RESEARCH / INVESTIGACIÓN

Determination of the prevalence of *blaoxa-like* gene and IS*Aba*1 elements among extensive-drug resistant (XDR) *Acinetobacter boumannii* isolates

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Abstract: The capacity of Multi-drug resistant (MDR) *Acinetobacter baumannii* to survive in any state of affairs concerning the gaining of various gene types of virulence and antimicrobial agent resistance are the main anxiety in the hospital's environments. So, it is very crucial to determine the prevalence of insertion sequences in *A. baumannii* in the hospitals. Detecting the *blaoxa-51* gene through the polymerase chain reaction (PCR) was performed to confirm Acinetobacter baumannii and the search for IS*Aba*1 element. Between October 2020 and February 2021, 540 distinct clinical specimens were gathered from five hospitals in Baghdad. Thirty-eight *A. baumannii* isolates were obtained from various clinical specimens. The isolates were initially identified phenotypically using standard microbiological techniques and by the Vitek2 compact automated machine. Isolates of *A. baumannii* were identified genotypically by amplification of the *blaoxa-51-like* gene. Antimicrobials are studied by Kirby-Bauer (disc diffusion) technique on Muller-Hinton agar as specified by the recent clinical and laboratory standard institute (CLSI) guidelines (2020). The actual results of the current study indicated that from total isolated (38) *A.baumannii* isolates, 23 isolates (61%) were resistant to meropenem and 25 isolates (66%) were resistant to imipenem. The *blaoxa-51* gene was identified in all strains examined, IS*Aba*1 was also present in all *A. baumannii* isolates. IS*Aba*1 has a high predominance between drug-resistant *A. baumannii.* Identifying these parameters can assist in the control of infection and decreasing the microorganism's prevalence rate.

Key words: Insertion sequence, The *blaoxa-51-like* gene, *Acinetobacter baumannii.*

Introduction

An opportunistic infectious agent, *A.baumannii* encompasses a high rate of occurrence among immunocompromised people, significantly those that have experienced long (more than ninety days) hospital residence[1]. Commonly related to aquatic environments[2]. It's been recognized as a "red alert" human infectious agent in recent years, causing concern among medical professionals, owing to its extensive spectrum of antibiotic resistance[3].

The development of multidrug-resistant (MDR) pathogens has more and more become a cause for profound importance concerning each healthcare facility and community-acquired infections[4]. According to the World Health Organization (WHO), Antimicrobial resistance has recently been recognized in concert as one of the 3 most vital issues facing human health[5]. The therapeutic selections are restricted, typically leading to unsuitable medical care and resulting negative consequences on patient[6].

The primary antibiotic resistance mechanisms are enzymatic (production of β-lactamases and enzymatic modification of aminoglycosides) and non-enzymatic (changing membrane permeability, activating efflux pumps) and altering of the target site)[7].

Insertion sequences (IS) are among the most basic mobile genetic elements (MGEs) and are found across the animal kingdom. To present, more than 4500 IS from 29 families have been discovered[8,9]. In Acinetobacter spp., more than thirty different types of Insertion Sequences have been discovered, suggesting that ISs had a significant role in developing this species and contributing to the multidrug-resistant phenotype shown in this genus[10].

Insertion elements have two distinct characteristics: short transposable elements (up to 2500bp) and only code for proteins involved in transposition[11].

In *A. baumannii*, IS*Aba*1 has been found in conjunction with numerous antibiotic resistance genes[12]. IS*Aba*1 has been shown to function in the expression of the *Bla* ampC gene, the antibiotic resistance gene of *A. baumannii*, which encodes the naturally occurring cephalosporins enzyme, and the blaOXA-23 gene, which encodes a carbapenem-degrading oxacillinase. Nevertheless, it could also act in the case of other resistance genes[13,14]. A composite transposon (defined as Tn2006) formed by two copies of IS*Aba*1 bracketing this β-lactamase gene, responsible for the movement of blaOXA-23[15].

IS*Aba*1 has been found to regulate the expression of the *bla* ampC gene, which encodes the naturally occurring cephalosporins enzyme, and the *blaOXA*-23 gene, which encodes a carbapenem-hydrolyzing oxacillinase enzyme. However, it may also play a role in the development of additional resistance genes. IS*Aba*1 has been demonstrated to produce carbapenem resistance in *A. baumannii* by causing overexpression of the naturally existing *blaoxa-51-like* gene[16].

The expression of the *blaOXA*-23 gene has been linked to IS*Aba*1 and IS*Aba*4[15,17]. The expression of the *blaOXA*-58 gene has been related to the insertion sequences *ISAba1*, *ISAba2*, *ISAba3*, and *IS18*[18]. Therefore, determining the prevalence of insertion sequences genes in A. baumannii in hospitals is very crucial.

Materials

Specimens' collection

Between October 2020 and February 2021, 540 distinct clinical specimens were collected from five hospitals in Baghdad, including The Burns Hospital, Gazi Al-Hariri Hospital, Baghdad Teaching Hospital, Welfare Teaching Hospital in the Medical City, and Al-Yarmouk teaching hospital. Collected

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specimens were sputum, blood, fluids such as (cerebrospinal, pleural, and peritoneal), urine, and swabs.

Isolation of Bacteria

In the laboratory (Teaching Laboratories/Medical City, Baghdad) under aseptic conditions, the collected specimens were cultured directly on MacConkey agar and blood agar, incubated for 24 hrs. at 37ºC. The colonies were non-hemolytic opaque creamy on blood agar, while on MacConkey agar were non-lactose fermenting colonies. For obtaining pure, well-isolated colonies, they were subcultured on another MacConkey agar plate and incubated for another 24 hrs. at 37ºC[19].

Bacterial Identification

Microscopical examination

One isolated colony was transferred to a microscopic slide, fixed then stained with Gram stain (GS). Gram reaction, cell shape, and arrangement were recorded. The results were compared with Brooks *et al.*(2013)[20].

Biochemical tests

To phenotypically identify the isolates as A. baumannii, biochemical tests such as the ability to grow at 42°C, culture on selective medium, negative for oxidase test, absence of lactose fermentation, and others were utilized.

Identification of *Acinetobacter baumannii* using VITEK® 2 system.

As stated by the manufacturer's instructions, identification cards of Gram-Negative Bacteria (ID-GNB) were used on the VITEK® 2 system to recognize isolates at the species level. The bacterial isolates were inoculated at 37°C on MacConkey agar plates and, after incubated overnight, taken a single colony then suspended. In 0.45 % sodium chloride, the turbidity measurement for the bacterial suspension to meet the McFarland (0.5) standards, The (Gram-Negative Vitek 2 Identity card) then was manually placed into the Vitek-2 system, along with the bacterial suspension tub, the software also prepared according to (BioMerieux, France) the manufacturer's instructions[21].

Identification of *A.baumannii* by PCR

Using a primer specific for *bla OXA51-like* genes, PCR was utilized to amplify *bla OXA51-like* genes used for *A. baumannii* isolate recognition.

Test of antimicrobial susceptibility profile

According to the latest clinical and laboratory standard institute (CLSI) criteria (2020), the isolates were tested for antimicrobial susceptibility to 18 antimocrobial agents using the Kirby-Bauer disc diffusion technique on Muller-Hinton agar (Oxoid /England)[22]. The antibiotic discs (Mast Group /UK) used throughout the study for *A.baumannii* isolates are Piperacillin-Tazobactam (100/10 µg/disc), Ampicillin-sulbactam (13/10 µg/disc), Ticarcillin-Clavulanate (55/13 µg/disc), Cefepime(33 µg/disc), Cefotaxime (33 µg/disc), Ceftazidime (33 µg/disc), Ceftriaxone (33 µg/disc), Imipenem (13 µg/disc), Meropenem (13 µg/disc), Colistin sulphate (25 µg/disc), Tobramycin (13 µg/disc), Gentamicin (13 µg/disc), Amikacin (33 µg/disc), Doxycycline(30 µg/disc), Tetracyclin (30 µg/disc), Ciprofloxacin (5µg/disc), Levofloxacin (5µg/disc) and Trimethoprime-Sulphamethoxazole(1.25/ 23.55 µg/disc).

Genomic DNA extraction from bacterial isolates

Extraction of bacterial DNA from isolates under study using a commercial Extraction system (ZR Fungal/Bacterial DNA Miniprep Kit) designed to isolate DNA from Gram-negative bacteria according to the manufacturer's instructions. For each reaction, a totally of 4 µl of extracted DNA was used.

Molecular recognition of *BlaOXA-51-like* gene and Insertion sequence elements

To detect XDR A.baumannii isolates, PCR was used to detect the *Bla-OXA-51-like* gene and IS*Aba*1 elements. Primer sequences for each gene reported above are listed in table (1). These primers (Macrogen, South Korea) were received in a lyophilized state, dissolved in sterile deionized distilled water

Primer	The sequence of primers (5' ---3')	Product size	Accession number
OXA51	CTTTTTGGCTAAATGGAAGCG	434	CP081137.1
OXA51	CGGGTGTCTTAGTTATCCAAC		
ISAba1 F	CACGAATGCAGAAGTTG	549	CP029569.1
ISAba1	CGACGAATACTATGACAC		

Table 1. Sequences of primers used throughout the study.

Steps	OXA-51	*ISAba1*	Repeats
Activation	94°C/5min	94°C/5min	1 cycle
Denaturation	94°C/45s	94°C/45s	40 cycles
Annealing	56°C	50°C	
Extension	72°C/45s	72°C/45s	
Final extension	72°C/7min	72°C/7min	-

Table 2. Programs were used in the PCR for *OXA-51-like* gene and IS*Aba*1 element.

to a final concentration of 100 picomole/µl, and kept in a deep freezer until use, as advised by the vendor.

The PCR amplification procedure for the genetic level to detecting genes under study by follows steps: Final volume for PCR mixture was 25 µl (12.5 of Green Master Mix 2x, 4 µl extracted template DNA, 1.5 µl from each forward and reverse primer, 5.5 µl nuclease-free water were added in 0.2 ml PCR Eppendorf tubes, mixed for a short time via vortex then been loaded to Veriti™ 96-Well (applied biosystems) Thermal Cycler. The program used for each monoplex PCR reaction was set according to each primer. The best annealing temperature was chosen after the gradient runs through the optimization process of each oligonucleotide primer.

For amplification of the *Bla-OXA-51-like* gene, the DNA thermal cycler device Veriti™ 96-Well (applied biosystems) was programmed in the following amplification conditions: Following a 5-minute activation at 94°C, 40 cycles of 45 seconds at 94°C (denaturation), 56°C (annealing), and 45 seconds at 72°C (extension) were conducted. In contrary to other genes, the IS*Aba*1 annealing temperature was 50°C. The last cycle was followed by 7 minutes at 72°C (Table 2). Amplified PCR products were examined on 1.5% agarose gel at an electrical current of 7 volt\cm2 in 1X TBE buffer with added Red safe dye (INTRON) has been exposed till the tincture had reached the other side of the gel. The SiZer™-1000 Plus DNA Marker and SiZer™-100 DNA Marker (Intron / Korea) were used as markers during PCR products electrophoresis. After that, the agarose gel was removed from the tank and visualized by a UV transilluminator documentation system (Cleaver scientific /UK) at 336 nm, then photographed using a digital camera.

Sequencing was carried out by Macrogen DNA Sequencing (Seoul, Korea) using 3730xl DNA Analyzer (Applied Biosystems™, Foster City, CA). Two samples from IS*Aba*1 PCR products with forwarding primer (17 pmol/ µl) for each gene were selected and sent to sequencing. Raw reads generated in this study were trimmed or filtered to remove low-quality sequences using (SnapGene software). Once sequencing reads had been obtained, the data analysis process was started, the Basic Local Alignment Search Tool (BLAST) of the National Center for Biotechnology Information (NCBI) was used to analyze DNA sequences and do similarity searches.

Results

540 clinical specimens were collected between October 2020 and February 2021 from some hospitals in Baghdad, including Baghdad medical city and Al-Yarmouk hospitals. Thirty-eight bacterial isolates were obtained, which differentiated to *A.baumannii*. Following conventional identification techniques, antimicrobial sensitivity testing was carried out by examining the findings in (Figure 1), revealing a high degree of resistance of *A.baumannii* clinical isolates to the majority of the antimicrobial agents under test.

In this study, antibiotic resistance profile of *Acinetobacter baumannii* for 18 antibiotics as following: Trimethoprime/sulphamethoxazole 32 (84%), Ciprofloxacin 27 (71%), Piperacillin/tazobactam 26(68%), Ticarcillin/clavulanate 26 (68%),Ceftazidime 26(68%), Ceftriaxone26(68%), Cefotaxime 25 (66%), Imipenem 25(66%), Doxycycline 26(68%), Levofloxacin 25 (66%),Cefepime 24(63%),Tetracycline 24(63%), Meropenem 23(61%), Gentamicin 22 (58%), Tobramycin 15(39%), Amikacin 17(45%), Ampicillin/sulbactam 12 (32%), Colistin 0(0%). The exact and important results of current study indicated that from total isolated (38) *A.baumannii isolates*, 23 isolates (61%) and 25 isolates (66%) were resistant to meropenem and imipenem respectively.

All the *A. baumannii* isolates were positive for *blaoxa-51-like* genes and IS*Aba*1 genes. Figures 1 and 2 demonstrate agarose gel electrophoresis of PCR products of blaoxa-51-like genes and ISAba1 elements, respectively.

The sequence was analyzed by BLAST software at NCBI. Figure (4) shows the alignment result with the USA: San Diego isolates (Accession number CP053098.1). The sequence was found to share 99% nucleotide homology with the reference isolates. Tables 3 and 4 show nucleotide changes and Features of IS*Aba*1(Forward) from *Acinetobacter baumannii* (X9 isolate) with *Acinetobacter baumannii* ATCC 17978 chromosome from the USA: San Diego.

The sequence was analyzed by BLAST software at NCBI. Figure (4) shows the alignment result with USA: San Diego isolates (Accession number CP050388.1). The sequence was found to share 99% nucleotide homology with the reference isolates. Tables 5 and 6 show the nucleotide changes and features of IS*Aba*1(Forward) from *Acinetobacter baumannii* (X10 isolate) with *Acinetobacter baumannii* strain VB473 chromosome from India.

Discussion

A. baumannii has developed as a well-established nosocomial pathogen with a high level of antibiotic resistance. Various medical facilities frequently report extensively drug-resistant, and pan drug-resistant isolates[23]. By 2007, up to 70% of isolates in specific locations had evolved multidrug resistance, particularly resistance to carbapenems, which were formerly thought to be the gold standard for treating MDR *A. baumannii* infections[24].

The antibiotic of choice for treating *A. baumannii* is carbapenems. Due to rising resistance rates, *A. baumannii* infections are becoming increasingly ineffectual. Resistance to the newer antibiotic tigecycline is also quickly developing. Colistin, a previously abandoned antibiotic, is now used as a last option, yet resistance to this medication is increasing at an alarming pace throughout the world[23].

Aside from its proclivity for the critically ill in intensive care units, *A. baumannii* has lately been linked to a slew of infectious diseases among military troops injured in the Iraq and Afghanistan wars[4].

Resistance of Carbapenem is frequently connected to the making of oxacillinase enzymes. Metallo β-lactamases (MBL), on the other hand, can cause carbapenem resistance in *A. baumannii*[25].

The actual results of the current study indicated that of 38 *A.baumannii* isolates, 23 isolates (61%) and 25 isolates (66%) were resistant to meropenem and imipenem, respectively. The antibiotic resistance results of imipenem and meropenem are less than that found by al Al-Saadi (2018)[26]. From 162 *A.baumannii* isolates, 112 isolates (88.19%) and 107 (84.25%) were resistant to meropenem and imipenem, respectively. Prior investigators in Iran found that the resistance rates to imipenem and meropenem were (95.23%) and (98.09%) respectively[27], indicating that these bacteria have a wide range of resistance mechanisms. This would imply significant risks among hospitalized patients, mainly where this antibiotic class was previously considered the standard therapy for *A.baumannii* infections[28].

The recognition of the *Bla OXA-51-like* gene can be utilized to identify *A.baumannii* reliably and straightforwardly[29,30].

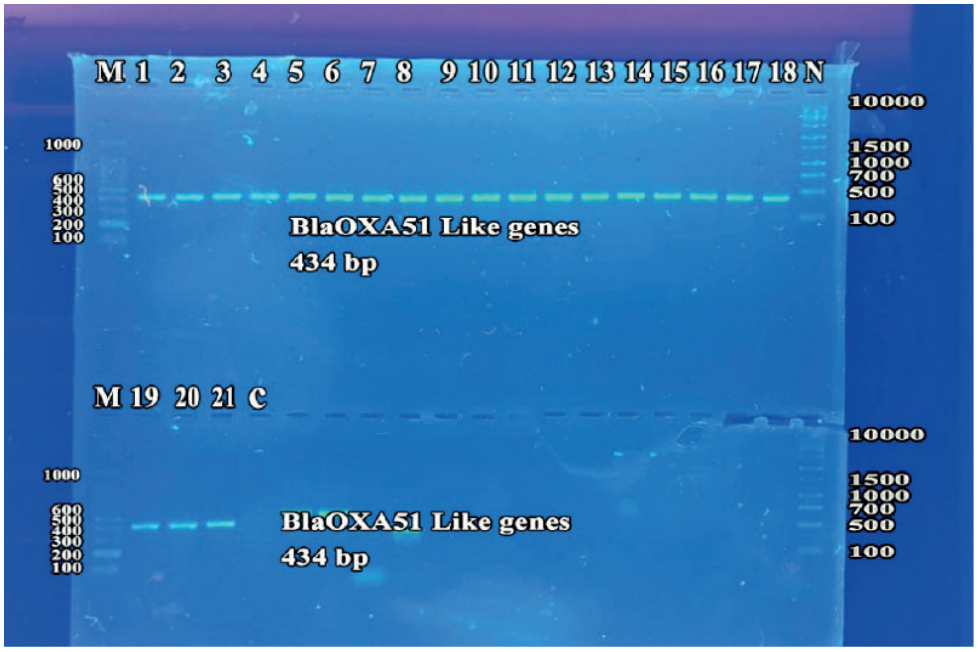

Figure 1. Detection of *bla*OXA51 like gene by monoplex PCR for *A.baumannii* isolates. lanes 1-21, XDR *A.baumannii*; Lane C, Negative control. Lane M, 100 bp DNA marker. Lane N, 1000 bp plus DNA marker. Detection was done on agarose gel (1.5%) at 5 Volt/cm for 1.5 hours, stained by Red Safe dye, and imagined on a UV transilluminator documentation system.

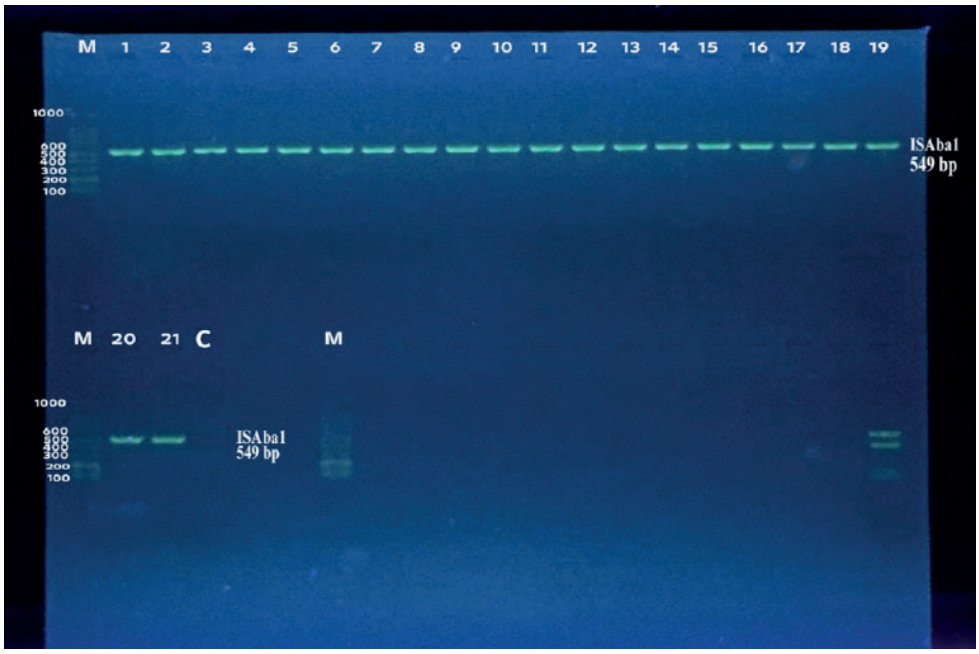

Figure 2. Detection of IS*Aba*1 gene by monoplex PCR of isolates. Lanes 1-21: XDR *A.baumannii* isolates. Lane C: Negative control. Lane M: 100 bp DNA marker. Detection was done on agarose gel (1.5%) at 5 Volt/cm for 1.5 hours, stained by Red Safe dye, and imagined on a UV transilluminator documentation system.

Furthermore, because this gene was controlled by insertion sequences such as IS*Aba*1, the presence of intrinsic chromosomally placed genes of the *bla OXA-51-like* gene did not correlate with the amount of carbapenem resistance of A.baumannii isolates[31].

Additionally, all isolates of *A.baumannii* carried the *Bla OXA-51-like* gene and attributed the imipenem resistance state to the presence of IS*Aba*1 upstream of the *blaoxa-51-like gene* serves as a promoter for gene expression as one of these isolates' resistance methods[32,33].

From 21 XDR *A. baumannii* isolates all have *blaoxa-51 like* genes. This corroborated those of previous local investigations[26,34,35].

A study in Egypt revealed that genes encoding *blaoxa-51* (belonging to class D carbapenemases) were found in 100% of the studied isolates[36]. According to research by Bahador et al., all 62 CRAB isolates tested positive for *blaoxa-51-like* genes[37].

The present data could affirm that all *A.baumannii* isolates were positive for the IS*Aba*1 gene. It was found that the prevalence of IS*Aba*1 was 100%[27,36]. IS*Aba*1 was the most common insertion element (90.6%)[38]. The prevalence of IS*Aba*1 is equal to that seen in 59 Spanish isolates (93.2%)[39]. While Taiwan (36%)[40] and India (33%)[41] have lower prevalence rates than the rest of the world. The presence of various insertion sequences in *A. baumannii* makes it resistant to carbapenems[42].

These insertion sequences are found near genes that code

Gene: *ISAba1*(Forward) from *A.baumannii*(X9 isolate)						
No.	**Type of substitution**	**Location**	**Nucleotide**	**Sequence ID with compare**	**Source**	**Identities**
1	Deletion	52	-/**A**	**CP053098.1**	***Acinetobacter baumannii***	**99%**

Table 3. Nucleotide changes of ISAba1(Forward) from *Acinetobacter baumannii* (X9 isolate) with *Acinetobacter baumannii* ATCC 17978 chromosome from the USA: San Diego.

Feature	Studied isolate	Reference isolate
Molecule Type	Genomic DNA	Genomic DNA
Isolation Source	Swab	Fatal meningitis
Host	Homo Sapiens	Homo Sapiens
Country	Iraq, Baghdad	USA: San Diego

Table 4. ISAba1(Forward) features from *Acinetobacter baumannii* (X9 isolate) with *Acinetobacter baumannii* ATCC 17978 chromosome from the USA: San Diego.

Gene: *ISAba1*(Forward) from *A.baumannii*(X10 isolate)						
No.	**Type of substitution**	**Location**	**Nucleotide**	**Sequence ID with compare**	**Source**	**Identities**
1	Deletion	83	-/**A**	CP050388.1	*Acinetobacter baumannii*	**99%**
	Deletion	85	-/**A**			

Table 5. Nucleotide changes of IS*Aba*1(Forward) from *Acinetobacter baumannii* (X10 isolate) with *Acinetobacter baumannii* strain VB473 chromosome from India.

Feature	Studied Isolate	Reference Isolate
Molecule Type	Genomic DNA	Genomic DNA
Isolation Source	Swab	Sputum
Host	Homo Sapiens	Homo Sapiens
Country	Iraq, Baghdad	India

Table 6. Features of IS*Aba*1(Forward) from *Acinetobacter baumannii* (X10 isolate) with *Acinetobacter baumannii* strain VB473 chromosome from India.

for several OXA-type carbapenemases and are implicated in their overexpression[13].

Conclusions

In conclusion, *A. baumannii* is a significant pathogen in several nations. According to the findings of this study, it has a high resistance rate against most antibiotics, threatening in patients as a red alarm bacterium in hospitals, producing a high rate of death and morbidity due to its numerous mechanisms of resistance and the fact that it is not or only rarely treated with conventional antibiotics.

This bacterium can cause dangerous and long-term infections, especially in youngsters and people with immunological deficiencies. Our research focused on specific mobile components transported between species to change the antimicrobial pattern and enhance antimicrobial resistance. IS*Aba*1 has a high prevalence among extreme drug-resistant *A. baumannii* isolated from several Baghdad hospitals. Identifying these parameters can aid in controlling infection and reducing the microorganism's prevalence rate.

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Acinetobacter baumannii ATCC 17978 chromosome, complete genome Sequence
ID: CP053098.1Length: 4005343Number of Matches: 1
Range 1: 3737775 to 3738256

Score	Expect	Identities	Gaps	Strand
883 bits(478)	0.0	481/482(99%)	1/482(0%)	Plus/Minus

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Query  2        CTCTGTCTGCGAACACATTCACAATACGGTCTTTACCAAAAATGGCTATAA-GCGTTGAA  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  3738256  CTCTGTCTGCGAACACATTCACAATACGGTCTTTACCAAAAATGGCTATAAAGCGTTGAA  3738197

Query  61       TCAAAGCAATACGCTCTTTCGTATCTGAATTTCCACGTTTATTAAGCAATGTCCAAAGGA  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3738196  TCAAAGCAATACGCTCTTTCGTATCTGAATTTCCACGTTTATTAAGCAATGTCCAAAGGA  3738137

Query  121      TAGGTATCGCTATTCCACGATAAACGATTGCGAGCATCAGGATATTAATATTTCGTTTTC  180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3738136  TAGGTATCGCTATTCCACGATAAACGATTGCGAGCATCAGGATATTAATATTTCGTTTTC  3738077

Query  181      CCCATTTCCAATTGGTTCTATCTAAAGTCAGTTGCACTTGGTCGAATGAAAACATATTGA  240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3738076  CCCATTTCCAATTGGTTCTATCTAAAGTCAGTTGCACTTGGTCGAATGAAAACATATTGA  3738017

Query  241      AAATCAACTGAGAAATTTGACGATAATCAAAATACTGACCTGCAAAGAAGCGCTGCATAC  300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3738016  AAATCAACTGAGAAATTTGACGATAATCAAAATACTGACCTGCAAAGAAGCGCTGCATAC  3737957

Query  301      GTCGATAAAATGATTGTGGTAAGCACTTGATGGGCAAGGCTTTAGATGCAGAAGAAAGAT  360
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Sbjct  3737956  GTCGATAAAATGATTGTGGTAAGCACTTGATGGGCAAGGCTTTAGATGCAGAAGAAAGAT  3737897

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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  421      TGTTCCATTTTAGATATTTGTTTAAGATAAGATATAACTCATTGAGATGTGTCATAGTAT  480
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Sbjct  3737836  TGTTCCATTTTAGATATTTGTTTAAGATAAGATATAACTCATTGAGATGTGTCATAGTAT  3737777

Query  481      TC  482
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Figure 3. Sequence alignment of IS*Aba*1(Forward) of *A.baumannii*(X9 isolate) with *Acinetobacter baumannii* ATCC 17978 chromosome from USA: San Diego.

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Acinetobacter baumannii strain VB473 chromosome, complete genome
Sequence ID: CP050388.1Length: 3948250Number of Matches: 27
Range 1: 164726 to 165214

Score	Expect	Identities	Gaps	Strand
891 bits(482)	0.0	487/489(99%)	2/489(0%)	Plus/Plus


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Query  2       GATAAACTCTCTGTCTGCGAACACATTCACAATACGGTCTTTACCAAAAATGGCTATAAA  61
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164726  GATAAACTCTCTGTCTGCGAACACATTCACAATACGGTCTTTACCAAAAATGGCTATAAA  164785

Query  62      GCGTTGAATCAAAGCAATACGCTCTTTCGTATCTGAATTTCCACGTTTATTAAGCAATGT  121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164786  GCGTTGAATCAAAGCAATACGCTCTTTCGTATCTGAATTTCCACGTTTATTAAGCAATGT  164845

Query  122     CCAAAGGATAGGTATCGCTATTCCACGATAAACGATTGCGAGCATCAGGATATTAATATT  181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164846  CCAAAGGATAGGTATCGCTATTCCACGATAAACGATTGCGAGCATCAGGATATTAATATT  164905

Query  182     TCGTTTTCCCCATTTCCAATTGGTTCTATCTAAAGTCAGTTGCACTTGGTCGAATGAAAA  241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164906  TCGTTTTCCCCATTTCCAATTGGTTCTATCTAAAGTCAGTTGCACTTGGTCGAATGAAAA  164965

Query  242     CATATTGAAAATCAACTGAGAAATTTGACGATAATCAAAATACTGACCTGCAAAGAAGCG  301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164966  CATATTGAAAATCAACTGAGAAATTTGACGATAATCAAAATACTGACCTGCAAAGAAGCG  165025

Query  302     CTGCATACGTCGATAAAATGATTGTGGTAAGCACTTGATGGGCAAGGCTTTAGATGCAGA  361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165026  CTGCATACGTCGATAAAATGATTGTGGTAAGCACTTGATGGGCAAGGCTTTAGATGCAGA  165085

Query  362     AGAAAGATTACATGTTTGCTTTAAAATAATCACAAGCATGATGAGCGCAAAGCACTTTAA  421
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165086  AGAAAGATTACATGTTTGCTTTAAAATAATCACAAGCATGATGAGCGCAAAGCACTTTAA  165145

Query  422     ATGTGACTTGTTCCATTTTAGAGATTTGTTTAAGATAAGATATAACTCATTGAGATGTGT  481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165146  ATGTGACTTGTTCCATTTTAGAGATTTGTTTAAGATAAGATATAACTCATTGAGATGTGT  165205

Query  482     C-T-GTATT  488
               | | |||||
Sbjct  165206  CATAGTATT  165214
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Figure 4. Sequence alignment of IS*Aba*1(Forward) of *A.baumannii*(X10 isolate) with *Acinetobacter baumannii* strain VB473 chromosome, from India.

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