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Drug Resistance and Virulence Traits of Acinetobacter Baumannii Isolated from Milk and Local Cheese in Al-Diwanyah /Iraq

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Abstract

Acinetobacter baumannii is a hazardous opportunistic bacterium that can thrive in a variety of settings, including food matrices, and acquire antibiotic resistance. This study was the first to successfully isolate this bacterium from samples of raw milk and cheese made locally.

They were subjected to microbiological tests. The isolates were first sub-cultured on selective media (Chrom agar and Gram staining) and subsequently identified more firmly with the VITEK 2 system, which produced a species identification certainty level at 99%,

The results indicated that the overall prevalence rate of the bacterium was 4.5%, but showed a higher occurrence in their samples in cheese (3%) than in milk (6%). The highest contamination rates in the area of the study were observed in the Al-Daghara region in Al-Diwanyah at the molecular level,

The isolates possessed full spectrum of virulence genes such as ompA and csuE associated with biofilm formation and host cell attachment. Health them with key antibiotic resistance genes such as blaOXA-51 and adeA, this suggests these isolates a multi drug-resistant (MDR) strain. Genomic analysis and DNA sequencing revealed high genetic similarity, up to 99.70% identical local isolates and pathogenic strains from all over the world published in GenBank (NCBI). These suggest that these bacteria are not only transients pollutants, but also developed strains which colonised and populate the local food environment. The data from this study demonstrates that the contamination of A. baumannii in traditional dairy products presents a serious public health hazard due to its high antibiotic resistance and virulence arsenal. Health restriction and control over the production and management of these products is necessary to minimize the risk of the transfer of resistant strains to human via the food chain.

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Introdaction

Acinetobacter baumannii is a Gram-negative coccobacillus, a significant opportunistic pathogen with the ability to withstand diverse environmental conditions and possess inherent resistance to commonly prescribed antibiotics ((Mohamed et al ,.2022). Also, it is considered one of the most common zmultidrug-resistant pathogens causing nosocomial infections. The incidence of multidrug-resistant A. baumannii infections is increasing because of several factors, including unregulated antibiotic use that contributed to global health concern due to increasing antibiotic resistance especially carbapenem resistance A. baumannii (CRAB) that associated to co-resistance to other antibiotics (Shi et al.,2024). The pathogenesis of A. baumannii initiates with its exceptional ability to colonize host biotic surfaces, particularly the respiratory tract and compromised skin, where the bacteria adhere firmly to epithelial cells to establish primary infection sites that resist mechanical clearance by the host's innate defenses (Ahmad etal.,2024).Pathogenesis progresses as the bacteria transition from local colonization to bloodstream invasion, a critical stage leading to "Bacteremia," where the pathogen disseminates through the circulatory system to reach vital organs like the kidneys and liver, triggering a massive systemic inflammatory response that damages healthy tissues.(Wang-Kan etal.,2023).The bacterium Acinetobacter baumannii is a formidable pathogen that has demonstrated an exceptional ability to adapt to diverse environments beyond clinical settings, emerging as a dangerous contaminant in the food chain—particularly in raw milk and dairy products (Hamidian & Nigro, 2019). Its presence in milk is hazardous not merely due to microbiological spoilage, but because it possesses a sophisticated system of virulence factors that enable it to stabilize and thrive in this nutrient-rich medium(Raza & Rehman (2025).

The pathogenicity of A. baumannii in milk is closely linked to its ability to withstand various environmental stresses, ranging from temperature fluctuations to the formation of biofilms on milking and processing equipment (Ghatak et al., 2020). These characteristics make it a highly competitive and pervasive microbe, utilizing its molecular arsenal to adhere to milk components and grow effectively, thereby posing a direct threat to public health upon consumption (Dahdouh et al., 2020). Acineto bacterbumanuii bacteria (GNB) are among the world's most significant public health problems due to their high resistance to antibiotics(Oliveira & Reygaert ,2023).

that pose a global threat to human health and a therapeutic challenge due to emerging and constantly increasing resistance(Whiteway et al., 2022).Carbapenem resistant A. baumannii (CRAB) was ranked in 2018 by WHO as number one priority for antibiotic research and development. Carbapenem was chosen as a marker, because carbapenem resistance is usually associated with a broad range of co-resistance to other antibiotic classes (Kyriakidis et al.,2021).

Method and material:

Collection of Samples:

Acinetobacter baumannii isolation and identification were the main goals of the current investigation. This was accomplished by gathering 100 samples of milk and 100 samples of locally made cheese in sterile, firmly sealed containers. After being kept cold in an ice box, the samples were brought to the lab for bacteriological analysis in order to produce representative findings.

Culture Method

On MacConkey and Chromagar isolated samples and incubated at 37C for 24 hr.

Microscopic Examination:

Pure bacterial colonies were taken and smeared onto a glass slide, then heat-fixed. Standard Gram staining was performed, and the slides were examined under a light microscope to determine the bacterial shape, arrangement, and Gram-negative classification.

DNA extract:

Pure bacterial colonies was taken into a tube with the lysis buffer and RNase from a commercial kit (DNA Extraction kit, RIBO RNA, Homi L. Rouhi, Tehran, Iran) according to the manufacturer's protocol instructions. The colonies were mixed well with the lysis buffer and incubated at the suitable temperature for a short time to lyse the bacterial cells. After centrifuging the samples, the supernatant was transferred to a clean tube. The supernatant was sequentially subjected to two wash steps and one elution step. The purified DNA was stored at -20°C until further analysis. The concentration of the extracted DNA was measured using a fluorometer or a spectrophotometer (if available) with the DNA concentration calculation formula.

PcR(Polymerase chain Reaction). :

A PCR assay was carried out on the bacterial isolates from milk and local cheese to detect the A. baumannii genes. The DNA of the bacterial isolates was used as a template for the PCR reaction. The PCR reaction mixture contained DNA polymerase, nucleotides and primers for the virulence genes, including ompA, adeA, cfuE, the resistance gene, blaOXA-51-like, and the 16S rRNA gene to confirm the bacterial identity, was incubated in a thermal cycler. The samples were subjected to the standard PCR program.

Table (1) PCR primer with their nucleotide sequence and product size.

Primers	Sequence 5'-3'		Product size	Genbank Reference code
16SrRNA gene	F	GCAGCAGTGGGGAATTTTGG	640bp	LN611374.1
	R	CCAGGTAAGGTTCTTCGCGT		
ompA gene	F	CGACAGCAAAATCAAGCCGT	356bp	PX680608.1
	R	AGAACACACGAAGTTCCATGT		
csuE gene	F	ACTGCCAGACTGCCGAATTT	159bp	DQ289017.1
	R	TTGCCATTTTGCGGGGAAAG		
blaOXA-51 gene	F	CCAACAAGGCCAAACTCAACA	125bp	MT157678.1
	R	TGGTTGCCTTATGGTGCTCA		
adeA gene	F	CGGAAACAGGCGATGTCACA	404bp	MN482160.1
	R	TCATGGTTGTGCCCCTTCAG		

The products of the PCR reaction were analyzed by agarose gel electrophoresis to determine the sizes of the expected fragments. The selected PCR products were purified and submitted for DNA sequencing to confirm the nucleotide sequences. The local isolates were compared with the isolates from the global isolates that are stored in the genetic database, by comparing 16S rRNA sequences and other targeted genes. The molecular analysis shows that the local isolates are genetically related to some hard pathogenic global isolates, which indicates that the same resistance and morphological characteristics are present and the minor differences in the nucleotide sequence between local and global isolates may be an indication that the local isolates are adapted to the local food matrix. This comparison gives us the possibility to estimate the potential health risk and also the genetic diffusion of bacteria among different sources and different geographic origins.

Statistical Analysis:

The data were tabulated and then subjected to statistical analysis using a personal computer program-Statistical Package for the Social Sciences (SPSS) version 26 (IBM Corporation, Armonk, NY, USA). The chi-square test was used for the qualitative data and compared among the groups. Statistical significance was assumed at a probability level of $P < 0.05$ (Field, 2013).

Result:

Nine AB isolates were recovered from 200 samples, with an overall prevalence of 4.5%. The isolation rates between the two sample types are presented in the table (1). The isolation rate from milk samples was slightly higher 6/100 (6%) than local cheese 3 /100 (3%). From the results of this study which are presented in the table, it is clear that there is a difference in the prevalence of positive cases between both samples (milk and local cheese). difference in prevalence was significant, as indicated by the two samples.

Table (2): Prevalence of *A. baumannii* in milk and local cheese samples

Sample source	Total samples	Positive	Percentage
Milk	100	6	6.0%
Local cheese	100	3	3.0%
Total	200	9	4.5%
Calculate X^2	1.047		
Calculated P	0.306*		

***No significant difference at P<0.05**

Bacterial isolation.

Primary isolation was carried out using MacConkey agar, appare circular smooth,mucoid and shiny colonies that are white pale to grayish in color and do not ferment lactose. colonies as show in figure (1). For the purpose of confirming the isolates ,it was culture on chrom agar and isolates formed circular colonies with smooth surfaces, displaying a distinct purple coloration with pale centers, which facilitated their differentiation from other bacterial species figure (2).

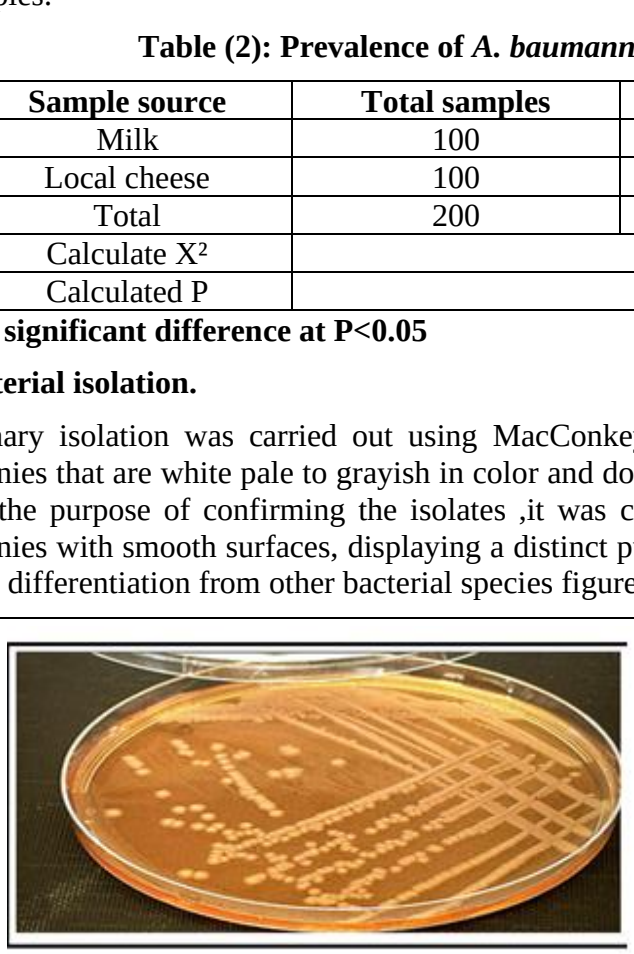


Figure (1) Colony growth of Acinetobacter baumannii MacConkey agar colonies with no color (lactose non- fermenter)

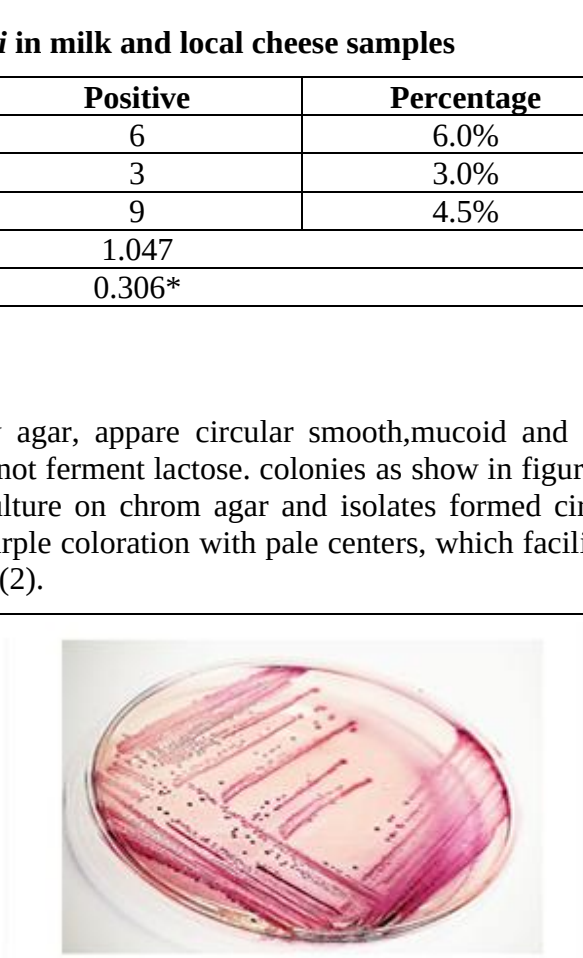


Figure (2) Colony growth of Acinetobacter baumannii on chrom agar that are appare purple colors with smoth surface.

Microscopic examination

Micrographically, Acinetobacter are short, Gram-negative rods,. appriximately 1-2m in length and 0.5-1 m in width. They occur singly, orpairs, or occasionally in very short chains. The cells may appear slightly rounded, giving a cocco-bacillary appearance. They are non-motile and lack flagella figure (3).

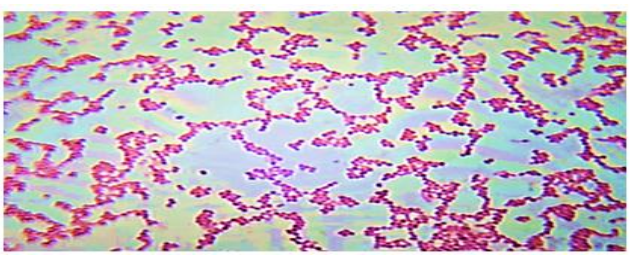


Figure (3) colony of A.baumannii show cocobacilla, singl, short chins in gram stain

Automated Biochemical Test (VITEK 2 System)

Whereas the Vitek II system was used to confirm the morphological and biochemical characteristics of the bacterial isolates Acinetobacter baumannii at with probability 99% utilizing biochemical profiles,as shown in figure (4).

ScientificReseracher.Co.LtD
bioMérieux Customer: Microbiology Chart Report Printed February 28, 2026 9:41:42 PM AST

Patient Name: . Patient ID: 3102025.2
Location: Physician:
Lab ID: 3102025.2 Isolate Number: 1

Organism Quantity:
Selected Organism : Acinetobacter baumannii

Source: Burn **Collected:**

Comments:	

Identification Information	**Analysis Time:** 5.82 hours	**Status:** Final
Selected Organism	99% Probability **Acinetobacter baumannii** **Bionumber:** 0241010103500350	
ID Analysis Messages		

Susceptibility Information	**Analysis Time:** 14.60 hours	**Status:** Final

Antimicrobial	MIC	Interpretation	Antimicrobial	MIC	Interpretation
Ampicillin/Sulbactam	16		Meropenem	>= 16	R
Piperacillin/Tazobactam	>= 128	R	Amikacin	>= 64	R
Cefotaxime	>= 64	R	Gentamicin	>= 16	R
Ceftazidime	>= 64	R	Ciprofloxacin	>= 4	R
Ceftazidime/Avibactam			Tigecycline		
Ceftolozane/Tazobactam			Colistin	<= 0.5	I
Cefepime	4	*R	Trimethoprim/ Sulfamethoxazole	160	R
Imipenem	>= 16	R			

*= AES™ modified **= User modified += Deduced drug #= Disabled BIOART Limitation Rule (-)= Susceptibility testing not recommended; species is a poor target for therapy IE= Insufficient Evidence that species is good target for therapy; MIC may be reported without interpretation SDD= Susceptible-dose dependent (SDD) implies that susceptibility of an isolate is dependent on the dosing regimen used. For further information, please refer to CLSI Performance Standards, or Product information. <= Missing required test @= Terminated antibiotic in family

Figure(4) identification A.baumannii using the VITEK®2 test.

The VITEK analysis time was 5.82 hours, with 99% probability for *Acinetobacter baumannii*, and the bionumber 0241010103500350 confirmed the identification with final status. All isolates were confirmed as *A. baumannii* (100% concordance). No other *Acinetobacter* species were detected. The chromogenic agar facilitated differentiation from other Gram-negative rods, and the VITEK results provided high-confidence identification. These findings demonstrate that *A. baumannii* is present in both milk and local cheese samples.

Amplification of 16S rRNA, virulence and resistance genes.

Regarding resistance gene amplification, the virulence genes, as well as genomic DNA from A.baumannii, produced distinct, isolated bands after ethidium bromide staining and viewing with UV light. Used for DNA separation according to size, agarose gel electrophoresis also helps in determining amplicon size in association with the 2,000 base pairs DNA ladder.

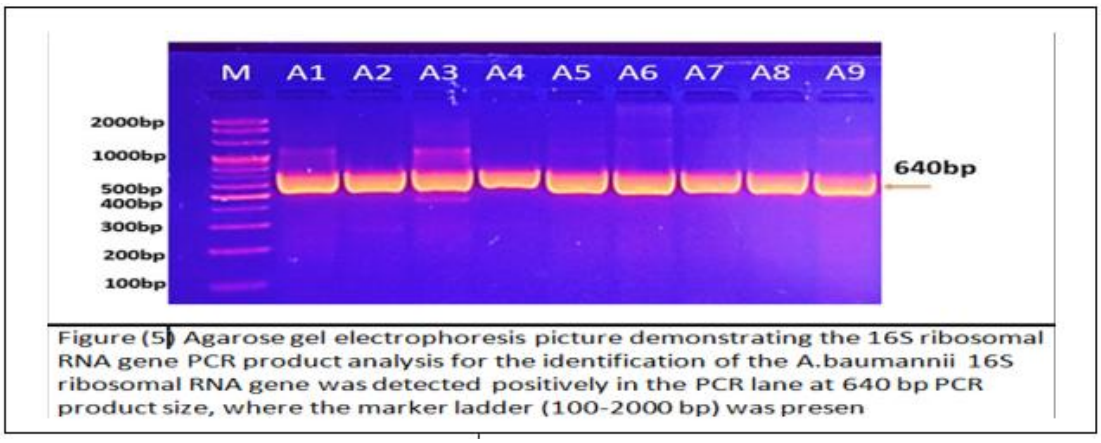
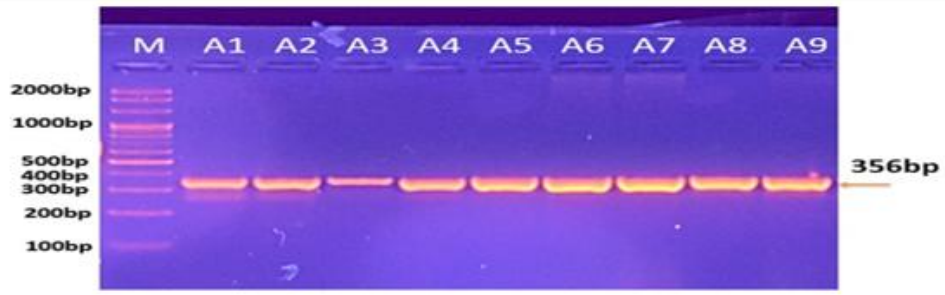


Figure (5) Agarose gel electrophoresis picture demonstrating the 16S ribosomal RNA gene PCR product analysis for the identification of the A.baumannii 16S ribosomal RNA gene was detected positively in the PCR lane at 640 bp PCR product size, where the marker ladder (100-2000 bp) was presen



Figure(6) Agarose gel electrophoresis picture demonstrating the omp A(outer membrane protein A) gene PCR product analysis for the identification of the A. baumannii. ompA adhesion gene was detected positively in the PCR lane at 356 bp PCR product size, where the marker ladder (100-2000 bp) was present.

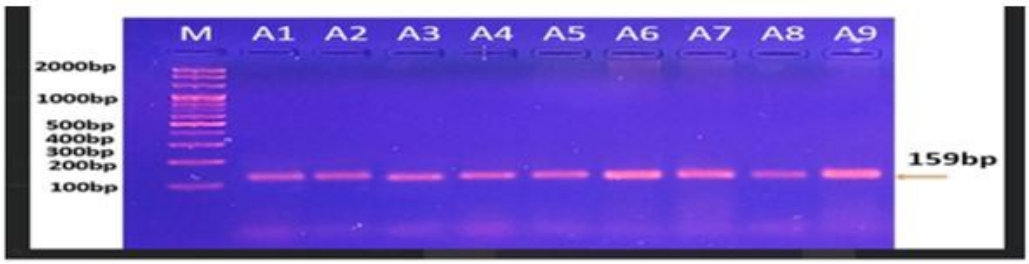


Figure (7) Agarose gel electrophoresis picture demonstrating the csuE (chaperone usher pili assembly)gene PCR product analysis for the identification of the A. baumannii. ompA adhesion gene was detected positively in the PCR lane at 159 bp PCR product size, where the marker ladder (100-2000 bp) was present.

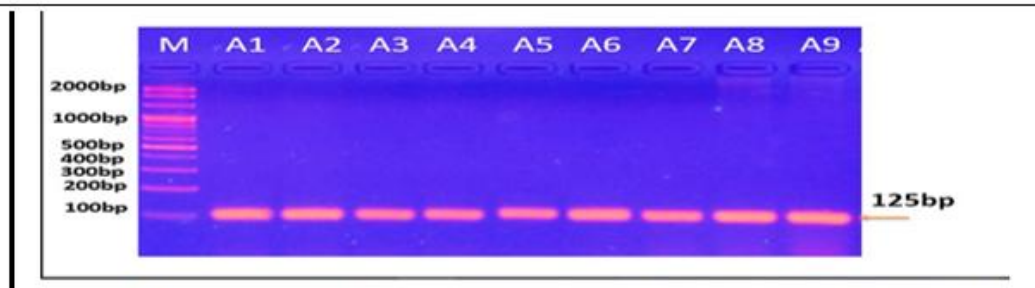


Figure (8) Agarose gel electrophoresis picture demonstrating the blaOXa-5 gene PCR product analysis for the identification of the A. baumannii. blaOXA destroy antibiotic gene was detected positively in the PCR lane at 125 bp PCR product size, where the marker ladder (100-2000 bp) was present.

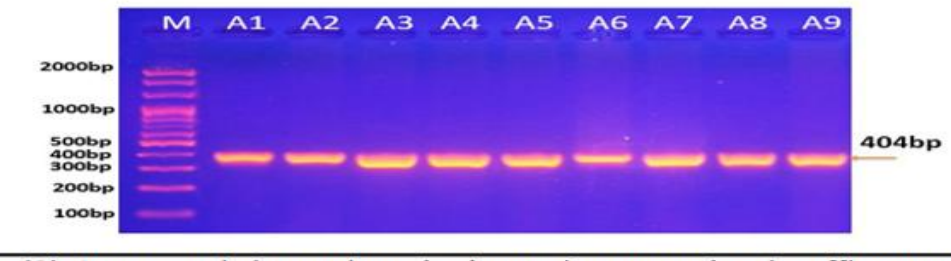


Figure (9) Agarose gel electrophoresis picture demonstrating the efflux pump gene PCR product analysis for the identification of the A. baumannii. Efflux pump gene was detected positively in the PCR lane at 404 bp PCR product size, where the marker ladder (100-2000 bp) was present.

Molecular confirmation of the isolates was performed by PCR targeting the 16S rRNA gene and two virulence-associated genes: *ompA* (outer membrane protein A), *csuE* (chaperone-usher pili assembly),

and two antibiotic resistance *bla*$_{OXA-51}$ gene and antibiotic resistance *efflux pump adeA* gene). All nine *A. baumannii* isolates produced the expected amplicon for 16S rRNA, confirming genus and species identity.

The antibiotic resistance gene were detected in 100% of isolates, consistent with its species-specific marker role. For virulence factors, *ompA* and csuE was present in all strains (100%), As show in agarose gel electrophoresis figure.(5,6,7,8,9).

DNA Sequencing results

The DNA sequencing method was carried out for genetic confirmative detection and genetic relationship analysis of Acinetobacter baumannii Iraq isolates based on 16S ribosomal RNA gene and compared with NCBI-Blast related Acinetobacter baumannii isolates. The phylogenetic tree was constructed using Unweighted Pair Group method with Arithmetic Mean (UPGMA tree method) and the evolutionary distances w0ere computed using the Maximum Composite Likelihood method in (MEGA 6.0 version).

The local Acinetobacter baumannii Iraq isolates IQ.No.1 and IQ.No.2 isolates were showed closed related to NCBI-BLAST Acinetobacter baumannii strain CUB_V5 (OP935683.1) at total genetic changes (0.00140-0.00020%) as showed in figure (10). The homology sequence identity between local Acinetobacter baumannii Iraq isolates IQ.No.1- IQ.No.2 isolates and NCBI-BLAST related Acinetobacter baumannii isolate were showed genetic homology sequence identity (99.70%) as show in table (3). Finaly the local Acinetobacter baumannii IQ.No.1-IQNo.2 isolates were submitted into Genbank and recorded as accession numbers (PZ194142.1-PZ194143.1).

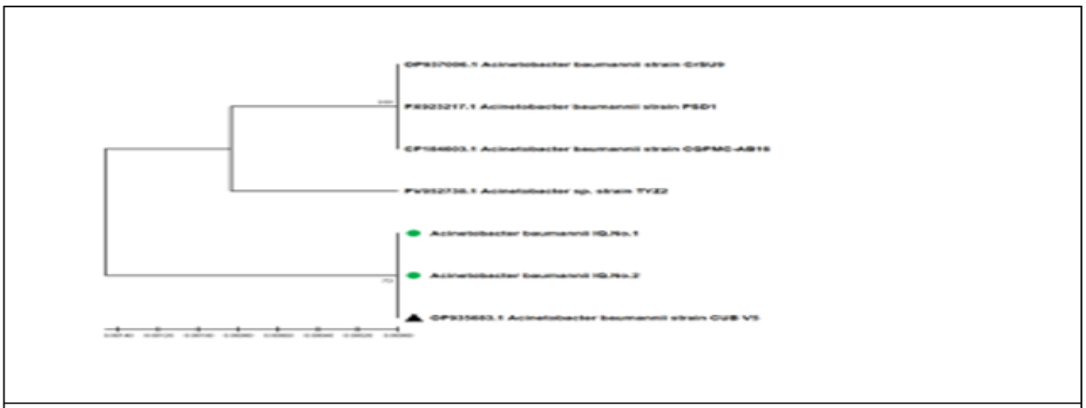


Figure (10): Phylogenetic tree analysis based 16S ribosomal RNA gene partial sequence in local Acinetobacter baumannii Iraq isolates that used for genetic relationship analysis.

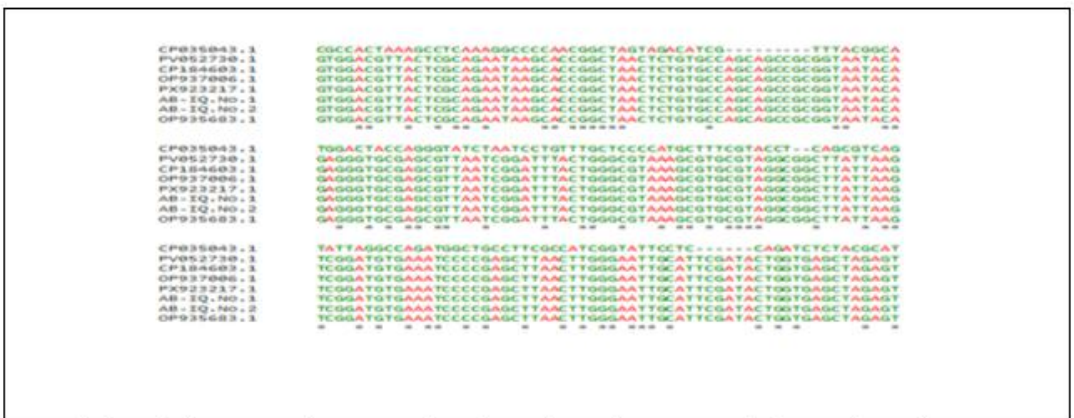


Figure (11): Multiple sequence alignment analysis of 16S ribosomal RNA gene in local Acinetobacter baumannii Iraq isolates and NCBI-Genbank Acinetobacter baumannii country related isolates. The multiple alignment analysis was constructed using (ClustalW alignment tool. Online). That alignment analysis was showed the nucleotide alignment similarity as (*) and substitution mutations in 16S ribosomal RNA gene between isolates.

The phylogenetic tree was constructed using Unweighted Pair Group method with Arithmetic Mean (UPGMA tree method) and the evolutionary distances were computed using the Maximum Composite Likelihood method in (MEGA 6.0 version). The local Acinetobacter baumannii Iraq isolates IQ.No.1 and IQ.No.2 isolates were showed closed related to NCBI-BLAST Acinetobacter baumannii strain CUB_V5 (OP935683.1) at total genetic changes (0.00140-0.00020%).

Table (3) the NCBI-BLAST Homology Sequence identity percentage between local Acinetobacter baumannii Iraq isolates and NCBI-BLAST closed related Acinetobacter baumannii isolate:

local isolate	Accession number	Homology sequence identity (%)	
		Accession number	Identity (%)
BS IQ No.1 isolate	PZ194142.1	OP935683.1	99.70%
BS IQ No.2 isolate	PZ194143.1	OP935683.1	99.70%

Antibiotic susceptibility profile of *A. baumannii* isolates by Automatic Biochemical.

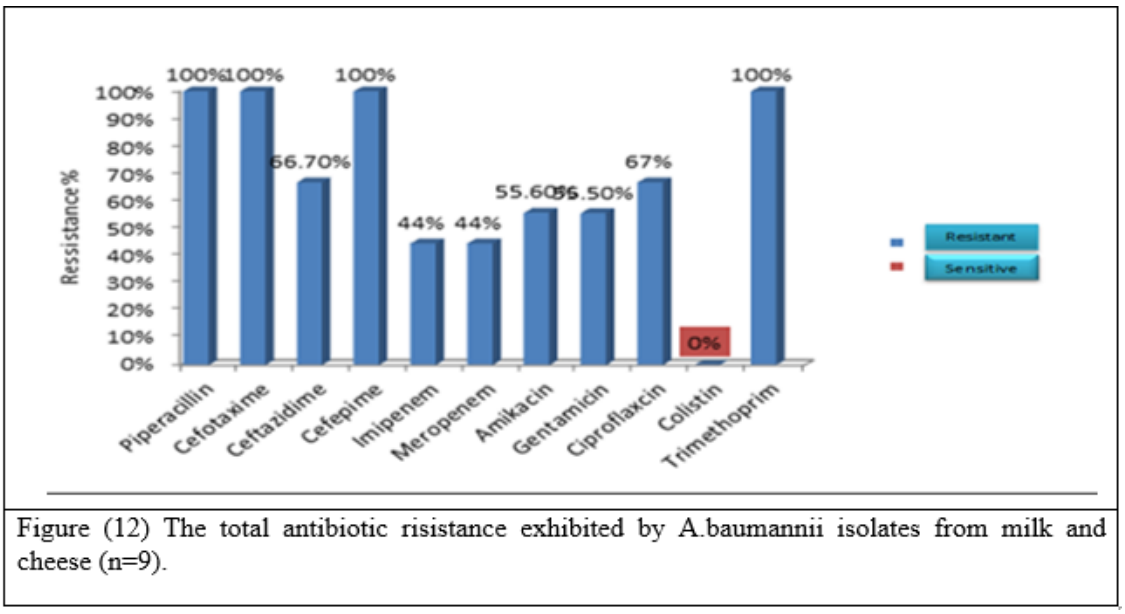


Figure (12) The total antibiotic risistance exhibited by A.baumannii isolates from milk and cheese (n=9).

All nine A. baumannii isolates recovered from milk and local cheese were subjected to antimicrobial susceptibility testing using VITEK® 2 AST cards. Minimum inhibitory concentrations (MIC, µg/mL) were interpreted according to CLSI breakpoints with AES™ modified interpretation. The detailed per isolate MIC values were presented earlier; here we summarize the resistance counts and percentages comparing milk (n=6) versus cheese (n=3) isolates. As shown in Table 4.3, resistance to piperacillin/tazobactam, cefotaxime, and cefepime was uniformly high: all six milk isolates and all three cheese isolates were resistant (100%). For ceftazidime, four out of six milk isolates (66.7%) and two out of three cheese isolates (66.7%) showed resistance; the remaining isolates exhibited intermediate susceptibility (not shown). Carbapenem resistance (imipenem and meropenem) was detected in three milk isolates (50%) and one cheese isolate (33.3%), indicating that not all strains were carbapenem resistant, but a considerable proportion (44.4% overall) carried resistance. Amikacin resistance was observed in four milk isolates (66.7%) and one cheese isolate (33.3%); gentamicin resistance in four milk (66.7%) and one cheese (33.3%); ciprofloxacin resistance in four milk (66.7%) and two cheese (66.7%). Notably, colistin resistance was absent in both groups (0% resistant), but several isolates showed intermediate MICs (≤1 µg/mL) – none were fully resistant. Trimethoprim sulfamethoxazole resistance was present in all six milk isolates (100%) and all three cheese isolates (100%). The comparative data highlight that cheese isolates were generally less frequently resistant to some aminoglycosides and carbapenems, but the small sample size limits definitive conclusions. The overall multidrug resistant

phenotype, especially the high rate of β lactam and quinolone resistance, underlines the importance of monitoring A. baumannii in dairy products. The data in Table (4) confirm that resistance to extended spectrum cephalosporins (cefotaxime, cefepime) and piperacillin/tazobactam was universal, while carbapenem resistance was present in about half of milk isolates and one third of cheese isolates. Ceftazidime resistance was observed in two thirds of isolates from both sources. Aminoglycoside resistance (amikacin, gentamicin) was more frequent in milk isolates (66.7%) compared to cheese (33.3%). Ciprofloxacin resistance was identical (66.7%) in both groups. Importantly, no colistin resistance emerged, and all isolates remained intermediate, which is clinically relevant as colistin is a last resort drug. Trimethoprim sulfamethoxazole resistance was uniformly 100%. These findings highlight the presence of MDR A. baumannii in dairy products, with variable resistance to carbapenems and aminoglycosides, and underscore the necessity for continuous surveillance and rational antibiotic use in animal and food sectors.

Table (4): Comparative resistance counts and percentages among *A. baumannii* from milk and cheese

Antimicrobial	Milk isolates (n=6)	Cheese isolates (n=3)	Total (n=9)
Piperacillin/tazobactam	100% (6)	100% (3)	100% (9)
Cefotaxime	100% (6)	100% (3)	100% (9)
Ceftazidime	66.7% (4)	66.7% (2)	66.7% (6)
Cefepime	100% (6)	100% (3)	100% (9)
Imipenem	50% (3)	33.3% (1)	44.4% (4)
Meropenem	50% (3)	33.3% (1)	44.4% (4)
Amikacin	66.7% (4)	33.3% (1)	55.6% (5)
Gentamicin	66.7% (4)	33.3% (1)	55.6% (5)
Ciprofloxacin	66.7% (4)	66.7% (2)	66.7% (6)
Colistin	0% R, 100% I (6)	0% R, 100% I (3)	0% R, 100% I (9)
Trimethoprim/sulfamethoxazole	100% (6)	100% (3)	100% (9)

nR = number of resistant isolates.

Discussion

The present study results raise a big concern about the contamination of locally consumed dairy products (raw milk and cheese) with Acinetobacter baumannii. The morphological and biochemical tests along with the VITEK 2 system confirmed the identity of isolates with a high probability of 99%. The pale-to-greyish colonies on the MacConkey agar and purple colonies on the Chromogenic agar are a direct reflection of the metabolic properties of this species, i.e. its inability to ferment lactose, as reported in (Mohamed et al. (2022) who have described the remarkable adaptability of this bacterium to various types of environmental stressors. Furthermore, the molecular detection of the 16S rRNA gene in all nine isolates, and the presence of the virulence factors ompA and csuE in 100% of the isolates, explain the high adhesion ability of the pathogen to the surfaces of milking equipment and its ability to form strong biofilm. This finding is strongly supported by (Ghatak et al. (2020) who established a direct relationship between the ability of the pathogenic bacteria to form a biofilm and its persistence in the food processing plant, where it is able to resist the routine cleaning process.

As for the antimicrobial resistance, the presence of the resistance gene blaOXA-51 and the efflux pump gene adeA in all the isolates indicate that the strains are Multidrug-Resistant (MDR). These findings indicate that the bacteria have acquired advanced defense mechanisms, either through the active extrusion of antibiotics or through the enzymatic degradation of antibiotics, especially carbapenems, where the isolates showed different patterns of resistance (44.4% for Meropenem and 44.4% for Imipenem). These findings are in perfect agreement with (Shi et al. (2024) who have warned of the increasing threat of Carbapenem-Resistant A. baumannii (CRAB) in the food chain due to the unregulated use of these

antibiotics in the livestock industry. Furthermore, the 100% resistance detected against Piperacillin/tazobactam and Cefotaxime is in agreement with (Kyriakidis et al. (2021) who reported that the carbapenem resistance was co-carried with other major antibiotic class resistance which would greatly restrict the clinical treatment options if these strains were to be transmitted to humans.

Genetic and epidemiological point of view, the high degree of genetic similarity between the local isolates and the known pathogenic strains worldwide, despite some limited nucleotide differences, suggest that these bacteria are not merely incidental contaminants, but evolved strains that can persist in the food. This supports the hypothesis proposed by (Hamidian & Nigro (2019) that A. baumannii has successfully transcended its traditional clinical boundaries to become a formidable environmental and foodborne threat this finding has direct implications for public health, as it contradicts the general public perception of safety regarding the traditional unpasteurized dairy products and highlights an urgent need for stricter health regulations and ongoing surveillance of the food chain to ensure that these highly resistant genes are not transferred to the human microbiome, which may cause public health emergencies that are increasingly difficult to manage.

Conclusion

The study demonstrates that A. baumannii has successfully transcended its traditional clinical boundaries to become a formidable environmental and foodborne threat. The results showed that raw milk and traditional dairy products sold in local markets are significant reservoirs for this opportunistic pathogen. This is mainly due to the poor quality of pasteurization and hygiene level in the dairy industry. And the natural ability of this bacterium to survive in harsh environmental conditions and the capacity to form biofilms, it is able to colonize milking equipment and storage vessels. One of the major conclusions of this study is that contamination is not only a quality concern but also a serious public health risk, as 100% of the isolates were found to have critical virulence genes such as ompA and csuE. Furthermore, the study provides evidence that these foodborne strains are multidrug-resistant (MDR) with total resistance to several major antibiotic classes, which severely restrict the options for clinical treatment. The presence of the blaOXA-51 genegene and efflux pump [Sri Lankan abberrancy of Acinetobacter baumannii resistant to all antimicrobials and abundant in traditional dairy products]

The presence of the mechanisms in all recovered isolates proves their high level of genetic readiness to resist the antimicrobial agents. That the unregulated use of antibiotics in the livestock sector is the main factor on the emergence of these resistant strains in the food chain. The molecular analysis of the local isolates shows a high level of genetic similarity to the globally known pathogenic strains, which proves that they are equally virulent and can cause severe human infections. The consumption of unpasteurized dairy products is a direct mode of transferring the highly resistant genes in the human microbiome. The current knowledge regarding the safety of traditional dairy products is largely erroneous and needs urgent revision. It is very important to implement strict health regulations and sterilization procedures in the dairy industry. The without constant surveillance and monitoring of the food supply, these resistant bacteria can cause a massive public health disaster. It is vital to now prioritize A. baumannii as an important foodborne pathogen in environmental health policies to avoid its spread.

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Conflict of Interest

The authors declare that no conflict of interest exists.

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Author Contributions

All authors have made substantial contributions to this work and approved the final manuscript for publication.

Data Availability

All data generated or analyzed during this study are included in this manuscript. Both sequences are deposited in NCBI GenBank under accession numbers PZ194142.1-PZ194143.1

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