ISOLATION AND IDENTIFICATION OF ZOONOTIC IMPORTANCE BACTERIA FROM MILK, MILK PRODUCTS AND HUMAN IN DIYALA, IRAQ

Rofeida Muhammad Hussein and AL-Khafaji Nazar Jabbar
Department of Medicine, College of Veterinary Medicine, University of Diyala, Iraq.

Abstract
To study bacteria of zoonotic importance, contaminated milk and milk products, a total 186 samples; represent 76 samples raw milk; 35 milk products, in addition to 75 swabs from workers in shops of milk products, were collected, from August, 2019 to April, 2020. The samples were submitted to laboratory examinations, for isolations and identifications. The results showed, that from 186 samples: 26 (13.98%) were free from bacteria, while from others, 160 samples (86.02%), 288 isolates were isolated, either in single form, 75 (40.3%) or mixed in two isolates in a sample 47 (25.3%), or there 33 (17.7%), or four 5 (2.7%) in a sample. The highest numbers of isolates was Staph.58/288 (20.1%); Sal 39/288 (13.5%); Lact.35/288 (12.2%); E. coli 30/288 (10.4%); Pseud. 30/288 (10.4%); Kleb. 29/288 (10.1%); Ent. 24/288 (8.3%); Prot.17/288 (5.9%); Cit.17/288 (5.9%); Strept. 5/288 (1.7%); List 4/288 (1.4%). From a total 76 samples of raw milk from udder and bulk tank from cow, buffalo, sheep and goat. 142 isolates were isolated: from which Sal. sp. 27/142 (19.0%); Staph. sp. 24/142(16.8%); Lact. 22/142 (15.5%); Ent. sp. 17/142 (12.0%); E. coli 15/142 (10.6%); Cit. sp. and Prot. sp., each 12/142 (8.5%); Kleb.8/142 (5.6%) and Pseud. sp., 5/142(3.5%). While from a total 35 samples of milk products (Cheese and Yoghurt), 62 isolates were isolated: Lactobacillus 14/62 (22.6%); Salmonella 12/62 (19.4%); E. coli., 10/62 (16.1%); Staph. 7/62 (11.3%); Pseudomonas 6/62 (9.7%); Proteus 5/62 (8.1%); Klebsiella 4/62 (6.5%); Enterobacter 3/62 (4.8%); Citrobacter 1/62 (1.6%).The highest isolates were from raw milk 141/186 (75.8%) then, workers 85/186 (45.7%), and milk products 62/186 (33.3%).

Key words: isolation; identification, zoonotic agents; milk, milk products

Introduction
Milk may serve as an ideal substrate for the growth and survival of an array of bacteria and fungi, thereby leading to the public health threat (Zucali et al., 2019). Milk in healthy udder cells is considered sterile, but thereafter contamination can originate from different sources, as teat apex, milking utensils, feed, grass, soil, surrounding air, feces, water or moisture content, and other environments (Verdier-Metz et al., 2012; Vacheyrou, et al., 2011). The aims of study were isolate the most common zoonotic pathogens from milk and milk products from, cow, buffalo, sheep and goats. Furthermore, identify these isolates.

Materials and Methods
All culture media, were prepared according to instruction of Manufactures Corporation and sterilization were, according to (Quinn et al., 2004).

Samples
The study was conducted in Department of Medicine, College of Veterinary Medicine, University of Diyala, Iraq, from August, 2019 - April, 2020.

Collection of raw milk samples
A total 186 samples, represent; (76) raw milk, from cow, buffalo, sheep and goat, collected either from udder or from bulk tanks; (35) cheese and yoghurt samples were purchased from shop, sales shops, in addition to (75) swabs obtained from workers and their equipment, utilized in shops or in preparation and transportation of milk and milk products in Diyala Province. Collected aseptically in clean, dry and sterile tubes, in a cool places, bring to laboratory, within 24 h. and examined upon arrival to the laboratory, for bacteriological analysis as described by (Fawole MO, Oso BA. Laboratory manual of Microbiology, 2001; Islam et al., 2016).

Bacterial examination
Initially, 25ml of each raw milk sample dispensed into a sterile flask containing 225 ml of 0.1% peptone water and mixed thoroughly. Subsequent serial decimal dilutions of each sample were prepared in 0.1% peptone water according to (APHA, 2001).

**Swabs culturing**

The swabs were submitted to culture by inoculation into nutrient broth and incubated at 37°C for 5 hr. Loop full from the incubated broth was distributed onto surface of MacConkey agar then incubated at 37°C for 24 hr. according to (Stromberg, 2015).

**Characterization and identification of the colony**

Characterization and identification of the colony isolates was achieved by initial, morphological examination of the colonies on plate. Gram staining and the biochemical tests, with standard reference organisms with those of known taxa, as described by Bergey’s manual for determinative Bacteriology(Syed et al., 2014; Bharathy et al., 2015).

**Results**

**Workers**

From a total 75 swabs, 85 isolates were isolated. Staph., 27/85 (31.7%); Pseud. 19/85 (22.4%); Kleb.17/85 (20.0%); *E. coli* and Strept each 5/85 (5.9%); List., Ent. and Cit. each 4/85(4.7%) table 1.

**Cow**

Total 45 samples obtained from cow, from which 81 isolates were isolated: Staph.15/81 (18.5%); Sal.13/81 (16.0%); Lact.12/81 (14.8%); Ent. 10/81 (12.3%); *E. coli* 9/81 (11.1%); Prot., 8/81 (9.9%); Citro. 6/81(7.4%); Kl. 5/81 (6.3%); Pseud.3/81 (3.7%) table 1.

**Buffalo**

A total of 15 raw milk obtained from buffalo from udder and bulk tank, from which, 30 isolates were isolated.

Sal. 6/30 (20.0%); Staph. and *E. coli*, 5/30 (16.6%); Lact. and Ent. each 3/30 (10.0%); Kleb.; Pseud.; Prot. and Citro. each 2/30 (6.7%) table 1.

**Goat**

From 6 raw milk samples obtained from goat, 13 isolates were isolated: Sal. 4/13 (30.7%); Staph. sp. 2/13 (15.4%); Prot. 1/13 (7.7%); Citro. sp. and Pseud. sp., each 1/13 (7.7%) table 1.

**Milk products:** Cheese

A total 25 samples of cheese local and kala were collected from which, 48 isolates were isolated. Sal. and Lact. 9/48 (18.8%); *E. coli*, 8/48 (16.7%) ; Pseud. 6/48 (12.5%); Staph. sp. 5/48 (10.4%); KL. and Prot. 4/48 (8.3%); Ent. 2/48 (4.2%); Cit. 1/48 (2.1%) table 1.

From 10 samples of Yoghurt; Sulaimania, Kanoon, 14 isolates were isolated 14: Lact 5/14 (35.7%) ; Sal 3/14 (21.4%); Staph. and *E. coli* 2/14 (14.3%); Ent. and Prot. 1/14 (7.1%) table 1.

From a total 35 samples of milk products, 62 isolates were collected from which, 48 were isolated. Sal. and Lact. 9/48 (18.8%); *E. coli*, 8/48 (16.7%) ; Pseud. 6/48 (12.5%); Staph. sp. 5/48 (10.4%); KL. and Prot. 4/48 (8.3%); Ent. 2/48 (4.2%); Cit. 1/48 (2.1%) table 1.

From a total 186 samples; represent 76 samples raw milk; 35 milk products and 75 swabs from workers in

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Work.</td>
<td>75</td>
<td>17</td>
<td>19</td>
<td>27</td>
<td>5</td>
<td>0</td>
<td>0</td>
<td>4</td>
<td>4</td>
<td>0</td>
<td>5</td>
<td>4</td>
<td>85</td>
</tr>
<tr>
<td>Cow teat</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>8</td>
</tr>
<tr>
<td>udder</td>
<td>30</td>
<td>4</td>
<td>1</td>
<td>10</td>
<td>6</td>
<td>8</td>
<td>10</td>
<td>4</td>
<td>7</td>
<td>5</td>
<td>0</td>
<td>0</td>
<td>55</td>
</tr>
<tr>
<td>Tank</td>
<td>11</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>18</td>
</tr>
<tr>
<td>Buff. Udder</td>
<td>10</td>
<td>1</td>
<td>1</td>
<td>4</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>18</td>
</tr>
<tr>
<td>Tank</td>
<td>5</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>13</td>
</tr>
<tr>
<td>Sheep</td>
<td>10</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>4</td>
<td>4</td>
<td>2</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>17</td>
</tr>
<tr>
<td>Goat</td>
<td>6</td>
<td>0</td>
<td>0</td>
<td>3</td>
<td>0</td>
<td>4</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>13</td>
</tr>
<tr>
<td>Cheese</td>
<td>25</td>
<td>4</td>
<td>6</td>
<td>5</td>
<td>8</td>
<td>9</td>
<td>9</td>
<td>1</td>
<td>2</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>48</td>
</tr>
<tr>
<td>Yoghurt</td>
<td>10</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>2</td>
<td>3</td>
<td>5</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>14</td>
</tr>
<tr>
<td>Total</td>
<td>186</td>
<td>29</td>
<td>30</td>
<td>58</td>
<td>30</td>
<td>39</td>
<td>35</td>
<td>17</td>
<td>24</td>
<td>17</td>
<td>5</td>
<td>4</td>
<td>288</td>
</tr>
</tbody>
</table>

Table 1: Total numbers of isolates in current study.
shops of milk products: 288 isolates were isolated. The highest numbers of isolates was Staph.58/288 (20.1%); Sal 39/288 (13.5%); Lact.35/288 (12.2%); E. coli 30/288 (10.4%); Pseud. 30/288 (10.4%); Kleb. 29/288 (10.1%); Ent. 24/288 (8.3%); Prot.17/288 (5.9%); Cit.17/288 (5.9%); Strept. 5/288 (1.7%); List 4/288 (1.4%) table 1.

Total numbers of samples in current study were 186. From which, 26 (13.98%) were free from bacteria, while from others, 160 samples (86.02%), a total of 288 isolates were isolated; from which 75 (26.0%) as single isolate, other as mixed with one or more isolates: in two isolates (47) :47×2 = 94 (32.6%); or there isolates, 33 (33×3) = 99 (34.5%); or four isolates 5 (4×5) = 20 (6.9%).

**Discussion**

In current study from 186 total samples, 26 (13.98%) did not yield isolates, while 160 (86.02%) yield isolates: 288 isolates were isolated. Among these isolates the Staphylococcus sp. was the most prevalent 58/288 (20.1%); followed by Sal 39/288 (13.5%); then Lact. 35/288 (12.2%); E. coli 30/288 (10.4%); Kleb. 29/288 (10.1%); Enterobacter 24/288 (8.3%); Proteus 17/288 (5.9%); Citrobacter 17/288 (5.9%); Streptococcus 5/288 (1.7%); List 4/288 (1.4%).

From 190 samples, 52 (27.37%) did not yield any isolates. Microorganisms were isolated from 138 samples. Among these, *Staphylococcus aureus* was with 52 (27.37%), followed by coagulase negative *Staphylococcus* spp. 24 (12.63%), *E. coli* 17(8.95%), *Pseudomonas* spp. 15 (7.89%), *Streptococcus* spp. 11(5.79%), mixed bacterial infection 9 (4.74%). *Klebsiella* spp. 3(1.57%) and Bacillus spp. 1(0.52%) isolates (Mohini et al., 2002; Grewal et al., 2005).

**Workers and equipment**

In current study, from 75 swabs obtained from worker, only four of them did not yield isolates. While from others 71 samples, 85 isolates were isolated either in single form, [Staph. 19, Cit. 3, Pseud.13, Kleb.13, Strept. 5, List.1, Ent. 2, E. coli 1], or in two isolates in a sample (14). The highest numbers of isolates was Staph 27/85 (31.7%); followed by Pseud 19/85 (22.4%); then Kleb.17/85 (20.0%); E. coli. and Strept each 5/85 (5.9%); List., Ent. and Cit. each 4/85(4.7%).

The milk can be contaminated directly by farm machinery and storage facilities. The microflora of the bacteria in the machinery varies greatly (Michel et al., 2006). Poor quality of milk, the use of unclean milking and transport equipment, poor hygienic quality, unhygienic conditions of manufacturing units, machinery, farm staff, unclean hands of workers, inferior quality of material used and water supplied for washing the utensils, the environment including bedding, air, grass, collection vessels, could be the source of accelerating the bacterial contamination of milk product and the post manufacturing contamination [Verdier-Metz et al., 2009; Quigley et al., 2013].

In current study 4 swabs were obtained from external surface of teat in cows, all were positive to bacterial contamination. 8 isolates were isolated, two isolates in each sample; Staph. and Sal. each of 2/8(25.0%), Enterobacter, Citrobacter and Proteus each 1/8 (12.5%).

Initial microbial colonization of raw milk comes from the teat surface, as the organisms present in unclean teats. These have been demonstrated to harbor a diversity of species, including members of the phyla Firmicutes, Actinobacteria, Proteobacteria and Bacteroides. [Verdier-Metz et al., 2012; Braem et al., 2012; Monaller et al., 2012]. The teat microbiota was shown to vary greatly, from cow to cow, and farm to farm, due to the manner in which it was acquired from, bedding, machinery, farm staff during milking and the environment [Verdier-Metz et al., 2012; Braem et al., 2013]. Braem et al., 2013, identified coagulase-negative Staphylococci as the dominant residents.

In current study, from 6 raw milk samples obtained from goat, 13 isolates were isolated, one in single form [Staph. 1], other in mixed, three isolates in a sample (4): The highest one is Sal. 4/13 (30.7%); Staph. 3/13 (23.1%); Citro. and Lact. each 2/13 (15.4%); Prot. and Ent. each 1/13 (7.7%).

In current study, from 10 raw milk samples obtained from sheep, two were free from contamination and 17 isolates were isolated from other samples, either in a single form (2) [Ent. 1; Sal.; 1], or in mixed forms, two isolates in a sample (4), three isolates (1): Sal. and Lact. each 4/17 (23.5%); Ent. 3/17 (17.6%); Cit. 2/17 (11.8%); Kleb.; Staph.; E. coli and Prot. each 1/17 (5.9%).

The predominant isolated coliform strains in the examined raw goat’s and ewe’s milk samples were *E. coli*, *Citrobacter amalonaticus*, *C. freundii*, *Escherichia adecarboxylata*, *Enterobacter aerogenes*, *Ent. agglomerans*, *Ent. cloacae*, *Ent. gergoviae*, *Klebsiella ozaenae*, *K. pneumonia* sub spp. *ozaaenae*, *K. pneumonia* sub spp. *pneumoniae* and *Hafnia alvei* at percentages varied between 0 to 17.14. The incidence of coliforms was 68.57% and 60% for raw goat’s and ewe’s milk respectively (Ombarak and Elbagory, 2017). Comparatively lower counts of coliforms were recorded by (Salem, 2003) for raw goat’s milk and
of the milk samples positive for *S. aureus* while studying 66 samples in Turkey. In Morocco, Bendahou et al., (2008) studied 27 samples and found 40% of the milk samples were containing *S. aureus*; while in India, 61.7% of the raw milk samples were found positive out of 60 samples studied (Lingathurai and Vellathurai, 2010).

Prevalence rate from Morocco, Palestine and Bangladesh reported by Bendahou et al., 2008, Farhan and Salk (2007) and Jahan et al., (2014) as (40%), 36.9%, and 25.53% respectively, which were higher to Patel et al., (2018) study. However, similar prevalence has been previously reported by Fagundes et al., (2010). From Sao Paulo State, Brazil, The ratio was (10.8%) by Ayano et al., (2013). (13.8%) from Holeta, Ethiopias. From all these study results of above mentioned indicates prevalence of *S. aureus* is varied from place to place and regions to regions around the world and it highlights that hygienic practice of milking and selling influence the prevalence of *S. aureus* in milk.

Thaker et al., (2013) showed that out of total 160 samples, (100) milk and (60) milk products *i.e.* curd (30), and pedha (30). *S. aureus* was isolated in 10 isolates from 160 samples (6.25%); as 6 (6.00%), of 100 milk samples, 3 (10.0%) from 30 pedha and 1 (3.33%) from 30 curd samples. Fagundes et al., (2010) recorded (7.3%) and Kumar and Prasad (2010) (6.6%).

Higher level of incidence of *S. aureus* have been reported by Singh and Prakash, (2008); Ekici et al., (2004); Santana et al., (2010); Zakary et al., (2010) and Lingathurai and Vellathurai (2010), who found 17.39%, 18.18%, 18.80%, 40% and 61.7% incidence respectively.

The finding of Thaker et al., (2013) study are in accordance with the findings; Ekici, et al., (2004); (9.5 %) Normanno et al., (2007) (12.8%); Singh and Prakash (2008) (10.34%); Kumar and Prasad, 2010 (6.6%) and Addis et al., (2011), (10%).

A total of 47 raw milk samples were tested and *S. aureus* was isolated from 12 (25.53%) samples (Jahan et al., 2015). The prevalence of *S. aureus* in raw milk and dairy product was found to be 56% in Turkey by Gundogun and Avei (2014) which were significantly higher than study of Jahan et al., (2015).

Jahan et al., (2015) from raw milk samples from dairy cattle. 12 samples were positive for *S. aureus* (25.53% (12/47). Zafolon et al., (2008) studied at Nova Odesa, Sao Paulo; showed that the prevalence of *S. aureus* was 54.4% . the results of Jahan et al., (2015) are higher when compared to those of (Shitandi and Sternesjo, 2004; Gundogun et al., 2006).
The high incidence of *S. aurus* is indicative of poor hygienic measures during production, handling and distribution, stated in the findings of Zakary *et al.*, (2011).

*Salmonella* sp. occupied the second position, post Staph. in current study (39/186 (21.0%), from raw milk 27/76 (35.5%), from milk product 12/35 (34.3%).

*Salmonella* spp. has been detected in raw sheep milk (Fotou *et al.*, 2011). However, this pathogen is one of the main microbiological hazards in raw cow milk (Claeys *et al.*, 2013).

In current study, Pseudomonas occupied the eighth position, 30/186 (16.13%), from raw milk 5/76 (6.6%); from milk product 6/35 (17.1%); from workers 19/75 (25.33%).

In current study, Listeria sp. was last position 4 out of 186 total samples in study, (2.15%), as it isolated from workers and equipment only 4/75 (5.33%).

In Asmaa *et al.*, (2017) milking equipment had the highest isolation rate of *Listeria* spp., followed by raw milk and hands swabs. There was no significant difference between *Listeria* spp. isolation rates between the three sources.

*Listeria monocytogenes* is ranked as the third major pathogen that is transmitted by food (Scallan *et al.*, 2012) and its occurrence in milk and dairy products has a negative impact on dairy industry and public health (Usman *et al.*, 2016).

The occurrence of *Listeria* spp. isolated from raw milk concurred with findings, 26% in Colombia (Vanegas *et al.*, 2009) and 23% in Iran (Rahimi *et al.*, 2010). A higher isolation rate of *Listeria* spp. in Asmaa *et al.*, (2017) study compared to previous studies in Egypt and other countries has been observed (Ismiel *et al.*, 2014 and Jamali *et al.*, 2013) and lower incidence (53%) than recently reported in Nigeria by Usman *et al.*, (2016). On the other hand, previous studies reported the occurrence of *Listeria* spp. in 1.5% of tested milking equipment [59]. Isolated from milking equipment and hand swabs in Asmaa *et al.*, (2017) study. It is known that the main sources of *Listeria* spp. contamination in dairy farms are infected animals, poor silage quality, and environment (Pantoja *et al.*, 2012). The infected animals and insufficient hygienic measures during milking and milk storage are likely the most common sources of *Listeria* spp. contamination. (Asmaa *et al.*, 2017).

El Marnissi *et al.*, (2013) exhibited 5.90% as an overall prevalence of *L. monocytogenes* in raw milk. Boubendir *et al.*, (2016) observed a comparable occurrence in bovine raw milk from the Northern Eastern Algaria, Jami *et al.*, (2011) reported a lower contamination rate for milk samples in Mashhad, Iran.

It has been shown that lactic acid bacteria (LAB) are the predominant microorganism in most fermented foods (Gulitz *et al.*, 2013; Guetouache *et al.*, 2015). They ferment lactose to lactate and are the dominant population in bovine, goat, sheep and buffalo milk prior to pasteurization. Raw milk contains about 30% of undesirable micro-organisms in total microbial count, therefore, this problem suggests inflexible hygienic measures must be followed in cheese making (Mekhamsew *et al.*, 2012; Pazakova *et al.*, 2001).

In current study, from 25 samples of cheese, only 4 were free from contamination and 48 isolates were isolated, either in single form 4 [Psed.1, *E. coli*, 2, Lact.1], or in two isolates 8, three isolates 8, or 4 isolates 1. The highest number was, Sal. and Lact. Each (36.0%), followed by *E. coli* (32.0%), Pseud. (24.0%), Staph. (20.0%), Kleb. and Prot. each (16.0%), Cit. (4.0%). While from 10 samples of Yoghurt, submitted for examination, 14 isolates were isolated, 5 in single form, [Staph. 1, Sal. 1, lact. 3], other in mixed forms, three isolates (3) in a sample. The highest one was Lact. (50.0%), Sal. (30.0%), Staph. and *E. coli* each (20.0%), Ent. and Prot. each (10.0%).

Cremonesi *et al.*, (2007) tested 33 samples of raw milk cheese and found all the samples were positive for *Staphylococcus aureus* contamination. *E. coli* was isolated from 76 samples out of 77 random samples, and 19.48% of isolates were belonged to EPEC serogroup in Kerman, Iran (Mekhamsew *et al.*, 2012; Pazakova *et al.*, 2001).

Coliform bacteria, *Escherichia coli*, *Staphylococcus aureus* and mold-yeast counts were detected in some dairy products in Kirklareli, Turkey (Çetin *et al.*, 2015).

The final microbiota of raw milk cheese varies depending on the type of cheese and ripening process used, as well as the location within the cheese that is sampled (Montel *et al.*, 2014; Irlinger *et al.*, 2015).

Microbiota of raw milk cheese comes not only from the raw milk, but also from added starters and the environment (Gatti *et al.*, 2014; Neviani *et al.*, 2013).

Traditional cheese making processes often involve the use of a wooden surface, either in the form of a storage vat or a ripening shelf. Wood is a natural reservoir for microbes and hence transfers this microbiota to the cheese (Settanni *et al.*, 2012). LAB species abundance and diversity increases after exposure to wooden vats (Licitra *et al.*, 2007; Lortal *et al.*, 2009), while ripening on wooden shelves leads to transference of coryneform...
bacteria, moulds, and yeasts (Mariani et al., 2007).

Despite improvements in dairy processing, domestic soft cheeses are still very popular. This type of cheese is usually made from raw milk with insufficient hygienic quality in rural regions. Hence, raw milk can be primarily considered the main source of microbial contamination (García and Díaz, 2011). In addition, worker’s hand, packaging, transportation and marketing can be the secondary cause in poor conditions of the soft cheese. Also, non-hygienic water rather than tap water mostly used in the cleaning of the utensils used in cheese making as well as general daily uses Hill et al., 2012; Uyttendaele et al., 2015.

Temelli et al., (2006) investigated the possible sources of the cheese contamination and found that starter culture was a possible contamination source for coagulase positive staphylococci, enterococci and psychrophilic bacteria, while floor and packaging material were as the contamination source of psychrophilic bacteria. Although soft cheese is a nutritious food, it may act as a good means for pathogenic microorganisms (Araújo et al., 2002). E. coli was isolated from milk products like Mawa, Khoa, Cream, Dahi, Cheese, Butter, Gulabjamum (Vernoz- Rozand et al., 2005).

The prevalence of E. coli in Ras cheese was 21.7%, while that of raw milk and Karish cheese was 76.4 and 74.5% respectively, out of 187 dairy products including raw milk samples, 55 Karish cheese and 60 Ras cheese, 222 E. coli isolates including 111; 89 and 22 were obtained from 55 raw milk samples (76.4%), 41 Karish cheese (74.5%) and 13 Ras cheese (21.7%) respectively. The higher E. coli contamination rate of Karish cheese, compared to Ras cheese, may be due to the differences in cheese making process and the characteristics of final product between these two cheese (Ombarak et al., 2016).

Higher prevalence of E. coli in cheese has been reported from Brazil (96 to 97.7%) Araújo et al., 2002; Araújo et al., 2002; Zimbabwe (66.6%) (Gran et al., 2003); South Africa (23.3%) (Lues et al., 2003); India (31.6 to 57%) (Nanu et al., 2007; Singh and Prakash, 2008).

Listeria monocytogenes has been found in a high percentage of hard cheese made from raw or low heat treated sheep milk in EU countries, including Italy (Ministry of Work, Health and Social Policies, (EFSA, 2015).

References


