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Original Article

Antimicrobial resistance profile and virulence gene prevalence in *Listeria monocytogenes* isolates from raw meat products

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Abstract

Background: Human listeriosis epidemics are often related to the intake of contaminated food, particularly meat products. **Aims:** This study aimed to investigate the prevalence, molecular and phenotypic determination of antibiotic resistance and pathogenicity of *Listeria monocytogenes* in beef, sheep, goat, camel, and buffalo meat in Chaharmahal and Bakhtiari province. **Methods:** A total of 300 raw meat samples were obtained from retail outlets. Biochemical analysis revealed that 129 samples (43%) were contaminated with *L. monocytogenes*. Using species-specific PCR (16S rRNA gene amplification), all 129 isolates obtained from the original samples were identified as *L. monocytogenes*. In this study, *actA1*, *hlyA*, *iap*, *plcA*, *prfA*, *intA*, and *intB* genes were evaluated using multiplex PCR. Multiplex PCR amplification of *aadB*, *aac(3)-IIa*, *penA*, *ermA*, *ermB*, *tetM*, *tetA*, *sulI*, and *sulII* was performed. **Results:** The average number of *L. monocytogenes* isolates in sheep, cow, camel, goat, and buffalo meat was 40%. *L. monocytogenes* isolates derived from raw meat exhibited the highest resistance to β -lactam antibiotics. In addition, the lowest resistance to Trimethoprim-sulfamethoxazole was observed. After the *hlyA* gene, the *iap* (44.18%) and *actA1* (40.31%) genes had the greatest frequency across isolates from various meat sources. The genes *penA*, *aadB*, and *aac(3)-IIa* were found in most *L. monocytogenes* strains. The most identified genes among *L. monocytogenes* strains were *penA*, *aadB*, and *aac(3)-IIa*. Few strains were resistant to SXT, although *penA* was widely distributed (92.24%). **Conclusion:** In conclusion, *L. monocytogenes* isolates from raw meat exhibited a high prevalence of virulence genes and considerable resistance to multiple antibiotic classes. It is necessary to continuously track these features throughout the food chain to improve control measures and reduce public health risks.

Key words: Antibiotic resistance, *Listeria monocytogenes*, Listeriosis, Meat products

Introduction

Food contains an enormous variety of nutrients that promote microbial growth, particularly pathogenic organisms (Kayode and Okoh, 2022). Numerous food products have been linked to listeriosis outbreaks throughout time, resulting in significant health consequences worldwide (Shonhiwa *et al.*, 2019). Foodborne listeriosis is typically linked to ready-to-eat (RTE) meals stored in refrigeration and to foods that require minimal or no processing. Microbiologically, product quality is of great importance to both the manufacturer and the individual who consumes it (Koopmans *et al.*, 2023; Maung *et al.*, 2023).

Listeria monocytogenes is a bacterium leading to listeriosis, a condition that may be managed by medications; however, it is a hazard to the general public since the organism has the capacity to acquire drug resistance (Moabelo *et al.*, 2023). It is a Gram-positive, facultative anaerobic bacterium found in food production

factories (Ranjbar and Halaji, 2018). This pathogen is very resilient to environmental conditions and can multiply even at 4°C. It also exhibits strong salt tolerance. These traits enable and survive for extended periods in food processing and manufacturing environments (Zamuz *et al.*, 2021). During food preservation, transportation, and preparation, contamination of animal products, eggs, frozen foods, fruits, vegetables, and seafood can result in human infection (Huang *et al.*, 2023). Listeriosis is an infectious complication that predominantly impacts expectant women, individuals at the extremities of age, or those with compromised immune systems. Consumption of food contaminated with *L. monocytogenes* is the predominant cause of infection, resulting in a self-limiting condition in immunocompetent individuals but linked to invasive disease and elevated mortality rates among high-risk patient populations (Mejía *et al.*, 2023).

The severity of *L. monocytogenes* infection is affected by many conditions that enhance the organism's

inherent capacity to endure in food-processing settings. *L. monocytogenes* produces virulence elements which involve the *hylA*, *actA*, *inlA*, *inlB*, *A Plc*, and *iap* genes (Gray *et al.*, 2021). The *hylA* protein is important for host cell invasion and phagosome avoidance (Duma *et al.*, 2024). *actA*, the actin building gene, helps cells migrate from one to another. The invasion-associated protein gene *iap* plays a role in the adherence and invasion of bacteria into host cells (Yoshikawa *et al.*, 2016). The *inlA-inlB* locus generates two membrane proteins, internalins InlA and InlB, which play a role in pathogen internalization by non-phagocytic cells upon the interaction of host cell receptors E-cadherin and Met, respectively (Schiavano *et al.*, 2023). *PlcA* and *PlcB* are responsible for escape from vacuoles (Gana *et al.*, 2024). Furthermore, *L. monocytogenes*' antimicrobial resistance efficiency might be enhanced through acquiring resistance genes from *Enterococcus* and *Streptococcus* species (Rippa *et al.*, 2024). Consequently, it is essential to perform an *in-vitro* evaluation of the antimicrobial drug beginning therapy, as well as to discover new and alternative antimicrobials. The main cause of the disease is the delay in treatment and the widespread of multidrug-resistant (MDR) *L. monocytogenes*, which has many virulence factors (Silva *et al.*, 2024). The present study aimed to investigate the virulence and antibiotic resistance genes harbored by *L. monocytogenes* strains obtained from red meat.

Materials and Methods

Collection of samples

In alignment with the National Disease Control and Food Safety Risk Monitoring Strategy, 300 raw red meat samples were collected over the course of one year from retail markets and meat processing facilities across Chaharmahal and Bakhtiari provinces, Iran. The samples consisted of beef (n=100), sheep (n=50), goat (n=50), buffalo (n=50), and camel (n=50). Samples were transferred to the food hygiene laboratory of Faculty of Veterinary Medicine, Shahrekord Azad University in an ice flask for further evaluation.

Screening and detection of *L. monocytogenes* strains

The FDA-BAM methodology was used to isolate and identify *L. monocytogenes* strains. The FDA-BAM technique is a standardized methodology created by the U.S. Food and Drug Administration for the isolation, detection, and confirmation of *L. monocytogenes* in food samples (Law *et al.*, 2015). After collecting the samples, 10 g of each sample was processed with 225 ml of Fraser broth (Fraser Broth is a selective medium used for the secondary enrichment of *L. monocytogenes*) (Condalab, Spain). The positive broth was placed on *Listeria* PALCAM agar (Condalab, Spain) and incubated at 37°C for 24 h. Gram-staining, oxidase, catalase, methyl-red, and Voges-Proskauer tests were used for biochemical diagnosis. *L. monocytogenes* colonies were verified via

β-hemolytic potential on blood agar, exhibiting hemolytic activity. The hemolytic activity of *Staphylococcus aureus* was utilized as a positive control. To validate the identification of *Listeria* species, gene-specific PCR was performed using 16SrRN-specific primers. The 16S *rRNA* region of *Listeria* strains was amplified with universal primers (F: 5'-GGA CCG GGG CTA ATA CCG AAT GAT AA-3' and R: 5'-TTC ATG TAG GCG AGT TGC AGC CTA-3') using a FlashDetect™ Mini8 Plus Thermal Cycler (Coyote, China) (Dapgh and Salem, 2022). *L. monocytogenes* bacteria with accession code PTCC 1298 were used as a positive control (Sharma *et al.*, 2024).

Antimicrobial susceptibility typing

The Kirby-Bauer disk diffusion technique was employed to examine the antibiotic susceptibility profiles of *L. monocytogenes* strains (Wiśniewski *et al.*, 2022). At first, a bacterial suspension of 0.5 McFarland was prepared. A 0.5 McFarland standard serves as a turbidity reference for estimating bacterial concentration in a liquid solution (Kawacka *et al.*, 2023). Twelve various antibiotic disks (Oxoid Ltd., Basingstoke, UK) representing nine distinct antibiotic groups were utilized: beta-lactams: ampicillin (AMP, 10 µg), penicillin (PEN, 10 µg), amoxicillin (AMX, 10 µg); aminoglycosides: gentamicin (GM, 10 µg); carbapenems: meropenem (MEM, 10 µg); macrolides: erythromycin (E, 15 µg), vancomycin (VA, 30 µg), oleandomycin (OL, 15 µg); sulphonamides: trimethoprim-sulfamethoxazole (SXT, 25 µg); tetracycline: tetracycline (TE, 30 µg), cephalosporin: Cefazolin (SE, 30 µg) and phenicols: chloramphenicol (C, 30 µg). Following the adjustment of the overnight bacterial culture in TSA (Tryptic Soy Agar, Condalab, Spain) to a 0.5 McFarland standard, a sterile swab was used to uniformly inoculate Müller-Hinton agar plates (Thermo Scientific, USA). Antibiotic discs were then positioned on the MHA agar using a disc dispenser, and the plates were incubated at 37°C for 24 h. After incubation, inhibitory zones were determined and classified as resistant (R), intermediate (I), or sensitive (S) (Kawacka *et al.*, 2023).

Molecular characterization

Extraction of DNA

A single *L. monocytogenes* colony was cultured overnight on TSA at 37°C. One colony from the culture was placed into 5 ml of TSB (Tryptone Soya Broth, Condalab, Spain) and incubated overnight at 37°C. The 2.5 ml broth culture was centrifuged at 4000 ×g for 10 min, the pellet rinsed in 1 ml of distilled water, and resuspended in an Eppendorf tube with 400 µL of phosphate buffer saline (PBS, Aminsar, Iran). The Qiagen DNA extraction kit was used to extract deoxyribonucleic acid (DNA) according to the product instructions.

Determination of virulence-associated and antibiotic resistance genes

This research investigated the presence of 7

virulence-related genes (*hlyA*, *actA*, *inlA*, *inlB*, *plcA*, *prfA*, and *iap*) in the *L. monocytogenes* isolates using multiplex PCR. Furthermore, isolates with resistance and intermediate resistance identified by phenotypic analysis were chosen for antimicrobial resistance gene screening. Isolates that showed sensitivity in phenotypic examination were not chosen for further investigation. Antimicrobial resistance genes were identified using PCR. Nine antimicrobial resistance genes were investigated, such as those encoding resistance to gentamicin (*aadB*, *aac(3)-IIa*, penicillin G (*penA*), erythromycin (*ermA* and *ermB*), tetracycline (*tetM* and *tetA*), and trimethoprim/sulfamethoxazole (*sulI*, *sulII*). PCR experiments were done in a final volume of 20 μ L, which included 12 μ L of Master Mix RED 2x (Ampliqon, Denmark), 2 μ L of template DNA, 1 μ L of each 10 μ M primer, and 5 μ L of DEPC water. The temperature protocol is described in Table 1. The primers used in this study listed in Table 2. The amplified DNA fragments were observed using safe stain (Cinaclone,

Iran) in a 2% agarose gel using UV light.

Statistical analysis

The statistical examination was carried out using SPSS 19.0 software. The Chi-squared test was used, with $P < 0.05$ indicating statistical significance.

Results

Prevalence of *L. monocytogenes* in collected meat samples

A total of 300 raw meat samples were collected from a variety of sources, with 129 (43%) identified as *L. monocytogenes* using biochemical analysis (Table 3). All 129 isolates (C1-C129) derived from the original samples were verified as members of the *Listeria* genus via PCR amplification of the *16S rRNA* gene. The frequency of *L. monocytogenes* isolates among sheep, cow, camel, goat, and buffalo meat samples was reported

Table 1: Temperature program used in the present study

Step	Temperature (°C)	Time	Cycles
Initial denaturation	95	10 min	1
Denaturation	95	10 s	
Annealing	55-65°C (depending on primer melting temperature)	30 s	35
Elongation	72	30 s	

Table 2: Primer sequences used in the investigation

Gene name		Sequence (5' to 3')	Annealing temperature (°C)	Product size	Reference
Listeriolysin O	<i>hlyA</i>	F: GCA GTT GCA AGC GCT TGG AGT GAA R: GCA ACG TAT CCT CCA GAG TGA TCG	62	456	Osman <i>et al.</i> (2014)
Actin polymerization protein	<i>actA</i>	F: CGC CGC GGA AAT TAA AAA AAG A R: ACG AAG GAA CCG GGC TGC TAG	62	839	Jallewar <i>et al.</i> (2007)
Internalin A	<i>inlA</i>	F: CCT AGC AGG TCT AAC CGC AC R: TCG CTA ATT TGG TTA TGC CC	58	255	Kawacka and Olejnik-Schmidt (2024)
Internalin B	<i>inlB</i>	F: AAA GCA CGA TTT CAT GGG AG R: ACA TAG CCT TGT TTG GTC GG	58	146	Mureddu <i>et al.</i> (2014)
Phosphatidylinositol-specific phospholipase C	<i>plcA</i>	F: CGA GCA AAA CAG CAA CGA TA R: CCG CGG ACA TCT TTT AAT GT	60	129	Mureddu <i>et al.</i> (2014)
Listeriolysin positive regulatory protein	<i>prfA</i>	F: GAT ACA GAA ACA TCG GTT GGC R: GTG TAA TCT TGA TGC CAT CAG G	49	274	D'agostino <i>et al.</i> (2004)
Invasion associated protein	<i>iap</i>	F: ACA AGC TGC ACC TGT TGC AG R: TGA CAG CGT GTG TAG TAG CA	56	131	Chen <i>et al.</i> (2025)
Resistance to GM	<i>aadB</i>	F: GAG CGA AAT CTG CCG CTC TTG R: CTG TTA CAA CGG ACT GGC CGC	57	310	Wiśniewski <i>et al.</i> (2022)
	<i>aac(3)-IIa</i>	F: CGG AAG GCA ATA ACG GAG R: TCG AAC AGG TAG CAC TGA G	60	740	Wiśniewski <i>et al.</i> (2022)
Resistance to PEN	<i>penA</i>	F: ATC GAA CAG GCG ACG ATG TC R: GAT TAA GAC GGT GTT TTA CGG	60	500	Srinivasan <i>et al.</i> (2005)
Resistance to SXT	<i>sulI</i>	F: CGG CGT GGG CTA CCT GAA CG R: GCC GAT CGC GTG AAG TTC CG	58	433	Iwu and Okoh (2020)
	<i>sulII</i>	F: GCG CTC AAG GCA GAT GGC ATT R: GCG TTT GAT ACC GGC ACC CGT	58	293	
Resistance to TE	<i>tetM</i>	F: GTG GAC AAA GGT ACA ACG AG R: CGG TAA AGT TCG TCA CAC AC	60	450	Swetha <i>et al.</i> (2021)
	<i>tetA</i>	F: GGC CTC AAT TTC CTG ACG R: AAG CAG GAT GTA GCC TGT GC	59	546	Gholami <i>et al.</i> (2019)
Resistance to E	<i>Erm A</i>	F: TAT CTT ATC GTT GAG AAG GGA TT R: CTA CAC TTG GCT TAG GAT GAA A	60	139	Gholami <i>et al.</i> (2019)
	<i>Erm B</i>	F: GAA AAG GTA CTC AAC CAA ATA R: AGT AAC GGT ACT TAA ATT GTT TAC	60	639	Gholami <i>et al.</i> (2019)

Table 3: The incidence of *L. monocytogenes* in various meat products

Sample	No. of samples	No. of positive isolates (%)
Sheep	50	20 (40%)
Cow	100	52 (52 %)
Camel	50	17 (34%)
Goat	50	10 (20%)
Buffalo	50	30 (60%)
Total	300	129 (43%)

in Table 3. The highest frequency of *L. monocytogenes* was observed in buffalo meat (60%), and the lowest frequency was observed in goat meat (20%). Statistical evaluations showed no statistically significant relationship between *L. monocytogenes* contamination in meat samples sold in Chaharmahal and Bakhtiari provinces ($P>0.05$).

Antimicrobial sensitivity

The antibiotic sensitivity patterns of *L. monocytogenes* strains collected from raw meat were determined using 9 antibiotic groups (Table 4). The results of this study showed that the highest prevalence of antibiotic resistance among *L. monocytogenes* strains is related to penicillin (96.89%) and ampicillin (89.14%). Antibiotic resistance in *L. monocytogenes* isolates from raw meat was most common in the β -lactam antibiotic. After that, the highest prevalence of antibiotic resistance was observed among aminoglycosides (gentamicin: 75.19%), tetracycline (tetracycline: 68.21%), and macrolide (erythromycin: 65.89%). Furthermore, the findings revealed that practically all the identified strains are susceptible to clindamycin (60.64%), trimethoprim-sulfamethoxazole (69.76%), and oleandomycin (62.01%). Vancomycin (51.95%), chloramphenicol (46.51%), and meropenem (42.63%) showed moderate sensitivity against *L. monocytogenes* isolates.

Investigating the prevalence of antibiotic resistance genes

To evaluate and determine the distribution of antibiotic resistance among isolates of *L. monocytogenes* isolated from different sources of meat, *aadB*, *aac(3)-IIa*,

penA, *ermA*, *ermB*, *tetM*, *tetA*, *sulI*, and *sulII* genes were evaluated using multiplex PCR (Fig. 1). The selection of genes was according to the antibiotic resistance pattern obtained from the disk diffusion test. The gentamicin resistance genes *aadB* and *aac(3)-IIa* were found in 74.41% and 77.59% of strains that showed phenotypic resistance. The *penA* gene with the highest frequency (92.24%) was found in 119 strains out of 129 strains of *L. monocytogenes*. Trimethoprim-sulfamethoxazole resistance genes *sulI* and *sulII* were found in 27.133% (35/129) and 21.70% (28/129) of the strains, respectively. The frequencies of the tetracycline resistance genes *tetM* and *tetA* were reported as 38.75% and 51.16%, respectively, which was consistent with the results obtained from the disk diffusion test. Also, the distribution of erythromycin resistance genes *ermA* and *ermB* among the isolates was 51.93% (67/129) and 55.03% (71/129), respectively. The highest frequency was related to the *penA* gene, and the lowest frequency was related to the *sulI* and *sulII* genes.

Distribution of virulence factors

Among 129 identified and confirmed *L. monocytogenes* isolates, the frequencies of the virulence genes: *hlyA*, *actA1*, *inlA*, *inlB*, *plcA*, *prfA*, and *iap* were reported as 70.84%, 40.31%, 34.88%, 24.80%, 24.80%, 34.88%, and 44.18%, respectively (Table 5). The highest pathogenicity factor found among isolates from different meat sources was related to the *hlyA* (70.84%) gene and the lowest was related to the *inlB* (24.80%), and *plcA* (24.80%) genes. The *hlyA* gene was found with the highest frequency in the strains isolated from sheep, cow, goat, camel and buffalo with 85%, 82.69%, 70%, 64.70%, and 83.33%, respectively. The results showed that the *intA* gene had the highest frequency among strains isolated from camel meat (70.58%), while its lowest frequency was observed in the strains isolated from buffalo meat (23.33%). The lowest prevalence of pathogenic genes is as follows: the *plcA* gene in goat (10%), camel (17.64%), and cow meat (13.46%); the *inlB* gene in cow meat (15.38%), and the *prfA* gene in cow meat (21.15%) and goat (20%) (Table 5).

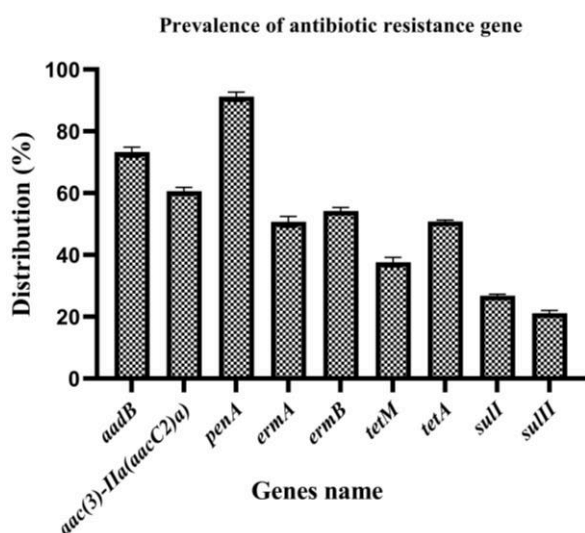
Table 4: The results of the antibiotic resistance pattern of *L. monocytogenes* strains isolated from different sources of raw meat

Antibiotic disc	Abbreviation	Concentration (μ g/ml)	Class of antibiotic	Phenotype resistance rate (%)					
				R (%)	No. of bacteria	S (%)	No. of bacteria	IM (%)	No. of bacteria
Ampicillin	AM	10	beta-lactam	89.14	115/129	0	0/129	22.48	29/129
Penicillin	PEN	10	beta-lactam	96.89	125/129	0	0/129	3.1	4/129
Amoxicillin	AMX	10	beta-lactam	73.64	95/129	7.75	10/129	18.6	24/129
Gentamicin	GM	10	aminoglycosides	75.19	97/129	3.87	5/129	20.9	27/129
Meropenem	MEN	10	carbapenems	42.63	55/129	34.88	45/129	22.48	29/129
Erythromycin	E	15	macrolide	65.89	85/129	13.17	17/129	20.9	27/129
Vancomycin	V	30	macrolide	51.93	67/129	5.42	7/129	42.63	55/129
Chloramphenicol	C	30	phenicols	46.51	60/129	13.17	17/129	40.31	52/129
Oleandomycin	OL	15	macrolide	23.25	30/129	62.01	80/129	14.72	19/129
Clindamycin	CC	2	lincosamide	19.37	25/129	60.46	78/129	20.15	26/129
Tetracycline	TE	30	tetracycline	68.21	88/129	0	0/129	31.78	41/129
Trimethoprim-sulfamethoxazole	SXT	25	sulphonamides	22.48	29/129	69.76	90/129	7.75	10/129
Cefazolin	SE	30	cephalosporin	37.20	48/129	55.03	71/129	7.75	10/129

Total=129, R: Resistance, IM: Intermediate, and S: Sensitive

Table 5: The results of distribution of virulence genes in *L. monocytogenes* isolates from beef, sheep, camel, goat and buffalo in Chaharmahal Bakhtiari province

Sample	No. of positive sample	Distribution of virulence genes						
		<i>hlyA</i>	<i>actA1</i>	<i>intA</i>	<i>intB</i>	<i>plcA</i>	<i>prfA</i>	<i>iap</i>
Sheep	20	17 (85%)	11 (55%)	8 (40%)	5 (25%)	5 (25%)	8 (40%)	10 (50%)
Cow	52	43 (82.69%)	21 (40.38%)	15 (28.84%)	8 (15.38%)	7 (13.46%)	11 (21.15%)	24 (46.15)
Camel	17	11 (64.70%)	5 (29.41)	12 (70.58%)	6 (35.29%)	3 (17.64%)	5 (29.41)	7 (41.17)
Goat	10	7 (70%)	3 (30%)	3 (30%)	5 (50%)	1 (10%)	2 (20%)	5 (50%)
Buffalo	30	25 (83.33%)	12 (40%)	7 (23.33%)	10 (33.33%)	13 (43.33%)	18 (60%)	11 (36.66%)
Total	129 (43%)	103 (70.84%)	52 (40.31%)	45 (34.88%)	32 (24.80%)	32 (24.80%)	45 (34.88%)	57 (44.18%)

**Fig. 1:** The results of investigating the prevalence of antibiotic resistance genes in *L. monocytogenes* strains isolated from different meat sources

Discussion

L. monocytogenes is a foodborne organism that can lead to listeriosis, a serious disease that may be deadly in those with immunocompromised conditions, such as the elderly, pregnant women, and their newborns (Shen *et al.*, 2022). This organism is prevalent in the environment and is commonly detected in food items, posing a severe hazard in the food chain, particularly for RTE meals (Cavalcanti *et al.*, 2022). Significant consumption of meat products in Iran increases the risk of listeriosis; therefore, evaluating the incidence rate of *L. monocytogenes* and determining the antibiotic resistance patterns of isolates found in different types of meat are very important.

The results of this study showed that among 300 meat samples collected from different sources, 129 samples were infected with *L. monocytogenes*. The total incidence of *L. monocytogenes* in meat was 43%. It validated both phenotypically and molecularly. In total, the prevalence of *L. monocytogenes* contamination in sheep meat was 40%, cattle 52%, camel 17%, goat 10%, and buffalo 60%. The results showed that the highest prevalence of *L. monocytogenes* is in buffalo meat and the lowest in goat meat. The results of the present study are in line with that of other studies. Previous studies have shown that the variable prevalence rates of *L. monocytogenes* in raw meat vary across several nations.

Yehia *et al.* (2020) identified *L. monocytogenes* in 16% of raw camel meat samples, but Boukili *et al.* (2020) reported a lower prevalence of 7.14% (10/140) in beef. Prevalence rates in several areas showed significant variation, with Egypt at 6.67%, Poland at 19.4%, and Ethiopia at 3.39% in beef and related products (Wieczorek *et al.*, 2012; Ismaiel *et al.*, 2014; Hailu *et al.*, 2024). In Turkey, elevated frequencies have been documented, with Arslan and Baytur (2019) identifying *L. monocytogenes* in 41.9% (26/62) of ground beef from Bolu. These investigations together underscore significant geographical disparities in the prevalence of *L. monocytogenes* in raw meat, highlighting the need for ongoing surveillance and food safety measures.

Numerous virulence genes have been identified in *L. monocytogenes* isolates from beef, meat derivatives, and other food sources (Chen *et al.*, 2019; Matle *et al.*, 2020; Li *et al.*, 2022). The prevalence of virulence genes in *L. monocytogenes* is higher than that of other *Listeria* species and varies according to the location, source, and type of sample (Arslan and Baytur, 2019). One of the key pathogenic component among these genes, *hlyA*, is responsible for phagosome escape and host cell invasion (Al Hulimi *et al.*, 2024). Among the seven investigated genes in *L. monocytogenes* strains, the *hlyA* gene was found in 70.84% of them. The *hlyA* gene in *L. monocytogenes* produces listeriolysin O (LLO), a virulence factor that helps the bacterium invade host cells and spread throughout the body (Saytekin *et al.*, 2025). This research traced *actA1*, *PrfA*, and *PlcA* genes from the *PrfA* virulence gene set (pVGC) in *L. monocytogenes* strains. After the *hlyA* gene, the highest frequencies were related to *iap* (44.18%) and *actA1* (40.31%) genes among isolates derived from different meat sources. The highest frequency of the *actA1* gene (55%) was observed among isolates from sheep, while the lowest was found in camel meat (29.41%). *L. monocytogenes*' main virulence factor, ActA, is an integral membrane protein necessary for intracellular motility, cell-to-cell transmission, and fast bacterial dispersion in the infected host (Travier and Lecuit, 2014). The *iap* gene of *L. monocytogenes* plays a major role in the pathogenesis of the bacterium. It encodes the p60 protein, which is important for cell survival and possesses bacteriolytic action (Pombinho *et al.*, 2020). The highest frequency of the *iap* gene was observed among isolates derived from sheep and camel meat, while the lowest was among isolates from buffalo meat (36.66%). The results showed that *intA* gene has the highest frequency among the strains isolated from camel

meat (70.58%), while its lowest frequency was observed in the strains isolated from buffalo meat (23.33%). So far, five internalin proteins (*InlA*, *InlB*, *InlC*, *InlF*, and *InlP*) have been identified as controlling *L. monocytogenes* infection. The internalins *InlA*, *InlB*, and *InlF* localize to the surface of *Listeria* and induce bacterial internalization into mammalian cells by interacting with unique host surface receptors (Iretton *et al.*, 2021). The *prfA* gene was abundant among *L. monocytogenes* strains isolated from buffalo meat (60%). *PrfA* positively controls the expression of virulence genes required for intracellular survival of *L. monocytogenes*, such as *hyl*, *mpl*, *plcA*, *actA*, and *plcB* (Ollinger *et al.*, 2009). The results of the present study are in line with that of other studies. Bouymajane *et al.* (2021) found *L. monocytogenes* in 15 of 520 samples, which is 2.9%. This included 3 isolates in conventional whey, raw minced beef, and raw sausage, 2 in raw milk, and 1 sample, 5.7%, in semen (traditional butter), raw beef, raw chicken, and raw fish whereas, no contamination was detected in salad and raib samples (traditional coagulated milk) (Bouymajane *et al.*, 2021). The results of this study showed that 15 isolates (100%) have the *actA* gene, 14 isolates (93.3%) have the *hylA*, *prfA*, and *plcB* genes, 13 isolates (86.7%) have the *inlA* and *inlC* genes, and 12 strains (80%) have the *inlJ* gene (Bouymajane *et al.*, 2021). Another study found that *hylA*, *prfA*, and *inlA* genes were present in 60.8% of *L. monocytogenes* isolates recovered from raw milk in Egypt (Tahoun *et al.*, 2017). The findings of another study revealed that all *L. monocytogenes* isolate obtained from beef and beef products had at least one of the seven virulence-related genes. The *inlA*, *hylA*, *plcA*, and *actA* genes were discovered in 97.3% of the isolates (Gana *et al.*, 2024). As a result, *L. monocytogenes* with a high incidence of virulence genes is extremely detrimental to public health, and consuming food contaminated with these strains regards a substantial risk to people, causing serious illness and death.

Antibiotic-resistant (AR) strains of *L. monocytogenes* pose a significant health concern connected with food intake. Despite its high vulnerability to the antimicrobials widely used in infection therapy, *L. monocytogenes* has recently been demonstrated to acquire enhanced antimicrobial resistance (Baquero *et al.*, 2020). *L. monocytogenes* antibiotic resistance can develop via the acquisition of resistance genes from other Gram-positive organisms (e.g., plasmid-mediated transfer). However, the misuse of antibiotics in healthcare and farming can also negatively affect pathogen's drug sensitivity (Komora *et al.*, 2017). Furthermore, *L. monocytogenes* cell components and processes involved in adaptation to stress circumstances occurring in the food chain have been postulated to be related to the increasing pathogen resistance to ampicillin, penicillin, and cephalosporins (Amajoud *et al.*, 2018). Furthermore, penicillin, ampicillin, and amoxicillin with or without gentamicin or trimethoprim-sulfamethoxazole are frequently prescribed as the primary option for the curative management of

listeriosis, while ciprofloxacin, tetracycline, and chloramphenicol are employed as the subsequent approach (Baquero *et al.*, 2020). Several investigations have confirmed that *L. monocytogenes* strains from meat are antimicrobial-resistant (Pesavento *et al.*, 2010; Noll *et al.*, 2018). In our study, 96.89% and 89.14% of *L. monocytogenes* strains isolated from different types of meat were resistant to penicillin and ampicillin. Gentamicin, an antibiotic successfully used to treat infections caused by *L. monocytogenes*, was found to be the least effective against strains recovered in our tests, with 97/129 (75.19%) isolates resistant. Furthermore, the results showed that almost all the isolates detected are sensitive to clindamycin (60.64%), SXT (69.76%), and oleandomycin (62.01%). However, research conducted in Malaysia on chicken carcasses found that the obtained isolates were resistant to penicillin (17.2%), ampicillin (6.9%), and erythromycin (6.9%) (Barbosa *et al.*, 2014). In Egypt, Tahoun *et al.* (2017) revealed that *L. monocytogenes* displays significant resistance to tetracycline (81%) and ciprofloxacin (66.7%), and susceptibility to ampicillin, erythromycin, and SXT.

In this study, the genes involved in the induction of aminoglycoside, macrolide, beta-lactam, tetracycline, and sulfonamide antibiotic-resistance were also investigated. In this investigation, *penA*, *aadB*, and *aac(3)-IIa* were the most discovered genes among *L. monocytogenes* strains. Few strains were resistant to SXT, although *penA* was very prevalent (92.24%). *tetA* and *tetM*, which encode resistance to tetracycline family antibiotics, were found in 51.16% and 38.75% of resistant strains, respectively. The frequencies of genes *ermA* and *ermB* genes responsible for erythromycin resistance were 51.93% and 55.03%, respectively. This was more prevalent than the distribution of genes responsible for tetracycline resistance. The high frequencies of antibiotic-resistant bacteria reported in this study is most likely due to the widespread use of these drugs in veterinary care. Indeed, the burden of selection brought to bear by the administration of antibiotics, particularly when done under improper settings, whether in people or in animals, must be considered as the primary risk factor in the formation of resistance to antibiotics (Parra-Flores *et al.*, 2022). The results obtained from this current research showed that there is resistance to antibiotics that are widely used in meat production and veterinary industries. According to the results of this study; Panera-Martínez *et al.* (2022) showed that *L. monocytogenes* strains isolated from chicken and turkey meat are 97.6% resistant to the ampicillin antibiotic of the beta-lactam family (Panera-Martínez *et al.*, 2022). This is due to the antibiotic's important function in treating listeriosis, as well as the growth in the proportion of resistant strains during the previous 20 years. Similar to previous studies, the present investigation found that the existence of antibiotic resistance genes in *Listeria* strains was not necessarily associated with phenotypic antimicrobial resistance. As a result, various mechanisms including decreased permeability, efflux pump activation,

mutations, or genes encoding enzymes with antibacterial activity may have contributed to the antibiotic resistance.

In this research, sheep, cow, goat, buffalo, and camel meat samples obtained from raw meat distribution stations in the Chaharmahal-Bakhtiari region had a high incidence of *L. monocytogenes*, indicating possible consumer hazards. In addition, many strains of *L. monocytogenes* have shown various resistances to penicillin, ampicillin, and amoxicillin, which is a significant finding in the field of food safety and health care, as these drugs often fail to manage listeriosis. 7 genes related to the pathogenicity of *L. monocytogenes* were found in this study with different prevalence. The highest frequency was related to *hlyA*, *iap*, and *actA1* genes. Finally, this study showed a high prevalence of *L. monocytogenes* in raw meat in Chaharmahal-Bakhtiari province, which poses a serious threat to consumers. However, this study has limitation such as lack of whole genome sequencing, focus on one province, and small sample size. Future research should use genetic monitoring and extensive temporal sampling to track patterns in developing resistance and pathogenicity. Future studies should also propose new strategies to improve regional food security.

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Conflict of interest

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References

- Al Hulimi, A; Al Hulimi, A and Nossair, MA (2024). Detection of some virulence factors of *Listeria* species isolated from chicken and their products. Alex. J. Vet. Sci., 82: 74-83.
- Amajoud, N; Leclercq, A; Soriano, JM; Bracq-Dieye, H; El Maadoudi, M; Senhaji, NS; Kounnoun, A; Moura, A; Lecuit, M and Abrini, J (2018). Prevalence of *Listeria* spp. and characterization of *Listeria monocytogenes* isolated from food products in Tetouan, Morocco. Food Control. 84: 436-441.
- Arslan, S and Baytur, S (2019). Prevalence and antimicrobial resistance of *Listeria* species and subtyping and virulence factors of *Listeria monocytogenes* from retail meat. J. Food Saf., 39: e12578.
- Baquero, F; Lanza, VF; Duval, M and Coque, TM (2020). Ecogenetics of antibiotic resistance in *Listeria monocytogenes*. Mol. Microbiol., 113: 570-579.
- Barbosa, LN; Alves, FCB; Andrade, BFMT; Albano, M; Castilho, IG; Rall, VLM; Athayde, NB; Delbem, NLC; Roca, RdO and Júnior, AF (2014). Effects of *Ocimum basilicum* Linn essential oil and sodium hexametaphosphate on the shelf life of fresh chicken sausage. J. Food Prot., 77: 981-986.
- Boukili, M; Filali, FR; Lafkih, N; Bouymajane, A; Sefiani, M and Moumni, M (2020). Prevalence, characterization and antimicrobial resistance of *Listeria monocytogenes* isolated from beef meat in Meknes city, Morocco. Germs. 10: 74-80.
- Bouymajane, A; Filali, FR; Oulghazi, S; Lafkih, N; Ed-Dra, A; Aboulkacem, A; El Allaoui, A; Ouhmidou, B and Moumni, M (2021). Occurrence, antimicrobial resistance, serotyping and virulence genes of *Listeria monocytogenes* isolated from foods. Heliyon. 7:e06169.
- Cavalcanti, AAC; Limeira, CH; de Siqueira, IN; de Lima, AC; de Medeiros, FJP; de Souza, JG; de Araújo Medeiros, NG; de Oliveira Filho, AA and de Melo, MA (2022). The prevalence of *Listeria monocytogenes* in meat products in Brazil: A systematic literature review and meta-analysis. Res. Vet. Sci., 145: 169-176.
- Chen, A; Chen, X; Zheng, Z; Wang, H and Hu, M (2025). Virulence gene profiling and molecular typing of clinical isolates of *Listeria monocytogenes* from Wenzhou, Eastern China. Infect. Drug Resist., 18: 3957-3966.
- Chen, M; Cheng, J; Zhang, J; Chen, Y; Zeng, H; Xue, L; Lei, T; Pang, R; Wu, S and Wu, H (2019). Isolation, potential virulence, and population diversity of *Listeria monocytogenes* from meat and meat products in China. Front. Microbiol., 10: 946.
- D'agostino, M; Wagner, M; Vazquez-Boland, J; Kuchta, T; Karpiskova, R; Hoorfar, J; Novella, S; Scotti, M; Ellison, J and Murray, A (2004). A validated PCR-based method to detect *Listeria monocytogenes* using raw milk as a food model—towards an international standard. J. Food Prot., 67: 1646-1655.
- Dagh, AN and Salem, RL (2022). Molecular detection of *Listeria monocytogenes* in milk and some milk products. Int. J. Vet. Sci., 11: 514-519.
- Duma, MN; Ciupescu, LM; Dan, SD; Crisan-Reget, OL and Tabaran, A (2024). Virulence and antimicrobial resistance of *Listeria monocytogenes* isolated from ready-to-eat food products in Romania. Microorganisms. 12: 954.
- Gana, J; Gcebe, N; Moerane, R; Ngoshe, YB; Moabelo, K and Adesiyun, AA (2024). Detection of pathogenic serogroups and virulence genes in *Listeria monocytogenes* strains isolated from beef and beef products retailed in Gauteng Province, South Africa, using phenotypic and polymerase chain reaction (PCR)-based methods. Int. J. Microbiol., 2024: 8891963.
- Gholami, A; Salehi, B and Jazi, FM (2019). The determination of the antimicrobial susceptibility and antimicrobial resistance gene patterns in *L. monocytogenes*. J. Med. Bacteriol., 8: 30-37.
- Gray, JA; Chandry, PS; Kaur, M; Kocharunchitt, C; Bowman, JP and Fox, EM (2021). Characterisation of *Listeria monocytogenes* food-associated isolates to assess

- environmental fitness and virulence potential. *Int. J. Food Microbiol.*, 350: 109247.
- Hailu, T; Gugsu, G; Tsegaye, Y; Ahmed, M and Awol, N** (2024). Occurrence and antimicrobial resistance pattern of *Listeria monocytogenes* isolated from bovine's milk and meat in Mekelle City, Ethiopia. *Adv. Public Health*. 2024: 8813787.
- Huang, C; Lu, TL and Yang, Y** (2023). Mortality risk factors related to listeriosis—a meta-analysis. *J. Infect. Public Health*. 16: 771-783.
- Iretton, K; Mortuza, R; Gyanwali, GC; Gianfelice, A and Hussain, M** (2021). Role of internalin proteins in the pathogenesis of *Listeria monocytogenes*. *Mol. Microbiol.*, 116: 1407-1419.
- Ismail, AAR; Ali, AES and Enan, G** (2014). Incidence of *Listeria* in Egyptian meat and dairy samples. *Food Biotechnol.*, 23: 179-185.
- Iwu, CD and Okoh, AI** (2020). Characterization of antibiogram fingerprints in *Listeria monocytogenes* recovered from irrigation water and agricultural soil samples. *PLoS One*. 15: e0228956.
- Jallewar, P; Kalorey, D; Kurkure, N; Pande, V and Barbuddhe, S** (2007). Genotypic characterization of *Listeria* spp. isolated from fresh water fish. *Int. J. Food Microbiol.*, 114: 120-123.
- Kawacka, I and Olejnik-Schmidt, A** (2024). High prevalence of virulence-associated genes and length polymorphism in actA and inlB genes identified in *Listeria monocytogenes* isolates from meat products and meat-processing environments in Poland. *Pathogens*. 13: 444.
- Kawacka, I; Pietrzak, B; Schmidt, M and Olejnik-Schmidt, A** (2023). *Listeria monocytogenes* isolates from meat products and processing environment in Poland are sensitive to commonly used antibiotics, with rare cases of reduced sensitivity to ciprofloxacin. *Life*. 13: 821.
- Kayode, AJ and Okoh, AI** (2022). Assessment of the molecular epidemiology and genetic multiplicity of *Listeria monocytogenes* recovered from ready-to-eat foods following the South African listeriosis outbreak. *Sci. Rep.*, 12: 20129.
- Komora, N; Bruschi, C; Magalhães, R; Ferreira, V and Teixeira, P** (2017). Survival of *Listeria monocytogenes* with different antibiotic resistance patterns to food-associated stresses. *Int. J. Food Microbiol.*, 245: 79-87.
- Koopmans, MM; Brouwer, MC; Vázquez-Boland, JA and van de Beek, D** (2023). Human listeriosis. *Clin. Microbiol. Rev.*, 36: e00060-00019.
- Law, JWF; Ab Mutalib, NS; Chan, KG and Lee, LH** (2015). An insight into the isolation, enumeration, and molecular detection of *Listeria monocytogenes* in food [Review]. *Front. Microbiol.*, 6: 1227.
- Matle, I; Mbatha, KR and Madoroba, E** (2020). A review of *Listeria monocytogenes* from meat and meat products: Epidemiology, virulence factors, antimicrobial resistance and diagnosis. *Onderstepoort J. Vet. Res.*, 87: 1-20.
- Maung, AT; Abdelaziz, MNS; Mohammadi, TN; Zhao, J; Mohamed, ET; Nakayama, M; Matsusita, K; Masuda, Y; Honjoh, Ki and Miyamoto, T** (2023). Comparison of prevalence, characterization, antimicrobial resistance and pathogenicity of foodborne *Listeria monocytogenes* in recent 5 years in Japan. *Microb. Pathog.*, 183: 106333.
- Mejía, L; Espinosa-Mata, E; Freire, AL; Zapata, S and González-Candelas, F** (2023). *Listeria monocytogenes*, a silent foodborne pathogen in Ecuador. *Front. Microbiol.*, 14: 1278860.
- Moabelo, KC; Gcebe, N; Gana, J; Ngoshe, YB and Adesiyun, AA** (2023). Contamination of beef and beef products by *Listeria* spp. and molecular characterization of *L. monocytogenes* in Mpumalanga, South Africa. *J. Food Saf.*, 43: e13055.
- Mureddu, A; Mazza, R; Fois, F; Meloni, D; Bacciu, R; Piras, F and Mazzette, R** (2014). *Listeria monocytogenes* persistence in ready-to-eat sausages and in processing plants. *Ital. J. Food Saf.*, 3: 20-26.
- Noll, M; Kleta, S and Al Dahouk, S** (2018). Antibiotic susceptibility of 259 *Listeria monocytogenes* strains isolated from food, food-processing plants and human samples in Germany. *J. Infect. Public Health*. 11: 572-577.
- Ollinger, J; Bowen, B; Wiedmann, M; Boor, KJ and Bergholz, TM** (2009). *Listeria monocytogenes* σ B modulates PrfA-mediated virulence factor expression. *Infect. Immun.*, 77: 2113-2124.
- Osman, KM; Zolnikov, TR; Samir, A and Orabi, A** (2014). Prevalence, pathogenic capability, virulence genes, biofilm formation, and antibiotic resistance of *Listeria* in goat and sheep milk confirms need of hygienic milking conditions. *Pathog. Glob. Health*. 108: 21-29.
- Panera-Martínez, S; Rodríguez-Melcon, C; Serrano-Galan, V; Alonso-Calleja, C and Capita, R** (2022). Prevalence, quantification and antibiotic resistance of *Listeria monocytogenes* in poultry preparations. *Food Control*. 135: 108608.
- Parra-Flores, J; Holý, O; Bustamante, F; Lepuschitz, S; Pietzka, A; Contreras-Fernández, A; Castillo, C; Ovalle, C; Alarcón-Lavín, MP and Cruz-Córdova, A** (2022). Virulence and antibiotic resistance genes in *Listeria monocytogenes* strains isolated from ready-to-eat foods in Chile. *Front. Microbiol.*, 12: 796040.
- Pesavento, G; Ducci, B; Nieri, D; Comodo, N and Nostro, AL** (2010). Prevalence and antibiotic susceptibility of *Listeria* spp. isolated from raw meat and retail foods. *Food Control*. 21: 708-713.
- Pombinho, R; Vieira, A; Camejo, A; Archambaud, C; Cossart, P; Sousa, S and Cabanes, D** (2020). Virulence gene repression promotes *Listeria monocytogenes* systemic infection. *Gut Microbes*. 11: 868-881.
- Ranjbar, R and Halaji, M** (2018). Epidemiology of *Listeria monocytogenes* prevalence in foods, animals and human origin from Iran: a systematic review and meta-analysis. *BMC Public Health*. 18: 1-12.
- Rippa, A; Bilei, S; Peruzzi, MF; Marrocco, MG; Leggeri, P; Bossù, T and Murru, N** (2024). Antimicrobial resistance of *Listeria monocytogenes* strains isolated in food and food-processing environments in Italy. *Antibiotics*. 13: 525.
- Saytekin, AM; Adiguzel, A; Alkilani, K; Yucetepe, AG and Keskin, O** (2025). Some virulence genes and biofilm formation capabilities of *Listeria monocytogenes* isolates from different sources. *Ankara Univ. Vet. Fak. Derg.*, 72: 35-45.
- Schiavano, GF; Guidi, F; Pomilio, F; Brandi, G; Salini, R; Amagliani, G; Centorotola, G; Palma, F; Felici, M and Lorenzetti, C** (2023). *Listeria monocytogenes* strains persisting in a meat processing plant in Central Italy: Use of whole genome sequencing and *in vitro* adhesion and invasion assays to decipher their virulence potential. *Microorganisms*. 11: 1659.
- Sharma, RK; Jalalpure, SS; Pathak, S; Ganapathy, S; Desvaux, M; Roy, S and Hegde, S** (2024). Molecular detection of *Listeria monocytogenes* from different dairy and street food sources in North Karnataka, India. *J. Infect. Public Health*. 17: 696-703.
- Shen, J; Zhang, G; Yang, J; Zhao, L; Jiang, Y; Guo, D; Wang, X; Zhi, S; Xu, X and Dong, Q** (2022). Prevalence, antibiotic resistance, and molecular epidemiology of

- Listeria monocytogenes* isolated from imported foods in China during 2018 to 2020. *Int. J. Food Microbiol.*, 382: 109916.
- Shonhiwa, AM; Ntshoe, G; Essel, V; Thomas, J and McCarthy, K** (2019). A review of foodborne diseases outbreaks reported to the outbreak response unit, national institute for communicable diseases, South Africa, 2013-2017. *Int. J. Infect. Dis.*, (Suppl 1), 79: 73.
- Silva, A; Silva, V; Gomes, JP; Coelho, A; Batista, R; Saraiva, C; Esteves, A; Martins, Â; Contente, D and Diaz-Formoso, L** (2024). *Listeria monocytogenes* from food products and food associated environments: Antimicrobial resistance, genetic clustering and biofilm insights. *Antibiotics*. 13: 447.
- Srinivasan, V; Nam, H; Nguyen, L; Tamilselvam, B; Murinda, S and Oliver, S** (2005). Prevalence of antimicrobial resistance genes in *Listeria monocytogenes* isolated from dairy farms. *Foodborne Pathog. Dis.*, 2: 201-211.
- Swetha, C; Porteen, K; Elango, A; Ronald, B; Senthil Kumar, T; Milton, A and Sureshkannan, S** (2021). Genetic diversity, virulence and distribution of antimicrobial resistance among *Listeria monocytogenes* isolated from milk, beef, and bovine farm environment. *Iran. J. Vet. Res.*, 22: 1-8.
- Tahoun, AB; Abou Elez, RM; Abdelfatah, EN; Elsohaby, I; El-Gedawy, AA and Elmoslemany, AM** (2017). *Listeria monocytogenes* in raw milk, milking equipment and dairy workers: Molecular characterization and antimicrobial resistance patterns. *J. Glob. Antimicrob. Resist.*, 10: 264-270.
- Travier, L and Lecuit, M** (2014). *Listeria monocytogenes* ActA: a new function for a 'classic' virulence factor. *Curr. Opin. Microbiol.*, 17: 53-60.
- Wieczorek, K; Dmowska, K and Osek, J** (2012). Characterization and antimicrobial resistance of *Listeria monocytogenes* isolated from retail beef meat in Poland. *Foodborne Pathog. Dis.*, 9: 681-685.
- Wiśniewski, P; Zakrzewski, AJ; Zadernowska, A and Chajęcka-Wierzchowska, W** (2022). Antimicrobial resistance and virulence characterization of *Listeria monocytogenes* strains isolated from food and food processing environments. *Pathogens*. 11: 1099.
- Yehia, HM; Elkhadragey, MF; Aljahani, AH and Alarjani, KM** (2020). Prevalence and antibiotic resistance of *Listeria monocytogenes* in camel meat. *Biosci. Rep.*, 40: BSR20201062.
- Yoshikawa, Y; Ochiai, Y; Mochizuki, M; Fujita, O; Takano, T; Hondo, R and Ueda, F** (2016). Genetic subtyping of *Listeria monocytogenes* via multiple-locus sequence typing using iap, sigB and actA. *J. Vet. Med. Sci.*, 78: 1831-1839.
- Zamuz, S; Munekata, PE; Dzuvoor, CK; Zhang, W; Sant'Ana, AS and Lorenzo, JM** (2021). The role of phenolic compounds against *Listeria monocytogenes* in food. A review. *Trends Food Sci. Technol.*, 110: 385-392.