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Acinetobacter baumannii Co-Resistant to Extended Spectrum Beta-Lactamases and Carbapenemases in Six Peruvian Hospital Centers

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Citation: Challapa-Mamani, M.R.; Yareta, J.; Fajardo-Loyola, A.; Asmat Marrufo, P.; Siesquen, C.P.; Pino-Dueñas, J.; Meza-Fernández, H.; Cruz-Vargas, J.A.D.L.; Marcos-Carbajal, P. *Acinetobacter baumannii* Co-Resistant to Extended Spectrum Beta-Lactamases and Carbapenemases in Six Peruvian Hospital Centers. *Microbiol. Res.* **2024**, *15*, 2650–2660. https://doi.org/10.3390/microbiolres15040175

Academic Editor: Gadi Borkow

Received: 24 May 2024
Revised: 29 November 2024
Accepted: 9 December 2024
Published: 11 December 2024

Abstract: Objectives: The aim of this study was to describe the phenotypic and molecular characteristics of *Acinetobacter baumannii* isolates carrying resistance genes to beta-lactams and carbapenems in six Peruvian public hospital centers. Materials and methods: The susceptibility of bacterial isolates was determined using the automated MicroScan system, with interpretation according to the M100 S30 CLSI 2020. Resistance genes were identified by conventional polymerase chain reaction (PCR), and PCR products were visualized by 1% agarose gel electrophoresis. Results: Nine strains (TRU1, PM1, PM2, CUS1, CUS2, CUS3, CAL1, CAL2 and CAL3) out of a total of 21 strains in the study were reactivated, showing resistance of 77.8% to imipenem, ciprofloxacin and cefepime, followed by 66.7% resistance to meropenem and ceftazidime, indicating marked multidrug resistance. In addition, the detection of the group A beta-lactamase genes *bla*CTX-M and *bla*TEM was confirmed, showing co-resistance in strains CUS1, CUS2 and CUS3, despite their unusual presence in this pathogen, also determined by the presence of the group D carbapenemase *bla*OXA in strain CUS3, the only strain to show co-resistance of the three groups. Conclusion: The prevalence of *Acinetobacter baumannii* resistant to extended-spectrum beta-lactamases and carbapenemases in Peruvian public centers represents a critical challenge for the treatment of infections. Rigorous surveillance, infection control strategies, and the development of alternative therapies are urgently needed to address this growing bacterial resistance.

Keywords: *Acinetobacter baumannii*; resistance genes; multidrug resistance; beta-lactamase

1. Introduction

The growing threat of antimicrobial resistance (AMR) and multidrug resistance (MDR) constitutes a critical challenge in contemporary healthcare [1]. This problem has emerged as a critical challenge in the global health sphere, triggering considerable concerns in the

medical and scientific community [2]. Within this context, *Acinetobacter baumannii* (*A. baumannii*), an opportunistic gram-negative microorganism, has emerged as a pathogen of particular interest due to its innate ability to acquire and develop resistance to multiple classes of antimicrobials [3]. This problem has been aggravated by its inclination to colonize and proliferate in hospital environments, where vulnerable patients are exposed to frequent antimicrobial treatments and compromised health conditions increase the risk of infections [4,5].

Multidrug resistance is a major problem in Latin America, especially in the hospital setting. According to data from the Latin American Antimicrobial Resistance Surveillance Network (RELAVRA), resistance of hospital pathogens such as *Klebsiella pneumoniae* has increased significantly in Latin America since 2014, reaching an average of 21% [6]. Furthermore, *A. baumannii* strains have been found to be highly resistant to multiple drugs, making their treatment difficult [7]. In Colombia, 100% of *A. baumannii* strains isolated from medical intensive care units were found to be resistant to carbapenems, suggesting that carbapenem resistance is a major problem in the region [8].

On the other hand, the pandemic of coronavirus disease (COVID-19) has led to the inappropriate use of antimicrobials, which has contributed to the increase in infections due to drug-resistant bacteria in the Americas region [9]. The Pan American Health Organization (PAHO) has urged countries to develop evidence-based treatment guidelines for doctors and to invest in new and better antimicrobial medications [9]. Public hospitals in Peru, as a microhabitat of this global problem, are not exempt from the constant pressure exerted by multidrug resistance in *A. baumannii* [10]. The prevalence of resistant strains in these medical settings not only threatens the efficacy of antimicrobial therapies but also drives the need for a comprehensive and rigorous evaluation of the phenotypic and molecular characteristics of this bacterium [11,12].

The present investigation was carried out to clarify the underlying dynamics of the phenotypic and molecular multidrug resistance of *A. baumannii* in six Peruvian hospital centers, allowing the identification of emerging resistance patterns and the detection of genes underlying this adaptive capacity. Addressing this problem in a local context, we not only seek to expand the current understanding of multidrug resistance in *A. baumannii* but also generate relevant information to inform management policies and control strategies in the hospital setting. Ultimately, we hope that the findings of this study will contribute to demonstrating which resistance genes circulate among the A. baumannii isolated from the six Peruvian hospital centers.

2. Materials and Methods

A descriptive and cross-sectional study was conducted, and 21 bacterial isolates were identified as *A. baumannii*. These isolates were obtained from endotracheal samples, bronchial aspirates and tracheal secretions from six public hospital centers of levels II and III between 2017 and 2019. The bacterial isolates were stored in vials with Trypticase Soy Agar at −20 °C in the microorganism collection of each hospital center, and from there, they were sent in cold chain to the Laboratorio de Investigación en Biología Molecular (LIBM) of the Universidad Peruana Unión (UPeU) for processing. The distribution of these isolates is detailed in Table 1.

Table 1. Peruvian public hospital centers.

Strain	City	Public Hospital Centers	Códe
04	Callao	Hospital Essalud Alberto Sabogal Sologuren	CAL
09	Trujillo	Hospital Belén	TRU
03	Cusco	Hospital Antonio Lorena	CUS

Table 1. *Cont.*

Strain	City	Public Hospital Centers	Códe
02	Loreto	Hospital Regional "Felipe Santiago Arriola Iglesias"	LOR
02	Puerto Maldonado	IPRESS Jorge Chávez	PM
01	Tarapoto	Hospital de Tarapoto	TAR

2.1. Phenotypic Characterization

Bacterial isolates were reactivated in trypticase soy broth and incubated at 37 °C for 18–24 h. These were then cultured on MacConkey agar and ESBL/SuperCARBA chromogenic agars to screen *A. baumanii* MDR bacterial isolates [13].

Strains were identified and evaluated for antimicrobial susceptibility by the broth microdilution (CMI) method using the automated MicroScan system, following the manufacturer's BECKMAN COULTER guidelines [14]. Conventional NC66 panels were used for bacterial identification and antimicrobial resistance assessment, and specific identification was performed through the "Biotype Lookup" program in labPro Diagnostics following the manufacturer's procedures. Interpretation of antibiotic susceptibility followed the guidelines of the 2020 Clinical and Laboratory Standards Institute (CLSI) document M100-S22.

As a last step, the antimicrobial susceptibility profile was evaluated for the following antibiotics according to the NC66 panel: amikacin (16–32 μg/mL), cefepime (1.4–8 μg/mL), ceftazidime (1.4–16 μg/mL), ciprofloxacin (1–2 μg/mL), gentamicin (4–8 μg/mL), imipenem (1–8 μg/mL), meropenem (1–8 μg/mL), tobramycin (4–8 μg/mL) and sulfamethoxazole/trimethoprim (2/38 μg/mL) [15].

2.2. Molecular Characterization

The bacterial isolates identified that were recovered on MacConkey agar were suspended in trypticase soy broth and incubated at a temperature of 37 °C between 16 and 18 h to achieve a necessary exponential concentration of 1×10^9 cfu/mL. Subsequently, the total DNA was extracted using the inmuPREP Bacteria DNA Kit (analitikjena) bacterial DNA extraction kit [16].

In the polymerase chain reaction (PCR) process, primers encoding beta-lactamase and carbapenemase were used, the details of which are specified in Table 2. A set of strains was also used as a positive control, which included ATCC BAA 1705 *Klebsiella pneumoniae*, ATCC 35218 *Escherichia coli* and ATCC 700603 *Klebsiella pneumoniae*, respectively. Additionally, a negative control with ultrapure water was incorporated. The composition of the PCR Mix consisted of 10X PCR Buffer (3 μL), dNTP (1 μL), Forward primer (0.5 μL), Reverse primer (0.5 μL), ultrapure water (17.3 μL), Taq polymerase (0.2 μL) and DNA (2.5 μL). The amplification protocols were adjusted according to the manufacturer's recommendations or the guidelines suggested in the literature [17] and to the described in the standardized protocol of the LIBM. Cycling conditions were established according to specific protocols for each gene [18], as detailed in Table 2.

PCR products were observed by electrophoresis on a RUNSTATION system with a 1% agarose gel using 1X TAE buffer. 8.0 μL of the PCR products were loaded with 1.6 μL of developer buffer and 5 μL of 100 bp molecular weight marker with 1 μL of developer buffer. Electrophoresis was carried out at 100 volts for 45 min, and visualization was performed on a RUNSTATION Cleaver photodocumenter.

Table 2. Primers used for the amplification of extended-spectrum beta-lactamase and carbapenemase resistance genes and thermocycling parameters.

Gen	Sequence	Size	Thermocycling Parameter	Ref.
*bla*CTX-M	F: GAA GGT CAT CAA GAA GGT GCG R: GCA TTG CCA CGC TTT TCA TAG	560 bp	Initial denaturation 94 °C × 5 min; Cycle denaturation 94 °C × 1 min; hybridization 52 °C × 1 min; cycle extension 72 °C × 1 min y final elongation 72 °C × 5 min for 35 cycles	[19]
*bla*TEM	F: TCC GCT CAT GAG ACA ATA ACC R: TTG GTC TGA CAG TTA CCA ATG C	931 bp	Initial denaturation 94 °C × 5 min; Cycle denaturation 94 °C × 1 min; hybridization 52 °C × 1 min; cycle extension 72 °C × 1 min y final elongation 72 °C × 5 min for 35 cycles	[19]
*bla*SHV	F: ATG CGT TAT ATT CGC CTG TG R: TGC TTT GTT CGG GCC AA	747 bp	Initial denaturation 94 °C × 5 min; Cycle denaturation 94 °C × 1 min; hybridization 51 °C × 1 min; cycle extension 72 °C × 1 min y final elongation 72 °C × 5 min for 35 cycles	[20]
*bla*KPC	F: AAC AAG GAA TAT CGT TGA TG R: AGA TGA TTT TCA GAG CCT TA	916 bp	Initial denaturation 94 °C × 5 min; Cycle denaturation 94 °C × 30 seg; hybridization 50 °C × 30 seg; cycle extension 72 °C × 1 min y final elongation 72 °C × 10 min por 35 cycles	[21]
*bla*NDM	F: AGC ACA CTT CCT ATC TCG AC R: GGC GTA GTG CTC AGT GTC	512 bp	Initial denaturation 94 °C × 5 min; Cycle denaturation 94 °C × 30 seg; hybridization 57 °C × 30 seg; cycle extension 72 °C × 30 seg y final elongation 72 °C × 5 min por 35 cycles	[21]
*bla*VIM	F: AGT GGT GAG TAT CCG ACA G R: ATG AAA GTG CGT GGA GAC	261 bp	Initial denaturation 94 °C × 5 min; Cycle denaturation 94 °C × 30 seg; hybridization 57 °C × 30 seg; cycle extension 72 °C × 30 seg y final elongation 72 °C × 5 min por 35 cycles	[21]
*bla*IMP	F: GGY GTT TWT GTT CAT ACW TCK TTY GA R: GGY ARC CAA ACC ACT ASG TTA TCT	404 bp	Initial denaturation 94 °C × 5 min; Cycle denaturation 94 °C × 30 seg; hybridization 50 °C × 30 seg; cycle extension 72 °C × 30 seg y final elongation 72 °C × 5 min por 35 cycles	[21]
*bla*OXA	F: AATGGCACCA-GATTCAACTT R: CTTGGCTTTTAT-GCTTGATG	599 bp	Initial denaturation 94 °C × 5 min; Cycle denaturation 94 °C × 30 seg; hybridization 50 °C × 30 seg; cycle extension 72 °C × 30 seg y final elongation 72 °C × 5 min por 35 cycles	[22]

F: forward, R: reverse; CTX-M: cefotaxime; TEM: temoniera; SHV: sulfhydryl variable; KPC: Klebsiella pneumoniae carbapenemase; NDM: New Delhi metallo β -lactamase; VIM: Verona encoded-integron metallo β-lactamase; IMP: imipenemase metallo β-lactamase; OXA: oxacillinase; bp: base pairs; bla: beta-lactamase genes.

The data derived from the determination of the percentages of antimicrobial resistance in *A. baumannii* were recorded in Microsoft Excel v. 2013 and the WHONET program (World Health Organization Net v. 2020) for the analysis of antimicrobial susceptibility data [23].

3. Results

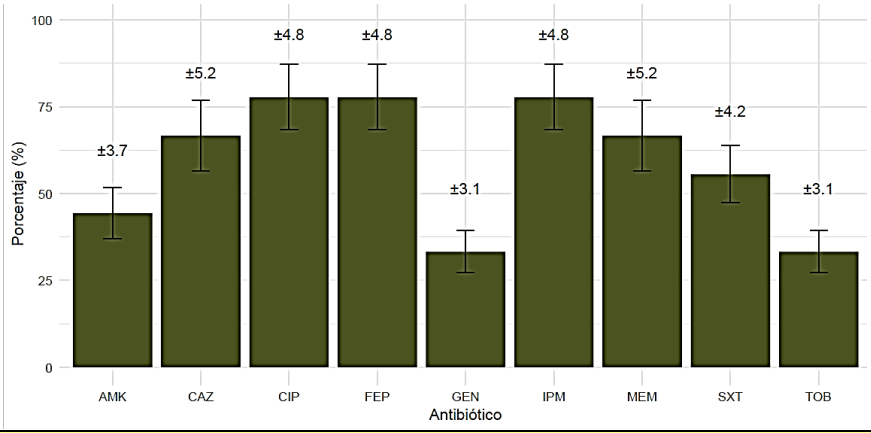
The bacterial isolates reactivated in the present study were 9/21 strains. Within this sample, a differential distribution was observed in terms of origin and clinical context. In more detail, it is established that 2/9 of these isolates came from patients undergoing hospitalization, while the remaining 7/9 were obtained from individuals under care in the intensive care unit (ICU). An even more in-depth analysis of this variability revealed that of the nine isolates, four were obtained from bronchial aspirate, two from endotracheal cultures, and three from tracheal secretion samples. This subdivision reflects the diversity of clinical sources used to obtain these isolates and points to the complexity of the scenarios in which *A. baumannii* can manifest its presence and activity. Specific details related to

this distribution are available in Table 3, where they are presented in a systematized and understandable manner for a more exhaustive analysis.

Table 3. Demographic data of the bacterial isolates.

Sample	Sex	Age	City	Hospital	Service	Códe
Bronchial aspirate	M	55	Trujillo	H. Belen	Intensive Care Unit	TRU1
Bronchial aspirate	M	37	Puerto Maldonado	IPRESS Jorge Chávez	Hospitalization	PM 1
Tracheal secretion	F	30	Puerto Maldonado	IPRESS Jorge Chávez	Hospitalization	PM 2
Bronchial aspirate	M	28	Cusco	H. Antonio Lorena	Intensive Care Unit	CUS 1
Tracheal secretion	F	2	Cusco	H. Antonio Lorena	Intensive Care Unit	CUS 2
Tracheal secretion	M	50	Cusco	H. Antonio Lorena	Intensive Care Unit	CUS 3
Endotracheal culture	M	44	Callao	H. Alberto Sabogal	Intensive Care Unit	CAL 1
Bronchial aspirate	M	24	Callao	H. Alberto Sabogal	Intensive Care Unit	CAL 2
Endotracheal culture	M	32	Callao	H. Alberto Sabogal	Intensive Care Unit	CAL 3

In this study, the growth of 100% of the *A. baumannii* strains reactivated in the ESBL and SuperCARBA chromogenic agars was highlighted. These specialized media were essential to detect and distinguish the bacterial isolates of interest. The susceptibility analyses revealed high percentages of resistance to beta-lactams, being 8/9 for *bla*CTX-M, *bla*TEM 3/9, and the presence of *bla*OXA was also evident in 1/9, which was followed by resistance to fluoroquinolones 7/9. In successive order, resistance profile was observed in the cephalosporins: ceftazidime (6/9) and cefepime (7/9), while resistance was less pronounced in the aminoglycosides: amikacin (4/9), gentamicin (3/9) and tobramycin (3/9), and in sulfamethoxazole/trimethoprim (5/9). The complete details of these results are graphically represented in Figure 1, which provides a visual and illuminating perspective of the antimicrobial resistance patterns exhibited by the strains analyzed.



PERCENT OF ANTIMICROBIAL RESISTANCE									
Microorganism	**AMK**	**CAZ**	**CIP**	**FEP**	**GEN**	**IPM**	**MEM**	**SXT**	**TOB**
A. baumannii	44.4	66.7	77.8	77.8	33.3	77.8	66.7	55.6	33.3

Figure 1. Frequency of antimicrobial resistance in *A. baumannii* strains producing resistance genes. CAZ: ceftazidime; FEP: cefepime; IPM: imipenem; MEM: meropenem; AMK: amikacin; GEN: gentamicin; TOB: tobramycin; CIP: ciprofloxacin; SXT: sulfamethoxazole/trimethoprim.

The analysis of antibiotic resistance data observed in Figure 1 shows that CAZ (ceftazidime) has a mean resistance of 66.7%, with a 95% confidence interval ranging from 61.5% to 71.9%, indicating moderate resistance with reasonable variability. FEP (cefepime) presents high resistance with a mean of 77.8% and a 95% confidence interval between 73%

and 82.6%, suggesting consistency and high resistance among the strains. IPM (imipenem), with a mean resistance of 77.8% and a confidence interval similar to FEP, also shows high resistance, indicating lower effectiveness against the studied strains. MEM (Meropenem) has a resistance profile similar to CAZ, with a mean of 66.7% and a 95% confidence interval between 61.5% and 71.9%, indicating moderate resistance. AMK (Amikacin) shows intermediate resistance with a mean of 44.4% and a 95% confidence interval between 40.7% and 48.1%, showing less variability in strain resistance. GEN (gentamicin), with a mean resistance of 33.3% and a 95% confidence interval between 30.2% and 36.4%, presents low resistance and high data consistency, suggesting that this antibiotic could be more effective. TOB (tobramycin) shows similar results to GEN, with a mean of 33.3% and a 95% confidence interval between 30.2% and 36.4%, indicating low resistance and high consistency. CIP (ciprofloxacin) also shows high resistance, with a mean of 77.8% and a 95% confidence interval between 73% and 82.6%, similar to FEP and IPM, indicating it is less effective against the studied strains. Finally, SXT (sulfamethoxazole/trimethoprim) has intermediate resistance with a mean of 55.6% and a 95% confidence interval between 51.4% and 59.8%, suggesting some variability but less than that of antibiotics with higher resistance.

In the field of molecular characterization, the identification of genes associated with beta-lactam resistance was conducted, specifically the *bla*CTX-M, *bla*TEM, and *bla*SHV genes. Additionally, genes linked to carbapenem resistance were detected and categorized into classes A (*bla*KPC), B (*bla*IMP, *bla*NDM and *bla*VIM) and D (*bla*OXA). Among all these molecular markers, three of the eight A. baumannii strains under study were detected (*bla*CTX-M, *bla*TEM, and *bla*OXA), whose graphical representation is provided in Figure 2.

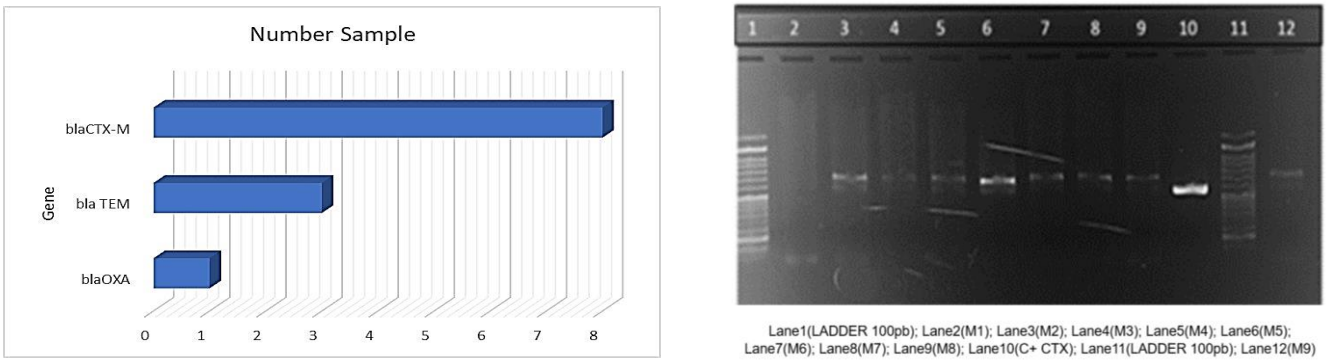


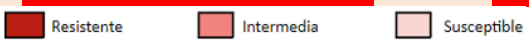
Figure 2. Number of *A. baumannii* samples with resistance genes detected and electrophoretic run photo for the ctx gene. CTX-M: cefotaxime; TEM: temoniera; OXA: oxacillinase; bla: beta-lactamase genes.

The presence of resistance genes was also detected in eight strains out of the nine investigated. In this context, strains CUS1, CUS2 and CUS3 were identified as having co-resistance genes (blaCTX-M, blaTEM and blaOXA) in the same strain CUS3. A notable case is that of the CUS3 strain, whose antimicrobial susceptibility profile showed total resistance (100%) to the antibiotics examined, defining it as an MDR (multidrug-resistant) strain. In the case of the PM1 strain, despite the detection of the *bla*CTX-M gene, no resistance was evident in its susceptibility profile, which suggests atypical behavior compared to other strains. In the case of the TRU1 strain, the *bla*CTX-M gene was detected along with a 55.6% resistance to the antibiotics evaluated. On the other hand, the presence of resistance genes was not detected in strain CAL1 despite presenting a resistance of 55.6% to the exposed antibiotics.

In line with these findings, Table 4 presents a detailed arrangement of the resistance genes detected for each strain analyzed, accompanied by their respective susceptibility profiles.

Table 4. Phenotypic and genotypic resistance profile of *A. baumannii* isolates.

Strain	Resistance Gene	AMK	FEP	CAZ	CIP	GEN	IPM	MEM	TOB	SXT
TRU1	*bla*CTX-M									
PM1	*bla*CTX-M									
PM2	*bla*CTX-M									
CUS1	*bla*CTX-M, *bla*TEM									
CUS2	*bla*CTX-M, *bla*TEM									
CUS3	*bla*CTX-M, *bla*TEM, *bla*OXA									
CAL1	*NDM*									
CAL2	*bla*CTX-M									
CAL3	*bla*CTX-M									



AMK: amikacin; FEP: cefepime; CAZ: ceftazidime; CIP: ciprofloxacin; GEN: gentamicin; IPM: imipenem; MEM: meropenem; TOB: Tobramycin; SXT: sulfamethoxazole/trimethoprim; ND: not detected).

4. Discussion

Recently, results have been reported showing a significant increase in the level of phenotypic resistance of this strain. Reports, such as those from SENTRY worldwide, indicated 1.6% resistance to carbapenems for the year 2016 [24], while the ECDC reported 31.9% for the year 2018 [25], and in our research, we reported resistance of 77.8% for imipenem (IPM) and 66.7% for meropenem (MEM), showing a notable increase. Furthermore, regarding the phenotypicity of multidrug resistance, another investigation reported that 46% of *A. baumannii* isolates were resistant to carbapenems, showing MDR and XDR phenotypes. Seven clonal groups were identified, with 36% related to international clone II. Oxacillinase genes for the *bla*OXA-51-Like genes were detected in all isolates, *bla*OXA-23-Like in 36% of isolates, and the metallo-beta-lactamase gene *bla*VIM in 71% of the isolates. In our study, expression of the *bla*OXA gene, in co-existence with two beta-lactam genes, *blaCTX-M* and *bla*TEM, was observed in the CUS3 strain. The wide distribution of these resistances in the population of strains studied highlights the importance of continuous surveillance and implementation of control strategies to mitigate their spread [26].

Importantly, resistance to carbapenems is of particular concern, as these antibiotics are considered last-line antibiotics for the treatment of serious infections caused by bacteria resistant to other antibiotics [27]. Carbapenem resistance has become a major problem worldwide, and Latin America is no exception [6]. It is important to highlight that this resistance does not originate solely from direct exposure to antibiotics but is also related to other determining factors. Among them, the transmission of resistance genes between bacteria stands out, which contributes to the spread of resistant strains [28].

In line with molecular characterization, the detection of the presence of resistance genes through the PCR technique provided valuable information on the molecular mechanisms underlying antimicrobial resistance. The genes detected in this investigation, such as *bla*CTX-M, *bla*TEM and *bla*OXA, are consistent with the resistance mechanisms observed in *A. baumannii* in previous studies [29]. The differential detection of these genes in the strains studied reinforces the notion that *A. baumannii* employs a variety of mechanisms to adapt and counteract the action of antibiotics, as determined in the CUS3 strain.

Dario R., et al. (2016) [30] reported in their research that at least 88.9% of the strains showed expression of resistance genes, highlighting the unusual presence of a class A Extended spectrum beta-lactamases (ESBL) in *A. baumannii* [31], led by the *bla*CTX-M gene followed by *bla*TEM, which has been verified and evidenced in our research since both beta-lactam genes were expressed in our isolates. Although they are not frequent, ESBL genes such as *bla*TEM, *bla*SHV and *bla*CTX-M have been reported [31,32]. Despite

its limited clinical importance compared to other genes, studies have pointed out the cellular distribution and invasion capacity of *bla*CTX-M [28]. The detection of *bla*CTX-M in a non-fermenting bacillus such as *A. baumannii* is striking, and its presence could be explained because *bla*CTX-M has the ability to distribute cosmopolitanly as well as the ease of invading human and animal cellular structures [33]. Furthermore, the presence of ESBL may facilitate the prevalence of these markers in nosocomial pathogens, as observed in the first report of MBL (NDM-1) [34].

Despite the low percentage 11.1% of carbapenemase genes blaOXA expressed in this study, it has been observed that *A. baumannii* commonly manifests carbapenemase genes, mainly of the *bla*OXA type [35], considered an intrinsic mechanism in this pathogen [36]. Carbapenemase genes, such as *bla*KPC, *bla*VIM, *bla*NDM and *bla*OXA, have been reported in bacteria such as *Klebsiella pneumoniae* and *Escherichia coli*, mostly acquired in hospital environments through plasmids, similar to what may have occurred with ESBLs in *A. baumannii,* increasing since its discovery in 1990 [37].

This study identifies a co-resistance group between Class A ESBLs and Class D Carbapenemases in the CUS1, CUS2 and CUS3 strains, evidencing an MDR susceptibility profile in *A. baumannii.* This co-resistance detected in some strains, which express multiple resistance genes, accentuates the complexity and adaptive capacity of *A. baumannii* in response to antimicrobial pressures. The identification of MDR strains and the observation of divergent susceptibility profiles based on gene expression suggest wide genetic variability in *A. baumannii* populations and highlight the need for an individualized approach in the selection of antimicrobial therapies [37].

In addition, unusual cases were observed, such as strain PM1, which expressed the *bla*CTX-M gene but did not show resistance in its susceptibility profile, suggesting atypical behavior compared to other strains. Similarly, the TRU1 strain presented the expression of the *bla*CTX-M gene along with partial resistance to the antibiotics evaluated. In contrast, strain CAL1 did not express resistance genes despite showing partial resistance to antimicrobial agents.

The uniqueness of the mutations that these strains can express is discussed by another study in which they report the appearance of a special type of bacteria, *A. baumannii,* in the Amazon region of Brazil. Four groups of these bacteria were identified through laboratory tests; one of these groups, called IC-6, turned out to be highly resistant to multiple drugs, similar to our findings in strains CUS1, CUS2 and CUS3. Resistance genes were found in these bacteria, and the *bla*OXA-72 gene is believed to be located on a small fragment of genetic material similar to our findings of the OXA gene in the CUS3 strain. Surprisingly, bacteria in Brazil share these resistance genes with bacteria found in another geographic area and at a different time. This suggests a connection between these resistant bacteria in different locations and highlights the importance of monitoring and understanding the spread of resistant bacteria even in less populated regions, as they pose a threat to public health [38].

The findings presented in this study are of great importance for both clinical practice and public health, emphasizing the pressing need to implement effective infection control strategies and promote the rational use of antibiotics. The constant evolution and adaptation of *A. baumannii* underline the relevance of maintaining continuous surveillance and carrying out a comprehensive analysis of antimicrobial resistance [39].

5. Conclusions

The present investigation has provided a detailed view of antimicrobial resistance and gene expression profiles in *A. baumannii* strain isolates from six Peruvian hospital centers, revealing high multidrug resistance, particularly to beta-lactams and carbapenems. Multiple key resistance genes, including *bla*CTX-M, *bla*TEM, and *bla*OXA, were identified using PCR. The findings highlight an urgent need for enhanced surveillance, infection control, and alternative treatment strategies to combat rising bacterial resistance.

Author Contributions: P.M.-C. and M.R.C.-M. Conceptualization. P.M.-C., J.Y., M.R.C.-M., A.F.-L., P.A.M., C.P.S., J.P.-D., H.M.-F. and J.A.D.L.C.-V. Methodology, Software, Validation. P.M.-C., J.Y., M.R.C.-M., A.F.-L., P.A.M., C.P.S., J.P.-D., H.M.-F. and J.A.D.L.C.-V. Investigation, Resources, Writing—Original Draft Preparation. P.M.-C., M.R.C.-M., J.Y. and A.F.-L. Supervision. P.M.-C., J.Y., M.R.C.-M., A.F.-L., P.A.M., C.P.S., J.P.-D., H.M.-F. and J.A.D.L.C.-V. Software and Validation. P.M.-C., J.Y., M.R.C.-M., A.F.-L., P.A.M., C.P.S., J.P.-D., H.M.-F. and J.A.D.L.C.-V. Writing—Reviewing and Editing. All authors have read and agreed to the published version of the manuscript.

Funding: This work was supported by the School of Medicine of the Universidad Peruana Union and the Research Institute in Biomedical Sciences (INICIB), Ricardo Palma University.

Institutional Review Board Statement: It is important to highlight that the execution of this research, by virtue of its bacteriological approach, fully adheres to the ethical principles of Autonomy, Beneficence, Justice and Non-Maleficence (in accordance with the Belmont Report) and the standards contemplated in Helsinki human studies. This research has due approval from the Research and Ethics Committee of the Universidad Peruana Unión, in accordance with Resolution No. 2019-CEPUPeU-001.

Informed Consent Statement: Not applicable.

Data Availability Statement: All the data obtained from the study are in the tables and figures.

Conflicts of Interest: All authors declare that they have no financial relationships with any organization that may have an interest in the work presented in previous years; no other relationship or activity could appear to have influenced the work submitted.

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