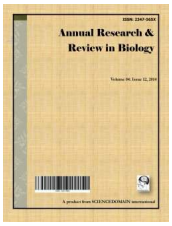

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Microbial Evaluation of Milk and Milk Products during a Past Two Decades, in Basrah Southern Iraq: A Review

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Authors' contributions

This work was carried out in collaboration between all authors. Author BAA designed the study, performed the statistical analysis wrote the protocol and the first draft of the manuscript. Author MKG collect the data of the study. Author AMA managed the literature searches and arrange tables and graphs. All authors read and approved the final manuscript.

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Review Article

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ABSTRACT

During the past decades, many researches have investigated the microbiological quality of milk and milk products. Milk was found to be contaminated with several types of bacteria. Most of these bacteria have been found to show different antibiotic resistance patterns against several known antibiotics. Different characterization methods such as conventional biochemical tests and DNA-based methods have been applied. Therefore, the aim of this study was to review the recent studies about the microbiological quality of milk and milk products.

Keywords: Basrah; milk; cheese; antibiotics; genes.

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1. INTRODUCTION

Milk is one of the most important foods for human beings. It is universally recognized as a complete diet due to its essential components [1]. Milk available is lower in food value due to high prevalence of mastitis in dairy animals [2]. Milk also serves as a good medium for growth of many microorganisms. Thus, the quality of milk is considered essential to the health and welfare of a community. Illnesses due to the consumption of milk occur because of the bacterial pathogens such as *Salmonella* sp., *Listeria monocytogenes, Staphylococcus aureus*, *Campylobacter sp., Yersinia sp.* [3,4].

Milk is contaminated by the organisms found on the exterior surfaces of the animal and the surfaces of milk handling equipment such as milking machines, pipeline, and containers resulting in infections and threating to consumer's health by the illnesses such as tuberculosis, brucellosis, typhoid fever, and listeriosis [5,6]. The investigation demonstrates that dairy cattle are a reservoir of *E. coil* 0157:H7 and other Shiga-like-toxin-producing *E. coli* [7]. Milk of buffaloes constituting an important source of market milk has some different characteristics. The fat content in this milk can exceptionally be as high as 15% and the overall average may be 7%. Most of these organisms are free living, widely distributed in soil, feeds, cows, buffaloes, goats, dairy utensils etc. Contamination usually occurs at the farm where milk is produced. *Escherichia coli* and coliform bacteria can enter milk and milk products very easily and their presence in the milk is an indication of contamination of milk. The presence of *E. coli* is the indicator of fecal contamination as well as it indicates the presence of toxigenic or enteropathogenic bacteria which are the major public health hazard [8-10]. Enteropathogenic *E. coli* can cause severe diarrhea and vomiting in infants and young children [11]. Methicillin–resistant *S. aureus* (MRSA) has become an important acquired pathogen in hospitals and also livestock (LA-MRSA) in recent years. MRSA associated with (LA-MRSA) have been reported worldwide in many species [12-14]. MRSA produces a low affinity penicillin binding protein (PBP2 or PBP2a) in addition to the usual PBPs [15]. Furthermore, MRSA strains are resistant to gentamicin, kanamycin, tobramycin, tetracycline and fluoroquinolones. Thus, multiple resistance of *S. aureus* strains occurs [16-18]. The objective of the study was to review more than 30 papers and thesis that studied microbiological quality of milk or milk products in Basrah province. These studies have used conventional biochemical tests and different molecular techniques for the identification organisms isolated from different sample types and determined the antibiotic susceptibility patterns.

2. ANIMAL ORIGIN

Different animals have been studied for collecting samples. These include cows followed by buffaloes, sheep goat and camel. This may be because of the availability of these animals. In addition, the milk of cows and buffaloes was traditionally used in Iraq. Camel milk has less attention during the mentioned period because its use is limited in the desert area. Many milk samples have been taken from market without specification of animals. Raw milk has a good chance of investigation since it is easy to collect and handle for laboratory analysis. In some cases, unpasteurized milk is used for the production of local cream and cheese (Table 1).

3. MICROFLORA AND DAIRY SAMPLES

As seen in Table 2, *E. coli* and *S. aureus* are the most prevalent organisms in this area. In addition, *Salmonella, Brucella, L. monocytogenes* have been isolated from these samples. The highest percentage, which refer to number of positive sample for isolation of microbes upon number of total collected samples, were found 62.66% for *E coli* and 53% for *S. aureus.*

4. ANTIMICROBIAL SUSCEPTIBILITY

Most of the studies have determined the antibiotic susceptibility patterns of isolated microorganisms (Table 3). They showed resistance to one or more antibiotics. Common used antibiotics such as tetracycline, cloxacillin, erythromycin, ampicillin, chloramphenicol, gentamycin and vancomycin were extensively used during the studies.

5. STUDIED GENES AND VIRULENCE FACTORS

Since 2012, many studies investigated the presence of virulence genes and toxin genes by DNA-based methods because they cause diseases in both animals and humans (Table 4). These genes such as verotoxin genes (*vet*), coagulase genes (*coa*), Emetic toxin genes,

enterotoxigeni genes (*see, sea, sec, seb and sed*), and other types of genes for *E coli* such as *pap, its, pai* and *icd* gene which used for species identification [30,34,36,37,41,49].

Table 1. The most studied animals used for milk and dairy products collection

Animal	Source of isolation	Microorganism(s)	References
Cow	Milk	*S. aureus, Streptococcus agalactia Streptococcus dysagalactia; Corynebacterium pyogenes, E, coli ,K. pneumonia ;Candida glabrata, Aspergillus fumigatus Candida albicans, Saccharomyces cerevisiae, Cryptococcus neoformans.*	[19]
Goat, buffalo	Milk	Hypersensitivity	[20]
unidentified	cheese , cream	*E. coli & S. aureus*	[21]
Buffalo, sheep	Milk	*Brucella*	[22]
Cow	Milk	*S. aureus, Streptococcus spp, E. coli, Klebsiella spp, Salmonella sp, Aspergillus spp, Candida spp*	[23]
Cow	Milk, Cheese	*Campylobacter* spp.	[24]
unidentified	Milk products	*Brucella*	[25]
unidentified	Cheese	*S. aureus*	[26]
unidentified	Milk product	*E. coli*	[27]
Cow	Milk	*Staphylococcus* Spp.	[28]
Cow, goat	Milk	*Burkholderia pseudomallei*	[29]
Animal , unidentified	Milk & milk products	*Bacillus cereus*	[30]
Animals	Milk	*E. coli*	[31]
Cow	Milk	*E. coli*	[32]
Animals	Milk	*S. aureus*	[33]
cow	Milk	*B. cereus*	[34]
Cow	Milk	*L. monocytogenes*	[35]
Cow	soft cheese	*E.coli*	[36]
Animal	Milk	*E. coli*	[37]
Animal	Milk	*S. aureus*	[38]
Cow	Milk	*S. aureus*	[39]
Animals	Milk, milk products	*B. cereus*	[40]
Cow	Milk	*S. aureus*	[41]
Cow	Milk	*E. coli*	[42]
Camel	Milk	*E. coli*	[43]
Camel	Milk	*E. coli*	[44]
unidentified	Milk	*Salmonella*	[45]
Cow	Milk	Lactic acid Bacteria	[46]
Cow, unidentified	Milk, yogurt, cheese	Coliform, *E. coli* & lactic acid bacteria	[47]
Animals	White cheese	*B. cereus*	[48]
Cow	Milk	*S. aureus*	[49]
unidentified	Milk	*Bacterial count*	[50]
Cow, buffalo, sheep	Milk	*L. monocytogenes*	[51]

Table 2. The percentage of recorded organisms during investigated period

Source	Product	Isolated organisms	Percentage %	References
unidentified	Chees	*E. coli*	62.66	[27]
unidentified	Milk	*Salmonella*	6.1	[45]
Cow	Milk	*Lactobacilli*	51	[46]
unidentified	Milk	*Staphylococci*	15.55	[28]
unidentified	Milk product	Coliform	-	[47]
unidentified	Milk, meat	*Campylobacter spp*	4-26	[24]
Cow milk	Milk	*B. Pseudomaleli*	33.33	[29]
Goat	Milk		26.66	
unidentified	Milk,	*Bacillus cereus*	30	[48]
	White cheese		20	
Buffalo	Milk	*S. aureus*	22.2	[52]
unidentified	milk	*Bacillus cereus*	32.7	[30]
	soft cheese		16.66	
	curls cheese		18.00	
	yogurt		6.00	
Cow, buffalo, sheep	Milk	*Brucella spp.*	24.2	[22]
unidentified	Cheese,	*Brucella spp.*	8	[25]
	cream,		1	
	ice-cream		0	
Camel	Milk	*E. coli*	7.44	[43, 44]
unidentified	soft cheese, curls cheese, yoghurt local cream	*E. coli*	-	[27]
Cow	Milk	*S. aureus*	48	[49]
Cow, buffalo, sheep	Milk	*L. monocytogenes*	7.3	[51]
Cow	Milk	*S. aureus*	53	[49]
cow	Milk	*S. aureus*	30	[39]
buffalo	Milk	*S. aureus*	27	[41]
unidentified	Chees	*S. aureus*	39	[26]
unidentified	Milk	*E. coli O157:H7*	14.3	[42]
Cow	Milk	*S. aureus*	33.12	[19]
		Streptococcus spp	24.84	
		E. coli,	12.88	
		Klebsiella spp,	1.84	
		Salmonella sp	0.92	
		Aspergillus spp,	20	
		Candida spp	80	

Table 3. Antibiotic susceptibility of isolated microorganisms

Microorganism	Antibiotic	Susceptibility	Reference
E. coli	Gentamycin, amikacin	S	[37]
	Amoxicillin, cefoxitim.	R	
Salmonella	chloramphenicol, rifampin	R	[45]
	ciprofloxacin	S	
Staphylococci	Ampicillin, novbiocin + penicillin, oxcillin	R	[28]
	ciprofloxacin, ghloramphenicol , gentamycin	S	
Campylobacter spp	Kanamycin, ampicillin, erythromycin, metronidazole	R	[25]
	Gentamycin, ceproflaxacin	S	
Bacillus cereus	Carbencillin, cephalothin, ampicillin	R	[48]
	Erythromycin, gentamycin, chloramphenicol, nalidixic	S	

Microorganism	Antibiotic	Susceptibility	Reference
	Sulfamethoxazole-trimethoprim.		
S. aureus	Cloxacillin	R	[49]
Bacillus cereus	Neomycin, chloramphenicol, gentamycin, streptomycin Erythromycin	S	[30]
	Penicillin	R	
E. coli O157:H7.	Cephalothin , cefoxitin ,cefixime, trimethoprim , amoxicillin,	R	[31]
	Azithromycin, amoxicillin/clavulanic, amikacin, Ciprofloxacin, imepenim, nitrofurantoin, gentamycin ,	S	
Listeria mononcytogenes	Cefotaxine, sulfamethoxazol, chloramphenical, tobramycin	R	[35]
	Rifampicin	S	
S. aureus	Nitrofurantoin, chloramphenicol, tobramycin, azithromycin	R	[39]
	Ceftriaxone, cefotaxime	R	

S, sensitive; R, resistant

Table 4. Genes present in organisms originated from animal samples

Microbe	Genes	Presence	Reference
E. coli	*Vet1, pap*	+	[37]
	Vet2	-	
S. aureus	*Coa*	+	[41, 49]
B. cereus	*cytK*	+	[30]
B. cereus	*hbl, nhe*	+	[40]
	bceT	-	
E. coli	*Its*	+	[43]
E. coli	*Pai*	+	[44]
	Icd	+	
E. coli O157:H7	*Vt1 , Vt2*	+	[36]
S aureus	*Sec*	+	[33]
	Sea, Seb,Sed, See	-	
E. coli O157:H7	*Tem*	+	[42]
	Shv	+	
B. cereus	Emetic toxin genes	+	[34]

5. CONCLUSION

From the above reviewed literatures, we can conclude that milk and its products at Basrah city are contaminated with different microorganisms. Most of them are infectious and can cause a disease for both humans and animals. In addition, many investigated microbes have multidrug resistance and harbor a virulence and toxin producing genes.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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