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The Whole genome sequence for *Acinetobacter baumannii* strain in Iraqi Hospitals Outbreak

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Abstract

A study was conducted to identify specialized F plasmid genes and regulatory systems in *Acinetobacter baumannii*. These genes could be very important for the capacity of these species to coexist with the human host and show a wide range of diversity in genes that contribute to antibiotic resistance. Identification of 50*A. baumannii* isolates was carried out through morphology and culture on CHROM agar and genotypic identification was performed using *blaOxa-51* gene. Out of 50, one AB isolate was chosen for whole genome sequencing (WGS) using Illumina MiSeq technology. The analysis identified specialized genes in these isolates that contribute to antibiotic stress and lipopolysaccharide barrier, including complex sets of partial and complete integrons and transposons. The recent findings, transferring of *A. baumannii* plasmid genes are inducing under the regulatory system to which the plasmid elements confer Adaptation such as F-plasmid genes transfer in *A.baumannii* induced by antibiotic stress under the control of transcriptional factor regulation system in order to antimicrobial drug resistance. The selected *A. baumannii* isolate, IS1- *A.baumannii* 32 contain five global regulator systems .Our study were provided detailed genomic picture in detected both innate and acquired plasmid-encoded AMR genes. Study aim is the role of genetic regulation to control the transcription, virulence factors and antibiotic resistance related mechanism in *A.baumannii* .

Introduction

The gram-negative, strictly aerobic, non-motile coccobacillus known as *Acinetobacter baumannii* does not produce the enzymes oxidase, urease, citrate, or indole and does not ferment glucose [1]. *A. baumannii* makes catalase and has a DNA sequence made up of 39–47% guanine–cytosine (GC) bases [2]. *A. baumannii* has lately evolved into a very serious nosocomial pathogen due to its multidrug-resistant (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR) strains, which are responsible for the majority of nosocomial infections globally [3]. *A. baumannii* has a normal genome size between 3.7 and 4.3 Mb, with a median GC content of 39% [4]. The genome size could increase to 9 Mb or more, though, because of the great flexibility of the genome and the capacity to take in foreign DNA. The auxiliary genome of *A. baumannii* is larger than the tiny core genome [5]. For the eradication or control of the possible spread of *A. baumannii* strains inside a hospital, molecular

epidemiology is a crucial tool [6,7]. Several molecular typing methods, such as whole-genome sequencing (WGS), pulsed-field gel electrophoresis (PFGE), and multilocus sequence typing (MLST), have been used to epidemiologically define *A. baumannii* strains. [8] Second-generation sequencers like Illumina platforms have made significant contributions to the molecular epidemiology of *A. baumannii* strains. WGS provides high resolution and information on *A. baumannii* Identification of pathogens, indicators of pathogen virulence, drug susceptibility, comparative genomics, and the identification and analysis of outbreaks.

Materials and Methods

A. baumannii isolates

February to April 2022,50 non-repetitive *A. baumnnii* isolates were obtained from clinical specimens such as blood, sputum and urine from patients (ranging age from 18to 65 years old) were hospitalized in ICUs of 3medical centers in different regions of Iraq, Bagdad. The biochemical interactions between the media in VITEK2 Identification Cards and the suspended bacterial isolates were used to characterize the A.B isolates using the VITEK 2 and Epi.20 test systems. Using transport medium, the samples were brought to the lab where they were grown on *A. baumannii*-selective media (Chrom agar) and MacConkey agar and incubated for 24 hours at a temperature of 37 °C in an aerobic environment. The colony's color, shape, edges, and texture were then examined.

DNA extraction and sequenceing

A. baumannii 3 were offered for WGS. The High-Pure template preparation kit (Roche Applied Sciences, Mannheim, Germany) was used to extract DNA in accordance with the manufacturer's instructions. A nanodrop spectrophotometer was used to measure the amount of extracted DNA and determine the sample quality for use in subsequent procedures. As previously described, *A. baumannii* strains underwent library preparation and paired-end sequencing on an Illumina MiSeq sequencer. Brefily, the Illumina TruSeq Nano DNA sequencing kit was offered by Illumina, Inc. in San Diego, California, the United States. The library was made using the Illumina MiSeq sequencer (Illumina, San Diego, CA, USA). Information from the Library Layout (paired), Library genomic Source, and Illumina were also included in the search results.

Results and discussion

Isolation and Identification

Acinetobacter baumannii isolated from sputum, urine and blood in Iraqi hospitals (The City of Medicine, Baghdad Hospital and Al-Hurok Hospital). The identification and characterization of the isolates were carried out according to certain morphology, cultural and biochemical test. To ensure this diagnosis of *A.baumannii*, isolates preliminary were cultured on CHROM agar, Blood agar, MacConkey agar, Kligler iron agar and Cetrimide agar plates in aerobic conditions at 37°C for 24h. The color, shape, edges, and texture of the colony were next studied. The Genetically identification of *A.baumannii* for all isolates has been done by housekeeping gene *16sRNA* to detect genus of *Acinetobacter* and *blaOxa$_{51}$* for detection the species of *Acinetobacter baumannii* using PCR technique as seen in Figure 1 . PCR assay have fingerprinted, 100% specificity and sensitivity for their intended targets.

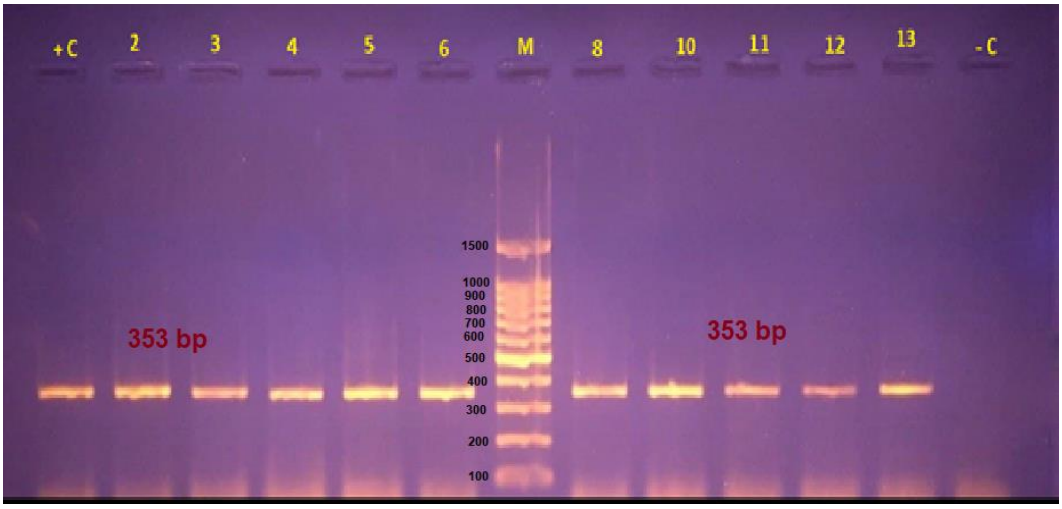

Fig. 1: The blaOXA-51 gene product size (band 353 bp) was detected using agarose gel electrophoresis (1% agarose, 7v/cm^2) with Ethidium bromide staining. Utilizing the template DNA that was prepared with the use of the boiling method. The molecular size of the DNA ladder was 100 bp, located in the middle (M). DNA isolated from *A. baumannii* samples has shown positive PCR, with a positive control on the left (lene + C) and negative control on the right (lene – C).

Whole Genome Sequencing of A.baumannii no.3 strain

In this context, it has been reported that after A. B3 isolate underwent whole-genome sequencing (WGS), the annotation statistics and comparison to other genomes of the same species revealed that the selected *A.baumannii* isolates had good genome quality. Whole-genome sequencing (WGS) is a powerful method increasingly used in clinical microbiology laboratories for identifying genetic components of nosocomial pathogens.

The number of overlapping DNA fragments binding with adaptor called contigs for AB3, were 158, considered low value when compared with the resulting of genomic length (were 7,709,828 bp, that may be due to the rubbish DNA functionless fraction *A.baumannii* genome .

A.baumannii 3 genome considered as transited isolate have been high G+C content(54.21%) because it have open pan-genome and obtained additional new genes from other bacterial isolates through horizontal gene transfer.

In this regarded, We found G+C content were considered one of the most important criteria in the WGS that a useful tool for distinguishing between different categories of *A.baumannii* isolates based on their genomic characteristics, and it has the potential to reveal valuable information about the bacterial diversity between bacteria and evolution of this important nosocomial pathogen. The conserved GC slandered found in the hospital type of *A.baumannii* but any increase or decrease in it ,that is explain bacteria genome exposed to mutation or recombination and acquired anew mobile genetic element from other related species.

Table1 is a list of the traits of the *A.baumannii* 3 genomes using the genome of AB strain GU71 (470.4681) as a reference sequence and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP). 7,552, open reading frame were predicted for *A.baumannii*

3(ST/ 1089). On other hand, *A.baumannii* 3 is environmental clone have been high CDS due to high genomic length (as listed above) with having different virulence factor genes . The genomes of *A.baumannii* 3 had complete ribosomal clusters with 134 tRNAs .Additionally, AB 3(ST/ 1089) had 6 rRNAs.

Table 1: Genomic characteristics of *A. baumannii* 3 strain.

Assembly details	*A.baumannii 3*
Contigs	158
GC Content	54.21
Contig L50	16
Genome Length	7,709,828 bp
Contig N50	156,509
Genome Quality	Good
CDS	7,552
tRNA	134
Repeated Region	12
rRNA	6

Regulation systems and mobile genetic elements (MGE)

The Controlling of F- plasmid genes transfer in *A.baumannii*

MGE in general and Plasmids in particular can explain how *A.baumannii* can colonize and adapt to various environmental conditions. The Plasmids facilitate the transfer and interchange of various features, including as antibiotic resistance, particular degradation pathways, symbiosis, and virulence and depressed or expressed mutant of genes within microbial populations. In order to better understand features of gene flux in ecosystems, studies concentrating on plasmid maintenance, diffusion, acquisition, and loss, we must explain the controlling results of regulatory systems.

A. baumannii can be conjugation the plasmid genes with same species and transformation with related species (plasmid DNA is packaged into phage particles during transduction, which releases DNA after the host is lysed. A cascade of transfers can start when the rare, transfer-efficient *A.baumannii* comes into contact with a potential recipient by accident and continues until all potential recipients have received the plasmid. The regulatory systems' transfer genes are expressed in response to particular stimuli. Small peptide signals from potential recipients activate the conjugative transfer genes in the pheromone-responsive F-plasmids of AB.

Finally, The transferring of plasmid genes are inducing under the regulatory system to which the plasmid elements confer Adaptation. For example, F-plasmid transfer in *A.baumannii* induced by antibiotic stress under the control of transcriptional factor regulation system in order to antimicrobial drug resistance . Understanding these control mechanisms could change how microbial communities are managed in situations where plasmid transfer is either desired or unwanted.

Regulation system types

The selected *A. baumannii* isolates, IS1- *A.baumannii* 3 contain five global regulator systems that could serve as potential therapeutic targets due to their roles in mediating AB virulence regulation, environment adaptation, and AB bacteria-specificity. These systems include two-component systems (TCS), transcriptional factor (TF), RNA polymerase binding protein, nucleoid-associated protein (NAP), and DNA polymerase binding protein.

By transferring a phosphate group from sensor histidine kinases to their cognate response regulators, which either physically bind to target proteins or recognize and bind to specific DNA sequences to control transcription. Two-component systems are a pair of regulatory molecules that regulates how microorganisms adapt to their environments. transcriptional factor is necessary for *A. baumannii's* intracellular mobility, survival, and persistence in host cells shortly after infection. While *BfmRS* (*D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase)* regulates elements of the cell envelope essential for the persistence of infections, *GacSA (Global Virulence regulator)* contributes to the expression of genes implicated in virulence and antibiotic resistance. As a crucial survival strategy in an animal host, *Fur* (Ferric uptake regulator) and *Zur* (Zinc uptake regulator) are used by *A. baumannii* to detect iron or zinc depletion and up regulate genes for metal scavenging.

In this study, we identified a dozen plasmid genes in the *A. baumannii* isolate IS1- *A. baumannii* 3 by analyzing the F-plasmids sequence in NCBI BLASTN and detecting genes in the gene bank. These genes could provide insight into plasmid-mediated antibiotic resistance and adaptation of *A. baumannii* to changing environments as seen in table 2.

Briefly, whiten our study provides information on different AMR mechanisms and genes associated with *A. baumannii* isolates. It also lists different antibiotics, their target mechanisms, and the corresponding resistance genes in *A. baumannii*. Additionally, provides information on different proteins and efflux pumps conferring antibiotic resistance, as well as regulators modulating the expression of antibiotic resistance genes. Overall, the table suggests that *A. baumannii* isolates have a diverse range of AMR mechanisms and genes that confer resistance to multiple antibiotics. Therefore, appropriate antibiotic stewardship practices and infection control measures are essential to prevent the spread of *A. baumannii* infections and limit the emergence of AMR in clinical settings.

Table 2: The regulatory systems in *Acinetobacter baumannii 3(IS1)*

Gene Name	The result	Type	Function	Reference
lptA_1 faoA, pstB	lysophosphatidic acid acyltransferase"	Two-component system	lptA_1 linked with phosphate uptake (pstB), lipid biosynthesis or metabolism (lptA, faoA)	[9]
gmhB	D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase"	Two-component system	In bacteria, GmhB promotes the l-glycero-d-manno-heptose-1-ADP pathway, which is involved in the synthesis of lipid A, and the d-glycero-d-manno-heptose-1-	[10]

			GDP pathway, which is involved in the synthesis of S-layer glycoproteins.	
tagX	DNA-3-methyladenine glycosidase I"	Two-component system	TagX, the first enzyme to be found, performs the important task of allowing the transit of T6SS machinery across the peptidoglycan layer of the T6SS-producing bacterium.	[11]
trkA	potassium transporter inner membrane associated protein"	Transcription factor	Potential K^+ transporter genes in A. baumannii	[12]
rsmB	ribosomal RNA small subunit methyltransferase B"	RNA polymerase binding protein	Given how important sRNAs are as regulators, it's probable that they contribute significantly to A. baumannii's drug resistance.	[13]
dinD	DNA-damage-inducible protein D"	Two-component system	all DNA damage-related genes that contain the outlined palindromic DNA motif are deregulated.	[14]
prlC	oligopeptidase A"	Two-component system	to better adapt to changing environmental conditions	[15]
coxB	Cytochrome c oxidase subunit 2	Transcription factor	Chaperones, chaperonins, porins, and the enzymes involved in the signal transduction cascade were among the proteins that were elevated in response to stress, especially in the early phases. The phenol-stressed bacteria produced more ABC-type transporters, membrane receptors, and efflux pumps to counteract its effects.	[16]
hasR, hasAp	heme uptake outer membrane receptor HasR" heme acquisition protein HasA	Transcription factor	It has been demonstrated that HasR and HasAp are essential for heme sensing and pathogenicity within the host.	[17]
hasE	metalloprotease secretion protein"	Transcription factor	Through a variety of ways, fimbrial protein has been found to promote mammalian cell apoptosis.	[18]
aprF	alkaline protease secretion protein AprF"	Transcription factor	has a crucial role in preserving membrane integrity, environmental stress adaptability, and virulence regulation.	[19]
hemO	heme oxygenase"	Transcription	Hb-iron and heme	[20]

		factor	consumption require a heme oxygenase.	
GacSA	Virulence regulator	Two-component system	Pilus synthesis, motility, biofilm formation, serum resistance, aromatic compound metabolism, regulat talk between two bacteria	[21]
znuB	Zinc acquisition	Transcription factor	In mouse models of A. baumannii infection, the Znu system is essential for pathogenesis and affects zinc acquisition by directly helping in the uptake of zinc into A. baumannii cells.	[22]
nrdJa nrdJb	ribonucleoside-diphosphate reductase	Two-component system	confirmed that the -oxidation pathway plays a role in the degradation of aliphatic alkanes	[23]
HipA ,RelE	toxin-antitoxin (TA) modules	Two-component system	It has been demonstrated that cells overexpressing either of the bacterial toxin-antitoxin (TA) module members, HipA or RelE, have the capacity to produce more persisters, indicating a specialized role for these toxins in the mechanism of persistence.	[24]
engB	putative GTP-binding protein EngB	Two-component system	Merlin's turnover is hampered by the contact between NGB and merlin, although merlin has no effect on NGB's GTPase or GTP-binding activities.	[25]
cc4	cytochrome c4	Two-component system	A.baumannii respiration at low oxygen concentrations and other bacteria relies on activity of cytochrome c4 oxidases	[26]
Cry	cryptochrome DASH"	Transcription factor	Blue light receptors.	[27]
ampDh2	virulence determinant	Transcription factor	AmpDh2 is a zinc protease that is present in Pseudomonas aeruginosa, a troublesome human infection. Its ability to flip the bacterial cell wall over is widely known. The relationship between AmpDh2 and the cell wall was examined.	[28]
AlgB, AlgR	alginate biosynthesis transcriptional	Transcription factor	The transcription of the tightly controlled gene algD, which	[29]

	regulatory protein AlgB"		codes for GDP-mannose dehydrogenase and is essential for P. aeruginosa and Acinetobacter alginate biosynthesis, is dependent on the response regulators AlgB and AlgR.	
abaR	Signal responsive	Transcription factor	A transcription factor that reacts to AHL and is involved in quorum sensing and the formation of biofilms.	[30]
recC, RecB, recD	RecBCD enzyme subunit RecC	Transcription factor	Both the restriction of foreign DNA and recombination-based DNA repair depend on the RecBCD enzyme.	[31]
phoR phoB	phosphate regulon sensor protein PhoR	Two component system	The expression of the pho regulon's genes is governed by a two-part regulatory system that consists of a response regulator, PhoB, and a sensor kinase, PhoR. Expression of the pho regulon is repressed when the extracellular phosphate content is too high because the genes of this regulon contain a regulatory promoter element known as the pho boxr.	[32]
ubiA , ubiC	4-hydroxybenzoate octaprenyltransferase	Transcription factor	ubiA (Coenzyme Q) is an essential component of bacterial respiratory chains.	[33]
rubA1_1 rubA2	Rubredoxin-1" Rubredoxin-2"	Transcription factor	The main pigment-protein complex in oxygenic organisms' photosynthetic electron transport chain has been hypothesized to participate in photosystem I assembly.	[34]
hupA	binding protein for DNA HU-alpha"	DNA-binding protein	Variations in growth temperature have an impact on the expression of the hupA gene as well.	[35]
dadA	D-amino acid dehydrogenase	Transcriptional regulator factor	A flavoenzyme called D-amino acid dehydrogenase breaks down free, neutral D-amino acids to produce the equivalent 2-oxo acids and hydrogen.	[36]

Information of closely related isolates to IS1-AB3 based on cgMLST (core genome Multi Locus Sequence Types) strategy

The cgMLST strategy was able to show close isolates to AB 3. For instance, Table 3 and figure 2 show some of clones globally registered have the same sequence type with AB-3 , infected same host (Human),isolated from different source which collected between Dec-2013 to 01-sep-2015, distributed in Ethiopia, Germany, Tunisia: Sousse, India, and Ghana: Kumasi with causes variable dangerous diseases while two novel clones with different ST have genetically close to it distributed in Spain and Tunisia which causes Bronchopneumonia and Urinary Tract Infection. These infections may have been transmitted by US occupation and American coalition soldiers.

Table 3: The prediction of closely related isolates to *A.baumannii* 3

Isolate	Accession number	ST	Host	Disease	Isolation Source	Country State	Collection Year	Antimicrobial resistance gene	Virulence gene	Different alleles
AB_B	LWSN01	1089	Human	inguinal abscess	wound swab	Ethiopia	Dec-2013	Show/ Hide	Show / Hide	121
AB_C	LWSO01	1089	Human	asthma/ laparotomy	wound swab	Ethiopia	Jan-2014	Show/ Hide	Show / Hide	122
AB_A	LWSM01	1089	Human	hem pneumothorax	wound swab	Ethiopia	Jan-2014	Show/ Hide	Show / Hide	124
Aci00859	VAGE01	1089	Human	Hem pneumothorax	wound swab	Germany: Heidelberg	2015-06-09	Show/ Hide	Show / Hide	136
MBL_M4	MWTU01	1089	Human	Septicemia	Blood	Tunisia: Sousse	19-mar-2015	Show/ Hide	Show / Hide	151
Ab_NDM_1	QBBY01	NA	Human	Bronchopneumonia	rectal swab	Spain: Cadiz	2017-04-19	Show/ Hide	Show / Hide	157
ACN21	CP038644	1089	Human	Bacteremia	blood	India	2018	Show/ Hide	Show / Hide	160
198	QTKC01	1418	Human	Urethritis	urethral swab	Ghana: Kumasi	2015	Show/ Hide	Show / Hide	172

Isolate	Accession number	ST	Host	Disease	Isolation Source	Country State	Collection Year	Antimicrobial resistance gene	Virulence gene	Different alleles
151	NXHM01	1418	Human	UTI	Urine	Ghana: Kumasi	2015	Show/ Hide	Show / Hide	173
MBL_M6	MWTW01	NA	Human	Urinary Tract Infection	urine	Tunisia: Sousse	15-Apr-2015	Show/ Hide	Show / Hide	180
MBL_M10	MWUA01	1089	Human	Septicemia	Blood	Tunisia: Sousse	01-sep-2015	Show/ Hide	Show / Hide	190

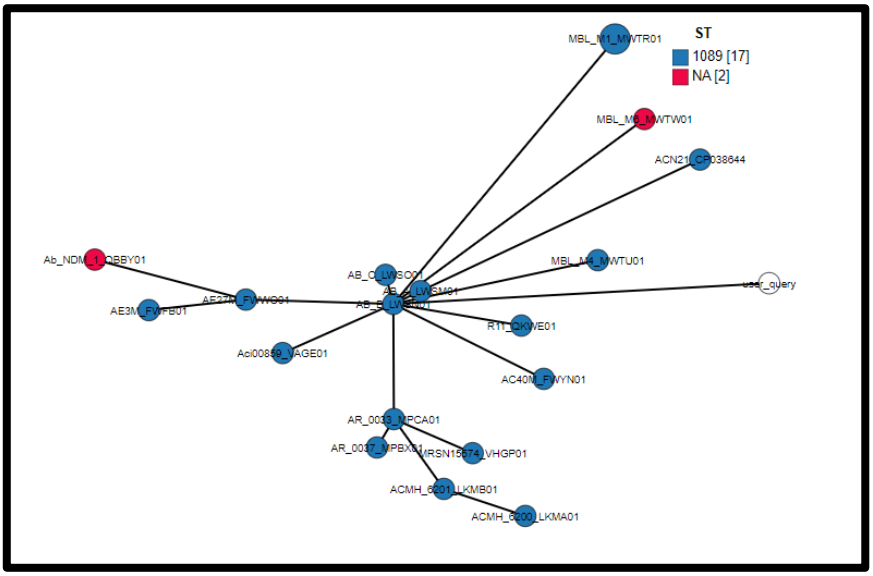

Fig. 2: Based on cgMLST characteristics, the minimal spanning tree for A.baumannii -3 isolate examined The numbers reflect amount of distinct alleles found in the pairs of related isolates. Close isolates are shown in the same color; other isolates are not.

Subsystem Analysis

Figure 3 shows a circular graph illustrating the distribution of genomic annotations. Contigs, CDS (coding DNA sequence) on the forward and reverse strands, RNA genes, CDS with homology to known virulence factors and antimicrobial resistance genes, GC concentration, and GC skew are included in this, listed from outer to inner rings. The forward and reverse strand CDS (coding DNA sequence) colors designate the subsystem to which these genes belong, as seen in Subsystems below. As part of PATRIC annotation, the subsystems unique to each genome are examined. A subsystem is a collection of proteins that work together to complete a certain biological function or structural complex. An overview of the subsystems for this genome is shown in Fig. 1.

There are Several housekeeping and acquired genes related to bacterial defense mechanisms were also observed in *A. baumannii* . Metabolism-associated genes were found in Ab isolate have been a high percentage of metabolic genes reached to 1382, followed genes related to stress response, defense, virulence, energy, and membrane transporter, DNA and RNA processing, cellular processer, miscellulanous, cell envelope and regulation cell signaling.

In this paper, we used a metagenomic subsystem analysis obtain functional gene data explained the difference between pathogenic and less pathogenic strains, describe the *A.baumannii* diversity and antimicrobial resistance over a long period in Iraqi hospitals .

The number of protein-processing genes reached 442 in *A.baumannii* 3, Each subsystem is made up of a group of proteins that work together to form a structural complex or perform a specific biological function (20). There were 240 virus genes in *A.baumannii* 3 that were in charge of stress and defense. The Pho (phosphate regulon) is essential for managing phosphate as well as for many bacteria's pathogenicity and stress responses, according to numerous studies [34]. The genes were encoded energy in A*.baumannii* 3 reached to 516 .The majority of membrane transporter genes were 325 in *A.baumannii* 3, The genes responsible for DNA processing in *A.baumannii* 3 equal 156 . The genes responsible for RNA processing in *A.baumannii* 3 equal 141 and cellular processer genes in *A.baumannii* 3 equal 244 . Cell envelope in *A.baumannii* 3 equal 244 . Finally, cell envelope and regulation cell signaling genes were in *A.baumannii* 3 equal 26 The genetic differences of subsystem differences in essential virulence traits of *Acinetobacter* species may aid in explaining why some species have a stronger clinical impact.

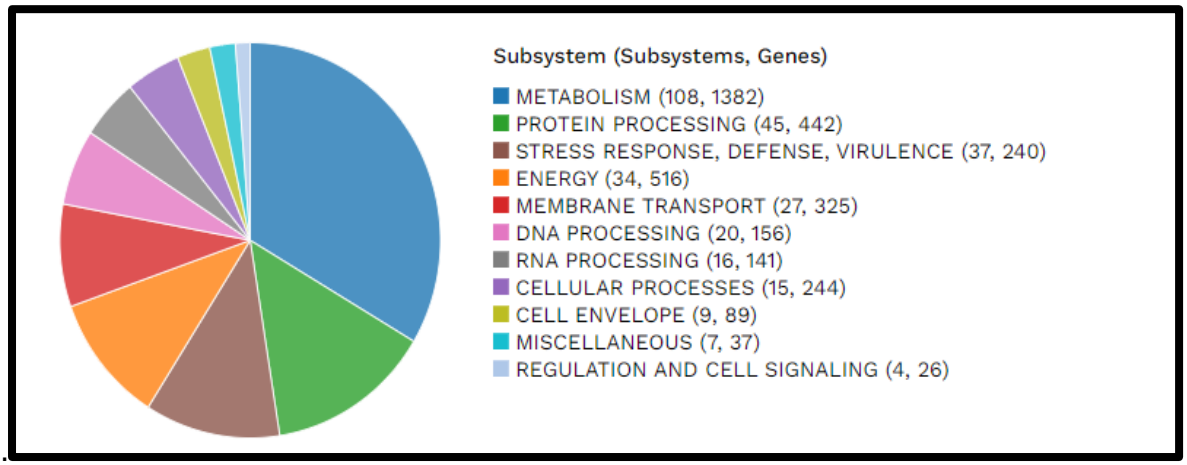

Fig. 3: A. baumannii 3 strains used in this study's analysis of the functional distribution subsystem of genes.

Conclusion

Using whole-genome sequencing (WGS) analysis, our work examined genetic epidemiology of *A. baumannii* strains selected from the hospitals in Iraq during an outbreak of antibiotic-resistant illnesses. *A. baumannii3* plasmid genes are being transferred as a result of the regulatory system's adaptation that the plasmid elements provide. As an illustration, antibiotic stress can cause the transfer of the F plasmid in *A.baumannii*, which is then regulated by the transcriptional factor regulation system to prevent the development of

antibiotic resistance. Five global regulator systems found in the chosen *A. baumannii* isolates, IS1- *A.baumannii* , be used as prospective therapeutic targets because of their functions in facilitating *A.baumannii* adaptation to changing environments, regulating virulence, and being specific to AB bacteria. These systems include DNA polymerase binding protein, RNA polymerase binding protein, nucleoid-associated protein (NAP), and two-component systems (TCS).

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تسلسل الجينوم الكامل لسلالة الراكدة البومانية في اندلاع المستشفيات العراقية

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الخلاصة:
أجريت دراسة لتحديد جينات البلازميد والانضمة المسيطرة عليها في بكتريا الراكدة البومانية. تكون هذه الجينات مهمة جدًا لقدرة هذه الأنواع على التعايش مع المضيف البشري وإظهار مجموعة واسعة من التنوع في الجينات التي تساهم في مقاومة المضادات الحيوية، تم التعرف على 50 عزلة من الراكدة البومانية من خلال الصفات المضهرية على وسط الكروم اكار والفايتك. وتم تحديد النمط الجيني باستخدام جين الاوكسا 51. من بين 50، تم اختيار عزلة واحدة لتسلسل الجينوم الكامل باستخدام تقنية الاليومنة Illumina MiSe وتعرف التحليل الجينومي على جينات تساهم في مقاومة البكترياضد المضادات الحيوية وحاجز عديدات السكاريد الدهنية، بما في ذلك مجموعات معقدة من الإنتجترونات الجزئية والترنبوزون. في الدراسة الحالية تم التعرف على ان انتقال جينات البلازميدات تكون تحت سيطرة خمس انواع من الانظمة. مثلا انتقال جينات تحت ضغط المضادات الحيوية يكون تحت سيطرة نظام اسمة عامل الاستنساخ لغرض المقاومة. في دراستنا هذه تم اكتشاف في عزلة الراكدة البومانية المختاره 32 ,خمس انواع من الانظمة المسيطرة. قدمت الدراسة الحالية صورة جينومية مفصلة في كل من جينات AMR الفطرية والمكتسبة المشفرة بالبلازميد.