes* isolated from milk, feces, urine, and vaginal secretion of bovine, ovine, caprine, buffalo, and camel species in Iran. *Jundishapur Journal of Microbiology*. 2013 May 31; 6(3):284-94.
- [5] Mousavi S, Dehkordi FS. Virulence factors and antibiotic resistance of *Helicobacter pylori* isolated from raw milk and unpasteurized dairy products in Iran. *Journal of Venomous Animals and Toxins including Tropical Diseases*. 2015 Jan 20; 20:1-7.
- [6] Pietrzak-Fiećko R, Kamelska-Sadowska AM. The comparison of nutritional value of human milk with other mammals' milk. *Nutrients*. 2020 May 14; 12(5):1404.
- [7] Berge AC, Baars T. Raw milk producers with high levels of hygiene and safety. *Epidemiology & Infection*. 2020; 148.
- [8] Ranjbar R, Farsani FY, Dehkordi FS. Phenotypic analysis of antibiotic resistance and genotypic study of the *vacA*, *cagA*, *iceA*, *oipA* and *babA* genotypes of the *Helicobacter pylori* strains isolated from raw milk. *Antimicrobial Resistance & Infection Control*. 2018 Dec; 7(1):1-4.
- [9] Dehkordi FS, Valizadeh Y, Birgani TA, Dehkordi KG. Prevalence study of *Brucella melitensis* and *Brucella abortus* in cow's milk using dot enzyme linked immuno sorbent assay and duplex polymerase chain reaction. *J Pure Appl Microbiol*. 2014; 8(2):1065-9.
- [10] Rostami F, Rahimi E, Yahaghi E, Khodaverdi Darian E, Bagheri Moghadam M. Isolation and evaluation virulence factors of *Salmonella typhimurium* and *Salmonella enteritidis* in milk and dairy products. *Iranian Journal of Medical Microbiology*. 2014 Jun 10; 8(1):54-61.
- [11] Mousavi S, Safarpour Dehkordi F, Valizadeh Y. Genotyping of *Helicobacter pylori* strains isolated from raw milk and dairy products. *Journal of Food Microbiology*. 2017 Nov 22; 4(3):41-53.
- [12] Safarpour Dehkordi F, Haghghi N. Detection of bovine viral diarrhea virus in bovine and buffalo milk thorough conventional and real-time reverse transcriptase polymerase chain reaction. *Research Opinions in Animal and Veterinary Sciences*. 2012; 2:263-7.
- [13] Dehkordi FS, Yahaghi E, Darian EK. Prevalence of antibiotic resistance in *Escherichia coli* isolated from poultry meat supply in Isfahan. *Iran J Med Microbiol: Volume*. 2014 Jul; 8(2).
- [14] Shakerian A, Rahimi E, Dehkordi FS. Identification and characterization of resistant *Arcobacter* spp. isolated from meat products. *Online Journal of Veterinary Research*. 2017; 21(12):766-76.
- [15] Dehkordi FS, Yahaghi E, Darian EK. Prevalence of antibiotic resistance in *Escherichia coli* isolated from poultry meat supply in Isfahan. *Iran J Med Microbiol: Volume*. 2014 Jul; 8(2).
- [16] Rahimi E, Yazdanpour S, Dehkordi FS. Detection of *Toxoplasma gondii* antibodies in various poultry meat samples using enzyme linked immuno sorbent assay and its confirmation by polymerase chain reaction. *J Pure Appl Microbiol*. 2014;8(1):421-7.
- [17] Hasanpour Dehkordi A, Khaji L, Sakhaei Shahreza MH, Mashak Z, Safarpour Dehkordi F, Safaee Y, Hosseinzadeh A, Alavi I, Ghasemi E, Rabiei-Faradonbeh M. One-year prevalence of antimicrobial susceptibility pattern of methicillin-resistant *Staphylococcus aureus* recovered from raw meat. *Trop Biomed*. 2017; 34(2):396-404.
- [18] Ekundayo TC, Okoh AI. Systematic assessment of mycobacterium avium subspecies paratuberculosis infections from 1911–2019: A growth analysis of association with human autoimmune diseases. *Microorganisms*. 2020 Aug 10; 8(8):1212.
- [19] Over K, Crandall PG, O'Bryan CA, Ricke SC. Current perspectives on *Mycobacterium avium* subsp. paratuberculosis, Johne's disease, and Crohn's disease: a review. *Critical reviews in microbiology*. 2011 May 1; 37(2):141-56.

- [20] Hosseiniporgham S, Biet F, Ganneau C, Bannantine JP, Bay S, Sechi LA. A comparative study on the efficiency of two mycobacterium avium subsp. Paratuberculosis (MAP)-derived lipopeptides of L3P and L5P as capture antigens in an in-house milk ELISA test. *Vaccines*. 2021 Sep 7; 9(9):997.
- [21] Hosseiniporgham S, Rebechesu L, Pintore P, Lollai S, Dattena M, Russo S, Ruiu A, Sechi LA. A rapid phage assay for detection of viable Mycobacterium avium subsp. paratuberculosis in milk. *Scientific Reports*. 2022 Jan 10; 12(1):1-1.
- [22] Bridges N, van Winden S. The occurrence of Mycobacterium avium subspecies paratuberculosis positive milk antibody ELISA results in dairy cattle under varying time periods after skin testing for bovine tuberculosis. *Animals*. 2021 Apr 23; 11(5):1224.
- [23] Krieger M, Eisenberg S, Köhler H, Freise F, Campe A. Within-herd prevalence threshold for the detection of Mycobacterium avium ssp. paratuberculosis antibody-positive dairy herds using pooled milk samples: A field study. *Journal of Dairy Science*. 2022 Jan 1; 105(1):585-94.
- [24] Dehkordi FS. Prevalence study of Coxiella burnetii in aborted ovine and caprine fetuses by evaluation of nested and real-time PCR assays. *American Journal of Animal and Veterinary Sciences*. 2011; 6(4):180-6.
- [25] Dehkordi FS, Tavakoli-Far B, Jafariaskari S, Momtaz H, Esmaeilzadeh S, Ranjbar R, Rabiei M. Uropathogenic Escherichia coli in the high vaginal swab samples of fertile and infertile women: virulence factors, O-serogroups, and phenotyping and genotyping characterization of antibiotic resistance. *New Microbes and New Infections*. 2020; 38:100824.
- [26] Dehkordi FS, Haghghi N, Momtaz H, Rafsanjani MS, Momeni M. Conventional vs real-time PCR for detection of bovine herpes virus type 1 in aborted bovine, buffalo and camel fetuses. *Bulgarian Journal of Veterinary Medicine*. 2013; 16(2):102-12.
- [27] Ghorbani F, Gheisari E, Dehkordi FS. Genotyping of vacA alleles of Helicobacter pylori strains recovered from some Iranian food items. *Tropical Journal of Pharmaceutical Research*. 2016; 15(8):1631-6.
- [28] Dehkordi FS, Gandomi H, Basti AA, Misaghi A, Rahimi E. Phenotypic and genotypic characterization of antibiotic resistance of methicillin-resistant Staphylococcus aureus isolated from hospital food. *Antimicrobial Resistance & Infection Control*. 2017; 6(1):1-1.
- [29] Dehkordi FS, Saberian S, Momtaz H. Detection and segregation of Brucella abortus and Brucella melitensis in aborted bovine, ovine, caprine, buffaloes and camelid fetuses by application of conventional and real-time polymerase chain reaction. *The Thai Journal of Veterinary Medicine*. 2012; 42(1):13.
- [30] Dehkordi FS, Momtaz H, Doosti A. Application of Real-Time PCR for detection of Aspergillus species in aborted ruminant fetuses. *Bulgarian Journal of Veterinary Medicine*. 2012;15(1):30-6.
- [31] Dehkordi FS. Prevalence study of Bovine viral diarrhea virus by evaluation of antigen capture ELISA and RT-PCR assay in Bovine, Ovine, Caprine, Buffalo and Camel aborted fetuses in Iran. *AMB Express*. 2011; 1(1):1-6.
- [32] Dehkordi FS, Parsaei P, Saberian S, Moshkelani S, Hajshafiei P, Hoseini SR, Babaei M, Ghorbani MN. Prevalence study of Theileria annulata by comparison of four diagnostic Techniques in southwest Iran. *Bulgarian Journal of Veterinary Medicine*. 2012; 15(2): 123-130.
- [33] Dehkordi FS, Khamesipour F, Momeni M. Brucella abortus and Brucella melitensis in Iranian bovine and buffalo semen samples: The first clinical trial on seasonal, Senile and geographical distribution using culture, conventional and real-time polymerase chain reaction assays. *Kafkas Univ Vet Fak Dergisi*. 2014; 20(6):821-8.
- [34] Naser SA, Thanigachalam S, Dow CT, Collins MT. Exploring the role of Mycobacterium avium subspecies paratuberculosis in the pathogenesis of type 1 diabetes mellitus: a pilot study. *Gut Pathog*. 2013;5(1):14
- [35] Safarpordehkordi F, Yahaghi E, Khodaverdi Darian E. Prevalence of antibiotic resistance in Escherichia coli isolated from poultry meat supply in Isfahan. *Iranian Journal of Medical Microbiology*. 2014; 8(2):41-7.

- [36] Safarpour Dehkordi F, Hosseini S, Rahimi E, Momeni M, Yahaghi E, Khodaverdi Darian E. Investigate the frequency of virulence genes *Vibrio parahaemolyticus* isolated from fish, lobsters and crabs caught from Persian Gulf. *Iranian Journal of Medical Microbiology*. 2014;8(2):1-7.
- [37] Safarpour Dehkordi F, Momtaz H, Esmailzade S, Khayyat Khameneie M, Yahaghi E. Detection of virulence factors of Uropathogenic *Escherichia coli* isolates from infertile women high vaginal swabs. *Iranian Journal of Medical Microbiology*. 2014; 7(4):1-8.
- [38] Ranjbar R, Seif A, Dehkordi FS. Prevalence of antibiotic resistance and distribution of virulence factors in the shiga toxinogenic *Escherichia coli* recovered from hospital food. *Jundishapur J Microbiol*. 2019; 12(5):8.
- [39] Dehkordi FS, Tirgir F, Valizadeh Y. Effects of Guajol® ointment synthesized from medicinal smoke condensate of jennet feces on burn wound healing on Wistar rat. *Veterinary Research Forum*. 2017; 8(3):215.
- [40] Nejat S, Momtaz H, Yadegari M, Nejat S, Safarpour Dehkordi F, Khamesipour F. Seasonal, geographical, age and breed distributions of equine viral arteritis in Iran. *Kafkas Univ Vet Fak Derg*. 2015; 21(1):111-6.
- [41] Ranjbar R, Yadollahi Farsani F, Safarpour Dehkordi F. Antimicrobial resistance and genotyping of *vacA*, *cagA*, and *iceA* alleles of the *Helicobacter pylori* strains isolated from traditional dairy products. *Journal of Food Safety*. 2019 Apr; 39(2):e12594.
- [42] Shirvani R, Rahimi E, Shakerian A, Momtaz H. Comprehensive study on the molecular prevalence and seasonal and age distribution of *Mycobacterium avium* subspecies *paratuberculosis* in raw milk and traditional dairy products. *Indian Journal of Dairy Science*. 2019; 72(6):631-8.
- [43] Okura H, Toft N, Nielsen SS. Occurrence of *Mycobacterium avium* subsp. *paratuberculosis* in milk at dairy cattle farms: a systematic review and meta-analysis. *Veterinary microbiology*. 2012 Jun 15;157(3-4):253-63.
- [44] Correa-Valencia NM, Ramírez NF, Arango-Sabogal JC, Fecteau G, Fernández-Silva JA. Prevalence of *Mycobacterium avium* subsp. *paratuberculosis* infection in dairy herds in Northern Antioquia (Colombia) and associated risk factors using environmental sampling. *Preventive veterinary medicine*. 2019 Oct 1; 170:104739.
- [45] Hendrick S, Duffield T, Leslie K, Lissemore K, Archambault M, Kelton D. The prevalence of milk and serum antibodies to *Mycobacterium avium* subspecies *paratuberculosis* in dairy herds in Ontario. *The Canadian Veterinary Journal*. 2005 Dec; 46(12):1126.
- [46] Marchetti G, Ricchi M, Serraino A, Giacometti F, Bonfante E, Arrigoni N. Prevalence of *Mycobacterium avium* subsp. *paratuberculosis* in milk and dairy cattle in Southern Italy: preliminary results. *Italian Journal of Food Safety*. 2013 Oct 15; 2(3):e35-.
- [47] Stephan R, Schumacher S, Tasara T, Grant IR. Prevalence of *Mycobacterium avium* subspecies *paratuberculosis* in Swiss raw milk cheeses collected at the retail level. *Journal of Dairy Science*. 2007 Aug 1; 90(8):3590-5.
- [48] Wolf R, Orsel K, De Buck J, Barkema HW. Calves shedding *Mycobacterium avium* subspecies *paratuberculosis* are common on infected dairy farms. *Veterinary research*. 2015 Dec; 46(1):1-8.