



## Phenotypic and genotypic of *Listeria Monocytogenes* isolated from raw milk in Assiut governorate

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### **Abstract:**

*Listeria monocytogenes* (*L. monocytogenes*) is a deadly foodborne pathogen affecting populations, although most foodborne pathogens cause considerable illness but little fatality. Raw milk and uncooked dairy products are frequently associated with notable *Listeria* attacks. Microbial virulence traits are potential markers for discriminating the invasive and environmental *L. monocytogenes* variants. So, this study explored the bacteriological and molecular aspects of *L. monocytogenes* isolates, their virulence genes (*hlyA*, *inlB*, and *prfA*), and antimicrobial sensitivity in raw milk in Assiut, Egypt. One hundred raw milk samples (40 Cow, 20 markets, 40 Buffalo) were analyzed. *L. monocytogenes* was detected in only 11 (27.5 %), 8 (40 %) and 6 (15 %) of collected samples from cow, market and buffalo raw milk, respectively. These isolates carried the virulence *hlyA*, *InlB*, and *prfA* genes and were sensitive to Sulfamethoxazole trimethoprim (SXT) and Ciprofloxacin (CIP) followed by Chloramphenicol (C), less sensitivity to Gentamicin (CN), and resistant to Erythromycin (E) and Amoxicillin (AX).

**Keywords:** *L. monocytogenes*, raw milk, PCR, *hly A*, *Inl B* and *prf A* genes.

## INTRODUCTION:

*Listeria monocytogene* is a facultative intracellular foodborne pathogen. Its growing prominence in recent years is entirely due to the changes in food preparation and distribution occurring in the so-called "global village" in the last decades of the 20<sup>th</sup> century and the rising pervasiveness of host variables that raise the infection risk. It has virtually nothing associated with the changing pathogenicity of the organism (Walter and Schlech, 2000). *L. monocytogenes* from a large-scale variety of food categories is linked to outbreaks in people and other animals Listeriosis (Renato et al., 2015). Hilliard et al., (2018) and Şanlıbaba and Tezel, (2018) assigned that listeriosis induces serious clinical manifestations such as meningitis or septicemia in immune-compromised hosts including infants, organ transplant recipients, cancer and AIDS patients, and in pregnant women with the fatality rates of 20 – 30%. It is responsible for about 99 % of cases after consumption of contaminated food. Immunocompromised individuals constitute high-risk populations for infection, especially pregnant women, infants, and the elderly (EFSA ECDC, 2015). *L. monocytogenes* was isolated from meat, milk, and milk products around the world (Ikeh et al., 2010; Khan et al., 2013). From 100 to 1000 *L. monocytogenes*/g of food is sufficient to produce listeriosis in humans as assigned by most experts (Ooi and Lorber, 2005). Gray et al. (2006) reported that as just as capable of living in the environment as it is of infecting humans and producing listeriosis, *L. monocytogenes* may also have a saprophytic life cycle. Throughout the past few years, experimental studies have shown that contaminated food is a significant means of bacterial transmission to people (O'Connor et al., 2010). *Listeria* has been linked to contaminants in food-processing facilities due to its ability to persist for several

months or years (**Lianou and Sofos, 2007**), its ability to colonize abiotic surfaces (**Poimenidou et al., 2016b**), and its ability to survive under harsh conditions (**Poimenidou et al., 2016a**), expanding the risk to food safety. Additionally, it can lead to miscarriages and nervous disorders in economically significant livestock animals like sheep and cattle. This caused the animals to produce less milk and eventually die. Many foodborne pathogens and opportunistic bacteria reside in the skin and digestive tract of livestock animals, which makes them ideal homes for foodborne pathogens and opportunistic bacteria like *L. monocytogenes*, which can contaminate meat and milk products during slaughter and milking. These bacterial infections can also infiltrate a variety of different natural settings (**Krawczyk et al., 2021**).

According to **Theivagt et al. (2006)** and **Listeria 2022 from the US Centers for Disease Control and Prevention**, *L. monocytogenes* is a gram-positive, non-capsulated bacterium that phenotypically forms single, short chains. It is a rod-shaped, non-spore-forming, facultative anaerobic bacteria that is 0.5 mm wide and 1-1.5 mm long (**Vazquez-Boland et al., 2001; Vera et al., 2013**). Taxonomically, it is divided into six species: *Listeria monocytogenes*, *Listeria ivanovii*, *Listeria seeligeri*, *Listeria innocua*, *Listeria welshimeri*, and *Listeria grayi*. The only pathogenic *L. monocytogenes* are *L. ivanovii*. Genotypic identification of bacterial virulence genes or gene products is the basis for characterizing *L. monocytogenes*. Listeriolysin O (LLO), according to **Ward et al. (2010)**, is a marker needed for the intracellular survival of invasive bacteria in mammalian hosts. *L. monocytogenes* also generates the virulence proteins PI-PLC and PC-PLC, which are encoded by the *hly-A* gene.

Due to the large number of cases and the roughly 30% overall death rate of these outbreaks, milk intake may be the primary source of listeriosis, which is raising outstanding worry in the dairy sector (**Amagliani et al., 2004**). For the identification of *L. monocytogenes* from samples taken from food and the environment using traditional techniques, enrichment cultures followed by selective plating are needed (**Reissbrodt, 2004**). Numerous novel and quick detection techniques based on molecular and antibody technologies have substantial overlap with methods for selective culture enrichment (**Reissbrodt, 2004; Gasanov et al., 2005**). PCR has been utilized more frequently than the other fast detection techniques for the quick, accurate, and focused detection of foodborne pathogens (**Olsen et al., 1995**). The purpose of this study was to estimate the prevalence of *L. monocytogene* in raw milk using a confirmatory PCR test and a traditional culture approach and screening their antimicrobial sensitivity.

## **MATERIALS AND METHODS**

### **1. Sample collection**

One hundred raw milk samples were aseptically collected from random different sources in Assiut City including market (20), buffalo (40), and cow (40) milk. The samples were put in sterile plastic bags in ice box and transported as fast as possible to the laboratory.

### **2. Microbiological analysis for *Listeria*:**

Following the instructions of ISO 11290, *L. monocytogenes* was isolated and identified as described by **Becker et al. (2006)**.

### **2. 1. Preenrichment: (Fraser and Sperber, 1988)**

After spinning the samples, 25 mL were added to 225 mL of half Fraser broth (Merck) as an initial enrichment culture, and the mixture was then homogenized using a stomacher (Lab blender 400, Seward Medical, London, UK) and incubated for 24 h at 30 °C.

### **2. 2. Selective enrichment:**

As a second enrichment culture, the incubated Fraser broth (10 mL) was added to 0.1 mL of half Fraser broth and re-incubated under aerobic conditions 3 hours at 37 °C for 48 hours.

### **2. 3. Isolation and identification:**

On the agar plates ALOA®, Merck agar (Merck), and OXFORD agar, a loopful of enhanced Fraser broth culture (the tubes that exhibit a blackening) was applied for selective plating. At 37 °C, cultures were incubated for 24 hours. Three to five presumed colonies were re-streaked on tryptic soy agar with 0.6% yeast extract (Oxoid, Basingstoke, UK).

Bacteriological analytical manual identification was done according to FDA (Hitchins, 1995). Biochemical assays such as the catalase, oxidase, methyl-red, vogues Proskauer, and urease tests were used to confirm colonies and fermentation of the xylose, rhamnose, and mannitol sugars. First, hemolysis on blood agar and the CAMP test were used to confirm isolates. Initially recognized the chosen colonies as *Listeria* spp. and transferred them to Columbia Agar with 5% sheep blood (bioMérieux) in accordance with the manufacturer's instructions. The kind of hemolysis was then evaluated. Finally, the PCR technique was used.

#### 2.4. Molecular analysis of the isolated *L. monocytogenes* and their virulence

The isolated *L. monocytogenes* colonies were molecularly analyzed according to **Kaur et al. (2007)**, **Shah et al. (2009)**, **Daniela et al. (2023)** and **Kumar et al. (2015)**. Briefly, pure colonies were dispersed in phosphate-buffered saline (5 mL) and centrifuged (3000 rpm for 10 min. at 4°C). This step was repeated 3 times till obtaining pellet. Pellets were used for DNA extraction using the QIAamp DNA Mini kit (Qiagen, Germany, GmbH) with modifications from the manufacturer's instructions. The extracted DNA was used as a template and amplified by polymerase chain reaction (PCR) using *L. monocytogenes* species-specific primer sets (Metabion, Germany) for 16 rRNA gene [Forward: (GGACCGGGGCTAATACCGAATGATAA) and Reverse: (TTCATGTAGGCGAGTTGCAGCCTA)] and EmeraldAmp® Master mix (Takara, Japan) in Veriti thermocycler (Applied Biosystems, Germany) following **Kumar et al., (2015)** cycling conditions. Exactly, an initial 94°C hot start for 5 minutes, followed by 35 cycles of denaturation at 94°C for 30 sec, annealing at 60°C for 1 min, and extension at 72°C for 1 min. then a final extension at 72°C for 12 min. The amplified products (5µl) were loaded in 1.5 % agarose gel stained with ethidium bromide (AppliChem, Germany, GmbH), electrophoresed (5V/cm, at room temperature), visualized with UV light in comparison to 100-1.500bp DNA ladder (Qiagen, Germany, GmbH) and photo'd by a gel documentation system (Alpha Innotech, Biometra). An amplicon size of 1200 bp is specific to *L. monocytogenes*.

#### 2.5. Determining virulence of the isolated *L. monocytogenes*

The *L. monocytogenes* DNA was analyzed for the virulence genes; internalin hemolysin (*hlyA*), internalin B (*inlB*), and positive regulatory factor A (*prfA*) genes

by PCR techniques using gene-specific primer set (**Table 1**). The DNA was amplified with the primer set specific to each gene as described above (**part 2.6.**) following the cycling conditions described in **table 2**. The amplified products were screened as mentioned above.

**Table 1: Primers sets specific to the virulence genes intended for determining the virulence of the isolated *L. monocytogenes***

Primer	Sequence	Amplicon size	Reference
<i>hlyA</i>	F 5'GCATCTGCATTCAATAAAGA 3'	174 bp	Deneer and Boychuk (1991)
	R 5'TGTCAGTGCATCTCCGTGGT 3'		
<i>inlB</i>	F 5'CTGGAAAGTTTGTATTTGGGAAA3'	343 bp	Liu <i>et al.</i> (2007)
	R 5'TTTCATAATCGCCATCATCACT3'		
<i>prfA</i>	F 5'TCTCCGAGCAACCTCGGAACCTGG3'	1052 bp	Dickinson <i>et al.</i> (1995)
	R 5'ATTGACAAAATGGAACA3'		

**Table 2: The cycling conditions followed in the PCR for the different primers intended for determining the virulence of the isolated *L. monocytogenes***

Gene	Initial denaturation	Amplification (35 cycle)			Final extension
		denaturation	Annealing	Extension	
<i>hlyA</i>		94°C (30 sec.)	50°C(30sec.)	72°C(30 sec.)	72°C(7min.)
<i>inlB</i>	94°C (5 min.)	94°C (30 sec.)	55°C(40sec.)	72°C(40sec.)	72°C(10min.)
<i>prfA</i>		94°C (30 sec.)	50°C(50sec)	72°C(1min.)	72°C(10min.)

#### 2.4 *In vitro* anti-microbial sensitivity testing:

As recommended by the European Committee on Antimicrobial Susceptibility test (EUCAST), the disc agar diffusion technique was used to explore the sensitivity of the isolated *L. monocytogenes* strains against 8 antibiotics; Erythromycin (E), ceftriaxone (CRO), Gentamycin (CN), Clindamycin (DA), Amoxicillin (AX), Ciprofloxacin (CIP), Chloramphenicol (C) Sulfamethoxazole-trimethoprim (SXT) and Ciprofloxacin (CIP) (NCCIS, 1999). In reality, a suspension with 0.5 McFarland turbidity of about 5-6 fresh overnight *Listeria* colonies and 1 mL normal saline solution was prepared. The produced suspension was flooded over Mueller-Hinton

agar (HiMedia, India) plates, and the antibiotic discs were then applied using a disc dispenser. The plates were incubated at 37° C for 24 h, and then after zones of bacterial growth inhibition were measured to the nearest mm. Results were interpreted following EUCAST principles.

#### **4. Statistical analysis**

The mean values were dependent on describing results and these data were analyzed by applying the Chi-square test using SPSS 18.0 (SPSS Inc., Chicago, IL, USA) to determine the relationship between the true/false positive results and the food categories.

## RESULTS

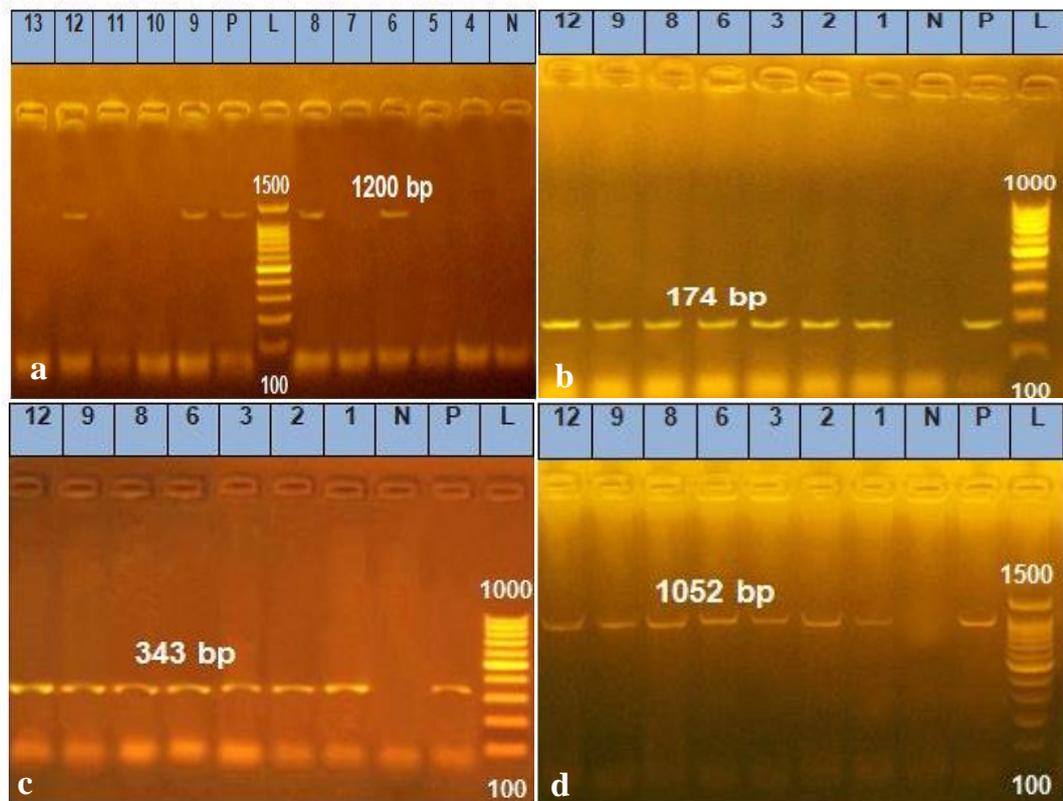
The results demonstrated in Table 3 showed the detection rate of *L. monocytogenes* in the examined Market, Buffalos, and cow milk samples in Assiut governorate. *L. monocytogenes* was detected in 8 out of 20 Markets, 6 out of 40 Buffalos, and 11 out of 40 cow raw milks with 40, 15, and 27 % detection rates, respectively.

**Table (3): *L. monocytogenes* percentage in the examined Market, Buffalos, and cow milk samples in Assiut governorate:**

Source	<i>L. monocytogenes</i> n/t (%)
Cow	11/40 (27.5)
Market	8/20 (40.00)
Buffalos	6/40 (15.00)
Total	25/100 (25.00)

### **Species identification within the tested isolates (PCR)**

Molecular characters of the recovered *L. monocytogene* isolates during the molecular analysis showed in **figure 1**. The isolates that positively reacted to biochemical reactions carried the *L. monocytogene* specific 16 rRNA gene and its virulence genes; *hylA*, *inlB*, and *prfA* genes.



**Fig. 1:** Agarose gel electrophoresis gel showing (a) 16 rRNA gene specific for *Listeria monocytogenes*, and its virulence genes (b) *hylA*, (c) *inlB*, and (d) *prfA* genes. Lane L:100-1000 bp DNA Ladder as a standard marker. N: Negative control. P: Positive control at 1200, 174, 343, and 1052 bp, respectively. Lanes 1-12: *L. monocytogenes* positive isolates.

### 3. Anti-microbial sensitivity of the isolated *L. monocytogenes*

In total, the detected *Listeria* isolates (25 isolates) were resistant to one or more of the tested antibiotics (table 4). They were sensitive to Sulfamethoxazole-trimethoprim (SXT) (25 µg /disc) and Ciprofloxacin (CIP) (10 mcg) followed by Chloramphenicol (C) (30 µg /disc), with weak sensitivity to Gentamicin (CN) (120 µg /disc). While they were resistant to Erythromycin (E) (15 µg /disc) and Amoxicillin (AX) (20 / 10 µg /disc)

**Table 4: *In-vitro* antimicrobial sensitivity test for isolated *L. monocytogenes*:**

Source	Anti-microbial								
	Sxt	CN	E	CRO-30	NV	D	AX	CIP	C
<b>Cow milk</b>									
<i>S</i> %	70	30	10	50	zero	20	zero	90	80
<i>R</i> %	20	40	90	10	90	40	100	0	10
<i>I</i> %	10	30	zero	40	10	40	zero	10	10
<b>Market milk</b>									
<i>S</i> %	83.3	16.7	00.0	33.3	00.0	33.3	00.0	83.3	00.0
<i>R</i> %	16.7	66.7	100.0	50	83.3	66.7	100.0	00.0	33.3
<i>I</i> %	00.0	16.7	00.0	16.7	16.7	00.0	00.0	16.7	66.7
<b>Buffalo milk</b>									
<i>S</i> %	100.0	33.3	00.0	33.3	00.0	66.7	00.0	66.7	33.3
<i>R</i> %	00.0	00.0	100.0	00.0	100.0	00.0	100.0	00.0	33.3
<i>I</i> %	00.0	66.7	00.0	66.7	00.0	33.3	00.0	33.3	33.3

*S*: sensitivity. *R*: Resistance. *I*: Intermediated

## DISCUSSION

**Adzitey et al. (2013)** and **Liao et al. (2021)** claimed that more than 200 diseases that are known to be dangerous to human health can spread through food. Among these food-borne bacteria, *L. monocytogenes* was discovered and has a major role due to its ability to flourish in refrigerator temperatures and high mortality rates (**Lida et al., 2014; Anonymous, 2021**). *L. monocytogenes* is an important pathogen in both human and veterinary medicine, inducing a number of illnesses in mammals, birds, and fish, as well as abortion and encephalitis in sheep and cattle (**Kalrey et al., 2008**).

According to **Lundèn et al. (2004)**, the consumption of ready-to-eat (RTE) food items is a key contributing factor to human listeriosis infections. The use of contaminated raw milk or post-processing contamination from environmental sources unrelated to raw milk can both lead to *L. monocytogenes* infection of fermented dairy products made from raw milk (**Kells and Gilmour, 2004**). Controlling *listeria* during

food processing is difficult because it is so prevalent in agricultural and food production areas (Sarfraz *et al.*, 2017). The expression of virulence factors and the immunological state of people determined the ability of *L. monocytogenes* to cause illness. The immunity mediated by cells of those who are most vulnerable to *L. monocytogenes* is typically compromised (Lecuit *et al.*, 2004).

The obtained data in this study revealed that *L. monocytogenes* was detected in 8, 6, and 11 in the cow, market, and buffalo raw milk respectively, samples out of 20, 40 and 40 samples respectively, 11 (27.5 %), 8 (40 %) and 6/40 (15.00) represented as in the market, buffalo, and cow raw milk that disagreed with that recorded by Zeinali *et al.*, (2017)

The virulence of *L. monocytogenes* was determined by the hemolytic activities of the isolated *Listeria* species (Maarouf *et al.*, 2007). Similar results were reported by Marrouf *et al.*, (2007) and Rahimi *et al.*, (2020), the result of virulence tests for isolated *listeria* showed that all *L. monocytogenes* were positive to CAMP test and showed narrow zone of  $\beta$ -hemolysis in sheep agar.

With dissimilar results to that reported by Cao *et al.*, (2018), the PCR results for *L. monocytogenes* isolated showed that 16rRNA, *hlyA*, *inlB*, and *perfA* genes were not detected in all isolates regarding the occurrence of 16rRNA genes in *L. monocytogenes* isolates, the obtained result revealed that, it was amplified in all tested isolates, that agreed with those recorded by Ciolacu *et al.*, (2015) and Abdelhamed *et al.*, (2022)

Disagreeing with Shen *et al.*, (2000), the PCR result for amplification of the internalin B (*inlB*) gene in *L. monocytogenes* showed that the *inlB* gene wasn't amplified in all tested isolates.

Similar to **Gelbicova and Karpiskova, (2012); Khan *et al.*, (2014); Ciolacu *et al.*, (2015) and Self *et al.*, (2019)**, the result of PCR for amplification of the listeriolysin O (hemolysin, hlyA) gene in *L. monocytogenes* showed that hlyA gene was amplified in all tested isolates giving the product of 174bp.

Dissimilar results with **(Gelbicova and Karpiskova, 2012 and Ciolacu *et al.*, 2015)** the result of PCR for amplification of the positive regulatory factor gene (*prfA*) in *L. monocytogenes* showed that the *prfA* gene wasn't amplified in all tested isolates.

In the present study, it is postulated that the detection rate of *L. monocytogenes* using the conventional method was 7.5 % in raw milk samples, almost similar results were studied by **Aygun and pehlivanlar, (2006)** who reported *L. monocytogenes* in 5% of raw milk samples, while, **(Kasalica and Oljačić 2007)** showed that in 30 samples of raw milk (sheep, goat and cow milk) the presence of *L. monocytogenes* was not established and **(Mohamed, 2010)** reported that listeria monocytogenes was present in 1.7 and 3.3 % in raw milk samples in farm A and b. also, **(Jami *et al.*, 2010)** found listeria monocytogenes in 4% of raw milk samples, cow milk is mentioned as carrier of the fatal listeriosis **(Farber and Peterkin, 1991; Sepahvand *et al.*, (2022).**

Sick animals on the farm were represented the most common way for transmission of *L. monocytogenes* to raw milk mainly, and healthy animals acted as a carriers of *listeria. monocytogenes* and source of contamination of the surrounded area, or milk. The poor quality of prepared silage was the main source of contamination of animals by these bacteria. *Listeria* was isolated in 1.2-60% samples as a result of poor quality of prepared silage (pH > 5-5.6) according to some literature

data (Vilar *et al.*, 2007). *Listeria* spp. was isolated in 2-6.1% samples of milk collected from cows fed silage (Vilar *et al.*, 2007) Brown, et al., (2021).

The presence of *L. monocytogenes* in food that reported by many researchers obtained in developed countries (Melanie and Siegfried, 2001; Karakolev, 2009). In Europe the incidence of *L. monocytogenes* that was recorded by microbiological studies has shown that 2.5 - 6 % of samples of raw milk can be contaminated with *L. monocytogenes*, these results come parallel with those recorded by their article according that there was a potential risk for the human population from dairy products manufactured from raw milk that reported by Donnelly, (2004).

The identification of several molecular virulence determinants plays an important role in cellular infection by *L. monocytogenes* and the detection of their mechanism of action which was made by *L. monocytogenes* acts as one of the most exciting models of host–pathogen interaction at the cellular and molecular levels that reported by Cabanes *et al.*, (2005), Cossart and Toledo-Arana, (2008), Shourav, *et al.*, (2020) and Sleator *et al.*, (2005). The most virulence determinants include *ActA* protein, two phospholipases, a metalloprotease, the internalin's, listeriolysin O (LLO), *Vip* protein, a bile exclusion system (BilE), and a bile salt hydrolase. Many articles have been found that a more sensitive and rapid technique for confirmation of the identification of suspect *L. monocytogenes* isolated on selective/differential agar plates was Polymerase chain reaction (PCR) which targeting the *hly* gene (Gouws and Liedemann, 2005) Dharshini. and Meera (2023)

The encountered *L. monocytogenes* isolates were sensitive to Sulfamethoxazole-trimethoprim (SXT) and Ciprofloxacin (CIP) followed by Chloramphenicol (C), with weak sensitivity to Gentamicin (CN). While they were

resistant to Erythromycin (E) and Amoxicillin (AX) recorded in-vitro antimicrobial sensitivity test, and these results came in accordance with those recorded by **Cabanes et al., (2005)** and disagreed with **Altuntas et al. (2012)** **Jibo. et al. (2022)**

### **Conclusion**

The research presented here ultimately leads to the conclusion that *L. monocytogenes* mainly serves as a food-borne pathogen that can spread through raw milk and cause listeriosis. The isolated *L.monocytogenes* were sensitive to Sulfamethoxazole-trimthoprim (SXT) and Ciprofloxacin (CIP) followed by Chloramphenicol ( C ), less sensitivity to Gentamicin (CN ). On other hand, the isolates were resistant to Erythromycin(E)and Amoxicillin (AX).

The isolated *L.monocytogenes* were CAMP Positive and produced  $\beta$ -zone of heamolysis. In PCR result assured that strains are *listeria monocytogenes* and have hlyA, inlB and prfA virulence genes genes.

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