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Dynamic Patterns of *Acinetobacter baumannii* Recovered from Local Dairy Chain and Human UTI cases in Baghdad

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Abstract

A specialized topic in the field of quorum sensing in naturally occurring highly resistant complex bacteria, that behaves likes a prohibited sophisticated emergent biohazard biofilm entity entitled a Iraqi bacteria *Acinetobacter baumannii* equipped with stress hardening resident within local dairy chain in Baghdad. These naturally resistant emergent highly infectious bioterror foci with or without recalcitrant biofilm barriers were isolated, identified and PCR primed from local Cows raw milk, paired fresh-brined soft cheese, paired fresh-soured yogurt, cream and butter. Samples collected randomly from Abu-Ghraib, Al-Sadrya and Al-Fudhaliyah sectors cascaded by verified modified processing protocols from February (2022) to proceed to February (2023). A HiCrome™ Acinetobacter Agar (M1938) with multidrug resistant (MDR) selective supplement vials either (FD271) or (FD335) was dependent for selective and differential isolation dogma. Cascaded series of VITEK®2 augmented with 16s rRNA PCR were confirmed recovery patterns. Experimental design was proceeds within veterinary public health / milk hygiene lab. Assessment risk design was aligned with urinary tract infection cases from associated worker and nosocomial hospital individuals. Recovery and segregation documentary records unveiled isolation of twenty-seven (27: 4.285 %) out of colloquy sixty and thirty-six (636) dairy samples units cascaded by four isolates (4: 11.11 %) out of thirty-six (36) urine samples of UTI patients from Baghdad. In conclusions: An emergent bioterrorism contamination cascaded ancestral Eco map of targeted forbidden denominator was resident and encountered from local dairy chain in association with Human UTI opportunity as a complex stress hardening in Baghdad.

Key Words: *Acinetobacter baumannii*, Stress Adaptation, Dairy Products, UTI

Introduction

Catastrophic sequels cascaded from contamination of the food chain in Baghdad by an emergent prohibited recalcitrant entity, well equipped with stress genes covered by a biofilm barrier. These genetically modified

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bacteria resident in the food chain with their mobile genetic elements as complex networks created and presented either from horizontal gene transfer via conjugated plasmids, foreign external DNA transformation and transduction prophages such as multi stress tolerant *Listeria monocytogenes* (1,2), methicillin resistant *Staphylococcus aureus* MRSA (3,4), vancomycin resistant *Enterococcus faecalis-faecium complex* (5,6), azoles resistant *Candida albicans* (7).

Acinetobacter baumannii, an ESKAPE chainsaw puzzle pathogen and emergent issue priority, A group of antibiotic-resistant bacteria that cause most nosocomial infections. A. *baumannii* is called "Iraqibacter" because it arose suddenly in Iraq War military treatment units. Veterans and soldiers from Iraq and Afghanistan still face it. Transporting sick soldiers between hospitals helps transmit multidrug-resistant A. *baumannii* to civilian hospitals. In the COVID-19 pandemic, multiple cases of SARS-CoV-2-A. *baumannii* coinfection have been reported (8–11).

Notorious broad-spectrum ability cascaded by genetic plasticity in learning, stress adaptation, developing and transferring resistance to diverse and versatile stimuli like antibiotics and cascaded prohibited chainsaw stressors like radiation, resident, deposited and displayed by genetically well-equipped *A. baumannii* as an emergent pandemic struggling. These superbugs can infect both man and animals causing difficulty in treatment like UTI, pneumonia, mastitis, etc. (12–15), An artificial intelligence (AI) deep learning machine could satisfy discovery of new combating antibiotics such as a shotgun “Abaucin” to fights struggling caused by prohiptrd bioterror targeted denominator *A. baumannii*(16).

Quorum sensing special topic targeted denominator *A. baumannii* associated with food chain and UTI cases in Baghdad sectors represent a challenge for us. Cascaded series of these torments including priority recovery of these emergent infectious agents cascaded and linked with MDR and ultraviolet irradiation tolerance behavior, then redirected by dynamic hygienic a termination processing with ecofriendly lytic bacteriophages cocktails.

Methodology

Sample Collection

Colloquially, randomized experimental design domain was dependent for scheduled collection and processing of samples units in which, six hundred and sixty-six (666) full samples units and their replicates were collected and categorized from scheduled experimentally built-in cascaded cross-sectional topic issue within specified timeline episodes. Segregation roadmap patterns were epidemiologically dependent for targeted denominator and scanned sector of Abu-Ghraib, Al-Fudhaliyah and Al-Sadrya in which, six hundred and thirty-six (636) randomly locally cascaded samples of Cows raw milk, fresh ropy versus curd sound yogurts, fresh soft versus brined cheeses, butters and creams brands. Five documented samples were collected monthly from each brand verified scanned sectors (Colloquially 35 units per sector and fully 105 units per month). Colloquially, segregation Eco-map of targeted Human urine samples of clinically UTI cases from both individuals’ genders (male and female) were collected as one sample from each

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gender per region per month to be colloquially six per month and fully thirty-six (36) per timelines episodes.

Processing of Samples

Segregated labeled pooled quantities of samples were collected via sterile disposable cups and hygienic durable plastic bags in which, population formulas as a half-liter versus 500 grams from each brand, transported freshly cooled preserved with ice box to workflow lab, mixed and homogenized well during accommodation directly with warm temperature in order to verify lipids sequestering hidden foci, or indirectly preserve under 4 C during processing proceeds. Colloquially, a representative unit from the fully homogenized original sample is double replicated in a volume of twenty ml or gram per each. These units were resuscitated indirectly via doubled strengthen powered an ATP dependent enriched tryptone soya yeast extract broth (TSBYE), vortexes well via Rotomixer upon incubation period at 37 C overnight. Modified verified dilution formulas were enrolled with or without 2 % buffered sodium citrate in case of soft cheese emulsifier, as one part sample to five- or ten-part decimal diluent TSBYE.

Bacterial Culturing and Identification

Culturing overnight inoculated units on surface of HiCrome *A. baumannii* agar via modified Cowan and Steel (17) identification formulas including buffering dilution culturing five droplets technique of Miles and Misra (18) with or without three lines swabbing procedure in which, each cascaded line from concentrated mixed decanted droplets (twenty microliter each for tenth ml whole) to titrated one represent approximately one valid log for each unit replicate. Synchronously, verified roll tube pour plate technique(19) was dependent for comparative metering's if facultative anaerobic respiration needed for resuscitation of sublethal targeted denominator. False positive cascaded by false negative results might reduce dramatically upon recovery dogmas.

Clinical UTI cases from human males versus females were tested by taken a urine sample by serial disposable cups as twenty ml, labeled and transported via ice box to lab, mixed well, then carefully cultured directly on *A. baumannii agar* and indirectly via resuscitation enriched TSBYE cascaded by selective and differential enrichment culturing on *A. baumannii* agar .Residence prevalence results of recovery scheme were scheduled later. Counting and calculating regimes cascaded concurrently with scanned units by equivocal procedures in which, a proximately, qualifications of semiconservative enumeration ecosystems oscillate between quantitative and qualitative built-in procedures in food microbiology. Counting of viable visible mass *A. baumannii* colonies or colloquially colony forming units per ml of original sample paraphrased as means Log counts ($CFU.ml^{-1}$ versus g^{-1}) reflect the nature and type conditions of microbial load either contamination or clinical infection or both. Decimal dilution a technique manually or automatically as with colony counters or biosensitive chips tensors probes represented in the known volume of a culture to verify and estimate its concentration in original one.

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A dose dependent curve was calculated for enrollment of modified verified adapted and improved dual decimal or logarithmic procedure reducing the aerobic and anaerobic environment for missing colonies and so counting errors. The mean log count of recovery of *A. baumannii* lineage-complex was dependent on colonial phenotypes variants like structures fingerprints and colonial biofilm behavior of isolates. The augmented reality of *A. baumannii* load log recovery titers calculated. Cascaded series of VITEK®2 Bifunctional visualized augmented GN automated BioMérieux Kit for laser dependent computerized biochemical segregation patterns (64a built-in reagents card ID series) (BIOMÉRIEUX) (20) and A 16s ribosomal RNA subunit dependent enrollment verify biodiversity of primed recovered *A. baumannii* isolates from dairy products and human origin (recovered from primed UTI positive patients) and adapted food chain ancestors. A phylogenetic interconnected genotypic relationship presents between Host Specific isolates and their linked ancestral tree. After amplification of the targeted special topic ribosomal RNA, we primed cascaded experimental methods, built in workflow analysis on sequences, and confirmed microorganism homogenic data using the rRNA database (NCBI).

Imaging Micrographs of *A. baumannii* with SEM Nano space scanning VEGA TESCAN built-in Electron Microscope (Nanotechnology center/University of Technology/Baghdad was presented and cascaded for imagine atomic scanning and viewing of ultrastructure's *A. baumannii* isolates recovered from cascaded chain of local dairy products and human UTI cases cascaded by biofilm ultrastructure (2,21–24).

Statistical Analysis

Built-in primordial statistical design dependent software of Statistical Analysis System- SAS (2018) program was used to detect the effect of difference factors in study parameters. Least significant difference –LSD test (Analysis of Variation-ANOVA) was used to significant compare between means. Chi-square test was used to significant compare between percentage (0.05 and 0.01 probability) for scan significance variations among data frequencies (percentages fitness and goodness).

Results and Discussion

Biostatistical integration was a predominant tool for deciphering and matching displayed calculated cascaded results series at confidence intervals 95 & 99 % in which, all observed results were analyzed by statistical analysis system (25) software program throughout interconnected values of significant and non or insignificant probability. Significant values mean significant clinical observed and calculated trials of experimental design and dissertation aim & objectives. Not always non or insignificant results means they were not important clinically or scientifically in accordance to pairs of null & alternative experimental hypothesis design but this dependent primarily on virulence indices cascaded by type of evolved isolate i.e., their genetic makeup in terms of genetically modified microorganisms as priority bioterrorism special topic issue within food chain with other interconnected predisposing factors and ecosystems in terms of zone of infection cascaded by episodes times intervals. In conclusions: Clinical observed trials were very important in spite of their statistical values were not significant in some situations.

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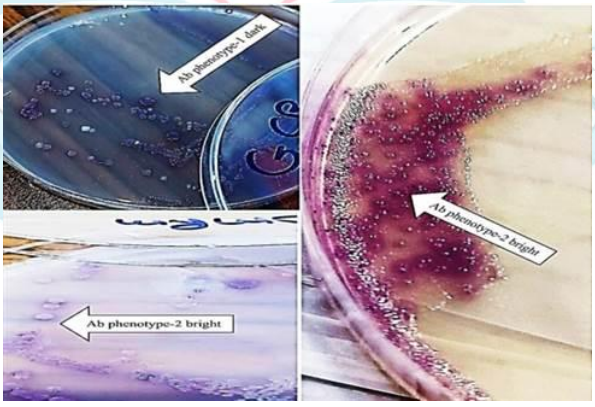
Emergent Risk Assessment Patterns illustrated and deciphered via an abnormal naturally and genetically modified to be resident and deposited within Iraqi environment with continuous stress adaptation and hardening. These emergent prohibited and biohazard *Acinetobacter baumannii* are genetically well-equipped foreign entity augmented to survive harsh environments with other infectious and contagious foci inside a recalcitrant barrier of biofilm to create an abnormal dangerous and sophisticated struggling entity with diverse and versatile, drift shift antigenic transformations ending with forbidden sequels. According to legendary futurist inventor and innovator Nikola Tesla and their researches in field of electromagnetic energy patterns constructions verification models with built-in prohibited sequels of negative energy and death irradiations oscillation poured by HARPA and DARPA projects for destroying every living thing and lifestyle changes, terminated with bioterrorism highly infectious agents' resident in food chain (26–31).

These emergent adapted multi-stress resistant entities to diverse antimicrobials antibiotics cascaded by irradiation tolerance behaviors (UVT) were encountered from dairy chain ecosystems inside Baghdad province with sequestered broad-spectrum genetic plasticity throughout cascaded Iraqi wars via infected and carrier USA solders to be resident and deposited within Iraqi environment as an emergent *A. baumannii* " figure1". These naturally and intentionally mutated entities to verified stressors had an ability and capacity to changes their genotypic contents from clinical phase to antigenic drift and shift food adapted contaminant phase with clever artificial intelligence behaviors in hiding and regulation virulence biomarkers. Modified mutated new progenies could be translated from generation timelines to cascaded brain like machines. Regulation of Quorum sensing networks behaviors with sigma factors via sophisticated cleaver strategies augmented by epigenetic drifted temporary tolerant transient phases cross environmental stimuli surrounding their genetic material to becomes persisters (32–37).



"Figure 1". Illustrate phenotypic colonies of A. baumannii as white purple circular convex surrounded by light purple zones on surface of Acinetobacter chrome agar adopted as phenotype-1 dark (left) & phenotype-2 bright (right)

These emergent entities were encountered in this special verified cross sectional topic torment from locally produced Cows dairy cascaded series prevalent inside Baghdad province. These investigated biohazard denominators dogmas were resident and deposited in frighteningly strange

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frequency and distribution growth patterns within randomly experimentally scanned sectors of Al-Sadrya, Abu-Ghraib and Al-Fudhaliyah. Verified scanned samples patterns with Ecomaps segregation categorized criteria including a built-in modified design for testing null cascaded alternative hypotheses about lunges cascades of seven predominant Iraqi dairy chain brands of raw milk, fresh ropy yogurts, curd soured yogurts, fresh soft cheeses, brined soft cheeses, butters, and creams; cascaded by associated cross linked cases of Human individuals infected and carriers (dairy workers & normal costumers) with urinary tract infections cases (UTI) (Table1-Table5) (1,4,7,23,38–41).

(Table 1). Distribution Patterns of PCR Primed Targeted Denominator MDR A. baumannii In Raw Milk Chain From Verified Districts Within Specified Episodes Cascaded By Recorded Mean Log Count (CFU.ml-1)

District	Sample	phenotypic MDR *A. baumannii*	16S rRNA PCR	distribution patterns of PCR primed denominator (630)%	Mean log count ($CFU.ml^{-1}$)
Abu-Ghraib	30	2 (6.66 %)**b**	1 (3.33 %)**b**	0.158**b**	2.62 ±0.07 **c**
Al-Fudhaliyah	30	2 (6.66 %)**b**	1 (3.33 %)**b**	0.158 **b**	2.93 ±0.13 **b**
Al-Sadrya	30	3 (10 %) **a**	2 (6.66 %)**a**	0.317 **a**	3.10 ±0.22 **a**
Total	90	7 (7.77 %)	**4 (4.44 %)**	**0.635**	2.88 ±0.08
Chi-Square: χ^2	---	**0.289 NS**	**0.506 NS**	---	**LSD= 0.371***
(P-value)		**(0.865)**	**(0.776)**		**P: (0.0427)**

Means with the different letters (a,b,c)in same column differed significantly at *(P≤0.05), Least significant difference –LSD test (Analysis of Variation-ANOVA) was used to significant compare between means.

(Table 2). Distribution Patterns of PCR Primed Targeted Denominator MDR A. baumannii In Yogurt Chain From Verified districts Within Specified Episodes Cascaded By Recorded Mean Log Count (CFU.ml-1)

District	Sample	phenotypic MDR *A. baumannii*	16S rRNA PCR	distribution patterns of PCR primed denominator (630 %)	Mean log count ($CFU.ml^{-1}$)
Abu-Ghraib	30	0	0	0	0
Al-Fudhaliyah	30	0	0	0	0
Al-Sadrya	30	2 (6.66 %)	2 (6.66 %)	0.317	1.1425 ±0.09
Total	90	2 (2.22 %)	**2 (6.66 %)**	**0.317**	**0.380 ±0.07**
Chi-Square: χ^2	---	**1.026 NS**	**1.026 NS**	---	---
(P-value)		**(0.109)**	**(0.109)**		

NS: Non-Significant, (Analysis of Variation-ANOVA) was used to significant compare between means.

(Table 3). Distribution Patterns of PCR Primed Targeted Denominator MDR A. baumannii In Cheese Chain From Verified districts Within Specified Episodes Cascaded By Recorded Mean Log Count (CFU.ml-1)

District	Sample	phenotypic MDR *A. baumannii*	16S rRNA PCR	distribution patterns of PCR primed denominator (630 %)	Mean log count ($CFU.ml^{-1}$)
Abu-Ghraib	30	6 (20 %) **b**	2 (6.66 %) **b**	0.317 **b**	3.539 ±0.25 **b**
Al-Fudhaliyah	30	6 (20 %) **b**	2 (6.66 %) **b**	0.317 **b**	3.710 ±0.31 **b**
Al-Sadrya	30	12 (40 %) **a**	6 (20 %) **a**	0.952 **a**	4.543 ±0.47 **a**
Total	90	24 (26.66 %)	**10 (11.11 %)**	**1.587**	**3.930 ±0.31**

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Chi-Square: χ^2	**---**	**3.032 NS**	**3.233 NS**	**---**	**LSD= 0.407 ***
(P-value)		**(0.219)**	**(0.198)**		**P: 0.0252**

Means with the different letters(a,b) in same column differed significantly at *(P≤0.05), NS: Non-Significant, Least significant difference –LSD test (Analysis of Variation-ANOVA) was used to significant compare between means.

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(Table 4). Distribution Patterns of PCR Primed Targeted Denominator MDR A. baumannii In Butter Chain From Verified Districts Within specified episodes cascaded by recorded mean log count (CFU.ml-1)

District	Sample	phenotypic MDR *A. baumannii*	16S rRNA PCR	distribution patterns of PCR primed denominator (630%)	Mean log count ($CFU.ml^{-1}$)
Abu-Ghraib	30	1 (3.33 %)	1 (3.33 %)	0.158	**1.531 ±0.03**
Al-Fudhaliyah	30	1 (3.33 %)	1 (3.33 %)	0.158	**1.778 ±0.04**
Al-Sadrya	30	1 (3.33 %)	1 (3.33 %)	0.158	1.832 ±0.04
Total	90	**3 (3.33 %)**	**3 (3.33 %)**	**0.476**	**1.713 ±0.03**
Chi-Square: χ^2	---	0.00 NS	0.00 NS	--	**LSD= 0.318**
(P-value)		(1.00)	(1.00)		**NS P: 0.096**

NS: Non-Significant at (P≤0.05), Least significant difference –LSD test (Analysis of Variation-ANOVA) was used to significant compare between means.

(Table 5). Distribution Patterns of PCR Primed Targeted Denominator MDR A. baumannii In Cream Chain From Verified Districts Within specified episodes cascaded by recorded mean log count (CFU.ml-1)

District	Sample	phenotypic MDR *A. baumannii*	16S rRNA PCR	distribution patterns of PCR primed denominator (630 %)	Mean log count ($CFU.ml^{-1}$)
Abu-Ghraib	30	5 (16.66 %)	2 (6.66 %)	0.317	4.414 ±0.25
Al-Fudhaliyah	30	4 (13.33 %)	2 (6.66 %)	0.317	4.380 ±0.30
Al-Sadrya	30	9 (30 %)	4 (13.33 %)	0.634	4.146 ±0.39
Total	90	18 (20 %)	**8 (8.88 %)**	**1.269**	**4.313 ±0.28**
Chi-Square: χ^2	---	**2.358 NS**	**1.010 NS**	0.317	**0.389 NS**
(P-value)		**(0.307)**	**(0.603)**		**(0.216)**

NS: Non-Significant, Analysis of Variation-ANOVA was used to significant compare between means. Chi-square test was used to significant compare between percentage .

Similarity index patterns of *A. baumannii* versus recorded upstairs foodborne Zoonotic reverse zoonotic transmissible pathogens cascaded by UTI cases series were recorded inside Iraqi ecosystems (Table 6).

(Table 6). Distribution Patterns of PCR Primed Targeted Denominator MDR A. baumannii In Human UTI cases From Verified Districts Within specified episodes cascaded by recorded mean log count (CFU.ml-1)

District	Gender		Phenotypic MDR *A. baumannii*			16S rRNA PCR			Mean log count ($CFU.ml^{-1}$)
	M (6)	F (6)	M	F	All	M	F	All	
Abu-Ghraib	12		N	2	2 (16.66%)**a**	N	1	1 (8.33%)**a**	0.845 ±0.14**b**
Al-Fudhaliyah	12		N	2	2 (16.66%)**a**	N	1	1 (8.33%)**a**	0.778 ±0.11 **b**
Al-Sadrya	12		2	2	4 (33.33%)**b**	1	1	2 (16.66%)**b**	1.23 ±0.19 **a**
Total	36		2	6	8 (22.22 %)	**1**	**3**	**4 (11.11 %)**	**0.951 ±0.15**
Chi-Square: χ^2	---		-	-	**1.010 NS**	-	--	**0.505 NS**	**0.310 ***
(P-value)			-	-	**(0.603)**	-		**(0.776)**	**(0.415)**

Means with the different letters(a,b) in same column differed significantly at *(P≤0.05), NS: Non-Significant, (Analysis of Variation-ANOVA) was used to significant compare between means. Chi-square test was used to significant compare between percentage

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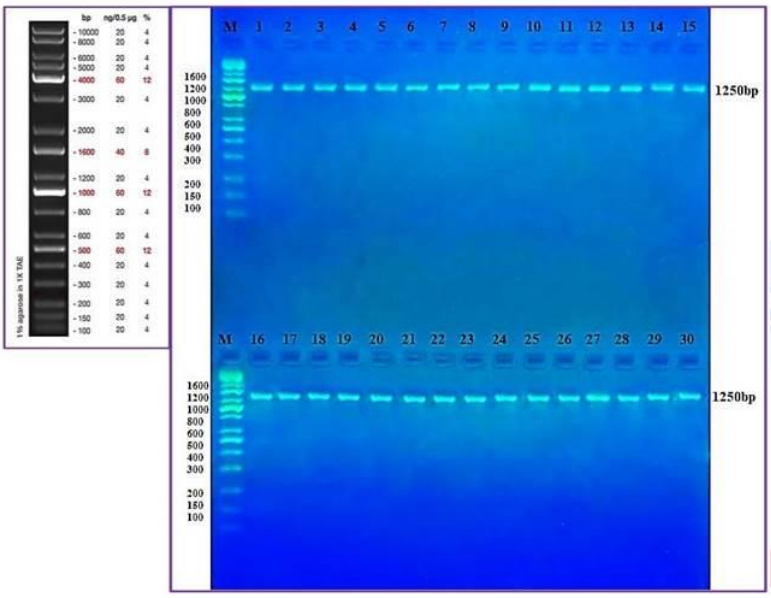
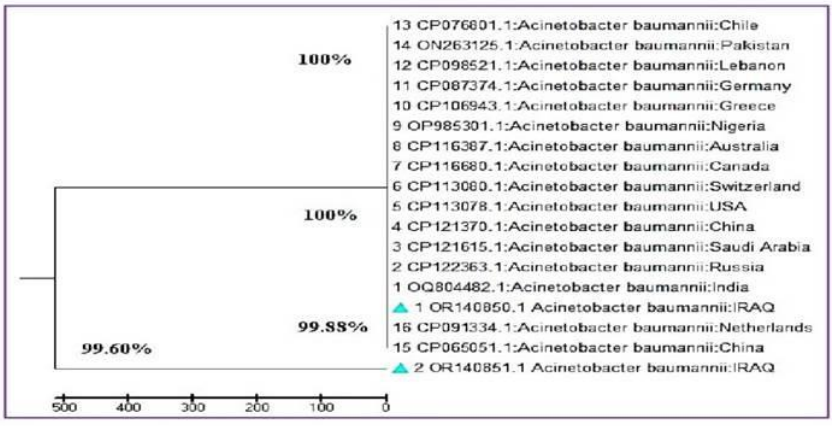
Recovery and Segregation Documentary Records Deciphered Eco-maps segregation incidence frequency and distribution patterns of targeted special topic denominator *A. baumannii* from locally dairy ecosystems in Baghdad within specified timelines episodes unveiled phenotypic isolation, biochemical segregation and 16S rRNA PCR confirmation of twenty-seven (27: 4.285 %) out of colloquy sixty and thirty-six (636) dairy samples units from Baghdad "figure2".



"Figure 2". 16s rRNA PCR fingerprint alignments bands of *Acinetobacter baumannii*. PCR amplification and PAGE analyzed genomic proteins bands of targeted denominator isolates. Results of the amplification of 16s rRNA gene for identified *A. baumannii* were fractionat

Phylogenetic Tree (UPGMA Clustering Index)

Phylogenetic trees are branching diagrams illustrating the evolutionary relationships among species. Usually, such trees are constructed based on sequence similarity between the highly conserved 16S rRNA genes or a set of housekeeping genes of several organisms. It is highly desirable to use all genes of the core genome as input for the tree calculation, which dramatically increases its reliability "figure3" (42)



"Figure 3". Phylogenetic tree, The evolutionary history was inferred using the UPGMA method (the isolate used in the current study labeled with light blue color)

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Sequence ID

PCR product were sent for Sanger sequencing using ABI3730XL, automated DNA sequences, by Macrogen Corporation – Korea.."Deciphered FASTA codes for each sample ecosystem within NCBI BLASTN authenticated with online certificate of identity (Table7 and Table8)

(Table 7). Illustrate and decipher 16s rRNA of Zainab A. baumannii recovered isolates from local dairy chain as (1) and Human UTI cases as (2) with ID accessions numbers and queries matching genetic sequence analyzed within NCBI databases cascaded by alignments

16S ribosomal RNA gene						
Type of subst-itution	Location	Nucleotide	Sequence ID with compare	Sequence ID with submission	Source	Identities
Dairy Series	Baghdad	dNTPs	ID: OQ804482.1	ID: OR140850.1	A.baumannii	100%
UTI	Baghdad	dNTPs	ID: OQ804482.1	ID: OR140851.1	A.baumannii	100%

(Table 8). Illustrate accessions numbers similarity genetic sequences of isolates according to UPGMA with other worldwide isolates. Local isolates were closer similar in coordinate cascaded patterns to India, Russia, Saudi Arabia, China, USA, Switzerland, Canad

	Accession	Country	Source	Compatibility
1	ID: OQ804482.1	India	----------	100%
2	ID: CP122363.1	Russia	Homo sapiens	100%
3	ID: CP121615.1	Saudi Arabia	Homo sapiens	100%
4	ID: CP121370.1	China	wastewater	100%
5	ID: CP113078.1	USA	Homo sapiens	100%
6	ID: CP113080.1	Switzerland	----------	100%
7	ID: CP116680.1	Canada	Homo sapiens	100%
8	ID: CP116387.1	Australia	----------	100%
9	ID: OP985301.1	Nigeria	Homo sapiens	100%
10	ID: CP106943.1	Greece	----------	100%
11	ID: CP087374.1	Germany	Homo sapiens	100%
12	ID: CP098521.1	Lebanon	----------	100%
13	ID: CP076801.1	Chile	----------	100%
14	ID: ON263125.1	Pakistan	----------	100%
15	ID: CP065051.1	China	Homo sapiens	99%
16	ID: CP091334.1	Netherlands	----------	99%

The targeted denominator was predominant and resident with subnormal cascaded levels in all tested brands collected from Al-Sadrya sector. Yogurts brands were hygienic not contaminated nor infected with A. baumannii (not recorded) in other cross sectional scanned territories of Abu-Ghraib and Al-Fudhaliyah. Fifteen isolates (15: 7.14 %) were PCR primed & confirmed from Al-Sadrya cascaded by six isolates (6: 2.85 %) from Abu-Ghraib and six isolates (6: 2.85 %) from Al-Fudhaliyah. Colloquially, not all documented and recorded phenotypic isolates (54: 8.571 %) via

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chrome agar cascaded by VITEK2 “Figure2” bio-informative chips were qualitatively confirmed via PCR due to complex genetic nature of foreign clonal isolates as well as verified antigenic variation of modified genetic makeup of targeted denominator resident & deposited with broad-spectrum transformation of genes sharing predicted alternatives within examined food chains (adding, deleting, reassortment genes within and outside biofilm) and Urinary tract infection patients.

ASCo

bioMérieux Customer:
System #:
Patient Name: Zainab Hazim, 1
Isolate: 82-1 (Approved)
Card Type: GN Bar Code: 241180710335480 7 Testing Instrument: 0000148FF939 (8538)
Setup Technologist: Laboratory Administrator(Labadmin)

Laboratory Report

Printed by: Labadmin
Patient ID: 82

Bionumber: 6727731553537673
Organism Quantity:

Selected Organism: Acinetobacter baumannii

Comments:	

Identification Information	**Card:**	GN	**Lot Number:**	2411807103	**Expires:**	Nov 7, 2022 12:00 CST
	Status:	Final	**Analysis Time:**	7.77 hours	**Completed:**	Apr 5, 2022 19:11 CDT
Organism Origin	VITEK 2					
Selected Organism	95% Probability		**Acinetobacter baumannii**			
	Bionumber: 6727731553537673			Confidence: Very Good identification		

Analysis Organisms and Tests to Separate:

Analysis Messages:

Contraindicating Typical Biopattern(s)
Acinetobacter baumannii

Biochemical Details

2	APPA	-	3	ADO	+	4	PyrA	+	5	lARL	+	7	dCEL	+	9	BGAL	+
10	H2S	-	11	BNAG	+	12	AGLTp	-	13	dGLU	+	14	GGT	+	15	OFF	+
17	BGLU	+	18	dMAL	+	19	dMAN	+	20	dMNE	+	21	BXYL	+	22	BAlap	-
23	ProA	+	26	LIP	-	27	PLE	-	29	TyrA	+	31	URE	-	32	dSOR	+
33	SAC	+	34	dTAG	-	35	dTRE	+	36	CIT	+	37	MNT	+	39	5KG	-
40	lLATk	+	41	AGLU	-	42	SUCT	+	43	NAGA	+	44	AGAL	+	45	PHOS	-
46	GlyA	+	47	ODC	+	48	LDC	+	53	lHISa	+	56	CMT	+	57	BGUR	+
58	O129R	+	59	GGAA	+	61	lMLTa	+	62	ELLM	(+)	64	lLATa	+			

(Figure 4). Biochemical ID certificate of A. baumannii via VITEK2 Adopted from ASCO center (Harthiya, Baghdad)

Predicted recovery of targeted denominator from linked associated cases of human UTI (both genders) unveiled opportunistic nature of *A. baumannii* as four isolates (4: 11.11 %) predominant in females out of thirty-six (36) collected urine samples from workers and normal consumers individuals within specified timelines episodes. Unacceptable contaminations log levels of targeted clinical isolates of prohibited denominator were documented and recorded in which, one detected CFU per ml or gm. in food chain considered a notifiable emergency must be carefully isolated as banded region until HACCP policy guided government call for hygienic biosafe termination. Cascaded split-split and decipher these interconnected events certificated by scanning electron micrographs (SEM) “Figurt3”, VITEK®2 and 16S rRNA PCR.

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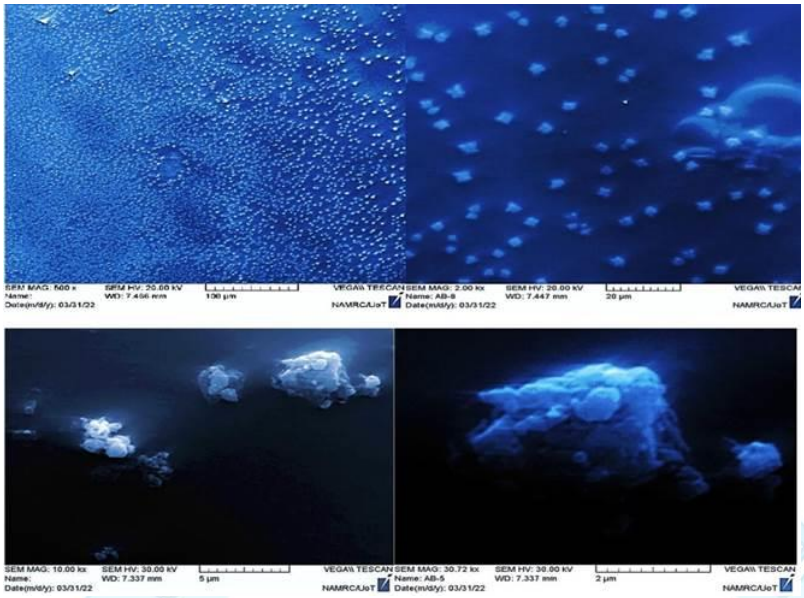

"Figure 5". Electron scanning micrographs of A. baumannii as sea stars like cocci adopted from Nanotechnology center/ University of Technology/ Baghdad.

In Conclusions:

Stress adaptation cascaded by stress hardening was evident in recovered contaminant *Acinetobacter baumannii* from local dairy chain and associated workers infected and carriers with UTI cases in Baghdad with an emergent and biohazard mutant entities in food chain.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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