



Article

In Vitro Activity of Sulbactam–Durlobactam against Carbapenem-Resistant *Acinetobacter baumannii* Clinical Isolates: A Multicentre Report from Italy

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Abstract: In the present study, the in vitro activity of the sulbactam–durlobactam (SUL–DUR) combination was evaluated against 141 carbapenem-resistant *A. baumannii* (CR*Ab*) clinical strains collected from six Italian laboratories. Over half (54.6%) of these isolates were resistant to colistin. The SUL–DUR combination was active against these CR*Ab* isolates with MIC₅₀ and MIC₉₀ values of 0.5 mg/L and 4 mg/L, respectively. Only eleven isolates were resistant to SUL–DUR with MIC values ranging from 8 to 128 mg/L. The SUL–DUR resistant *A. baumannii* exhibited several antimicrobial resistance genes (ARGs) such as *bla*_{OXA-20}, *bla*_{OXA-58}, *bla*_{OXA-66}, *bla*_{ADC-25}, *aac*(6')-Ib3 and *aac*(6')-Ib-cr and mutations in *gyr*A (S81L) and *par*C (V104I, D105E). However, in these isolates, mutations Q488K and Y528H were found in PBP3. Different determinants were also identified in these CR*Ab* isolates, including *adeABC*, *adeFGH*, *adeIJK*, *abeS*, *abaQ* and *abaR*, which encode multidrug efflux pumps associated with resistance to multiple antibacterial agents. This is the first report on the antimicrobial activity of SUL–DUR against carbapenem-resistant *A. baumannii* isolates selected from multiple regions in Italy.

Keywords: durlobactam; A. baumannii; WGS



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1. Introduction

Acinetobacter baumannii has emerged in the last two decades as one of the major causes of nosocomial infections associated with significant morbidity and mortality and it has been recognized by World Health Organization (WHO) as a "critical priority pathogen" (www.who.int, accessed on 2 August 2022) [1,2]. A. baumannii is ubiquitous and can be found in various environmental sources including soil, water, vegetables, meat and fish [3,4]. In hospital settings, especially in intensive care units, A. baumannii can cause

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ventilator-associated pneumonia and bloodstream infections [5–8]. The success of this organism is attributed to its ability to survive long-term in hospital environments and its prodigious capacity to acquire new antimicrobial resistance determinants [9]. The mechanisms of resistance in *A. baumannii* include enzymatic inactivation by β-lactamases, modification of target sites (e.g., Penicillin Binding Proteins, PBPs), alterations of porin proteins that result in decreased permeability and the upregulation of the activity of multidrug efflux pumps [9]. Currently, carbapenem-resistant A. baumannii (CRAb) pose a global threat to human health. CRAb is emerging worldwide, and the majority of these isolates show multidrug-resistant (MDR), extensively drug-resistant (XDR) and pandrug-resistant (PDR) phenotypes [10-13]. Currently, few therapeutic options are available for CRAb treatment [14,15]. Generally, colistin (CST), tigecycline and aminoglycosides are used against MDR A. baumannii, although there are limitations due to toxicity and poor pharmacokinetic properties [16]. CST has been successfully used to treat pneumoni and, bloodstream and meningitis infections caused by CRAb [17,18]. However, colistin-resistant isolates are emerging worldwide [19]. The intravenous fosfomycin is also used in combination with colistin or tigecycline or aminoglycoside for the treatment of hospital-acquired pneumonia caused by CRAb [20]. Cefiderocol, a novel siderophore cephalosporin, has recently been approved for the treatment of MDR A. baumannii [21]. Durlobactam (DUR), previously called ETX2514, is a non-β-lactam diazabicyclooctane (DBO) inhibitor with activity against Ambler class A, C and D β -lactamases [22,23]. Recently, some studies have shown that sulbactam in combination with durlobactam is active against MDR A. baumannii [24–31]. Sulbactam (SUL) is one of the first β -lactamase inhibitors used in combination with ampicillin for the treatment of class A β-lactamase-producing pathogens. In *A. baumannii*, SUL also has antibacterial activity by targeting PBPs (i.e., PBP1a/b and PBP3), enzymes required for cell wall synthesis [32]. DUR inactivates serine-β-lactamases by forming a reversible covalent bond with the active site serine [33]. This potent activity of durlobactam allows the susceptibility of CRAb to sulbactam to be restored [22,27]. The aim of the present study was to examine the in vitro activity of sulbactam–durlobactam (SUL–DUR) against 141 CRAb clinical isolates retrospectively collected from six clinical microbiology laboratories located across the national territories representative of northern, central and southern Italy.

2. Results

2.1. Antimicrobial Susceptibility

Antimicrobial susceptibility of CRAb isolates was previously assessed by each center using commercial systems in the context of normal clinical routine. Consistently, the associated traits were as follows: imipenem and meropenem, MICs > 8 mg/L; gentamicin, MICs > 8 mg/L; ciprofloxacin, MICs > 2 mg/L and SXT, MICs > 8 mg/L (based on trimethoprim concentration). Overall, 64 CRAb isolates were XDR (MIC values for colistin \leq 2 mg/L), while 77 CRAb isolates showed a PDR phenotype (MIC values for colistin > 2 mg/L).

The in vitro activity of SUL–DUR was evaluated for 141 CRAb clinical isolates using SUL, DUR and CST as comparators. Overall, 77 out 141 (54.6%) A. baumannii isolates exhibited resistance to CST with Minimal Inhibitory Concentration (MIC) values of ≥ 4 mg/L. The MIC $_{50}$ and MIC $_{90}$ for CST were 4 mg/L and >4 mg/L, respectively (Table 1). As shown in Table 1, 131 out of 141 CRAb isolates exhibited MICs > 4 mg/L for SUL and the MIC $_{50}$ and MIC $_{90}$ values were 16 mg/L and 128 mg/L, respectively. DUR had MIC $_{50}$ and MIC $_{90}$ values of 64 mg/L and 128 mg/L, respectively. The SUL–DUR combination was more potent against these CRAb isolates with MIC $_{50}$ and MIC $_{90}$ values of 0.5 mg/L and 4 mg/L, respectively. Only eleven isolates exhibited MIC values > 4 mg/L, the preliminary susceptible breakpoint for SUL–DUR (Table 1) [34,35]. All of the SUL–DUR resistant CRAb isolates were from the Clinical Microbiology Laboratory of Catania University located in southern Italy (Table 2).

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Table 1.	In vitro	activities	of sulbactam	–durlobactam	and	comparators	against	141	carbapenem-	
resistant	Acinetoba	acter baum	annii collected	d in Italy.						

Antimicrobial							Νι	ımber	of Iso	lates a	t Each	MIC	(mg/L)				
Agent	0.06	0.125	0,25	0.5	1	2	4	>4	8	16	32	64	128	>128	MIC RANGE	MIC ₅₀	MIC ₉₀
SUL	/	/	/	/	/	2	8	_	27	45	33	8	13	5	0.06->128	16	128
DUR	/	/	/	/	/	/	/	_	3	7	44	39	47	1	0.06 -> 128	64	128
SUL-DUR	/	4	25	51	30	14	6	_	4	2	/	/	/	5	0.06/4->128/4	0.5	4
CST	/	7	6	12	20	19	22	55	_	_	_	_	_	_	0.06 -> 4	4	>4

/ = the number of isolates equal to zero. _, no values available. In SUL–DUR combination, DUR was at fixed concentration of $4\,\mathrm{mg/L}$.

Table 2. MIC distribution of sulbactam–durlobactam and comparators against 141 CRAb isolates by location of the clinical microbiology laboratory.

City (No. Isolates)	Number of Isolates with MIC (mg/L)													
Antimicrobial Agents	0.06	0.125	0.25	0.5	1	2	4	>4	8	16	32	64	128	>128
Pavia (16)														
SUL	/	/	/	/	/	/	1	-	1	5	7	2	/	/
DUR	/	/	/	/	/	/	/	-	/	/	/	2	13	1
SUL-DUR	/	/	/	6	6	4	/	-	/	/	/	/	/	/
CST	/	/	1	6	9	/	/	/	-	-	-	-	-	-
Gemelli (26)														
SUL	/	/	/	/	/	1	2	-	4	11	7	1	/	/
DUR	/	/	/	/	/	/	/	-	/	2	6	11	7	/
SUL-DUR	/	/	3	16	7	/	/	-	/	/	/	/	/	/
CST	/	/	/	/	/	/	13	13	-	-	-	-	-	-
PE/AQ (9)														
SUL	/	/	/	/	/	/	/	-	/	1	6	1	1	/
DUR	/	/	/	/	/	/	/	-	/	/	3	2	4	/
SUL-DUR	/	/	1	2	2	4	/	-	/	/	/	/	/	/
CST	/	/	/	/	/	/	/	9	-	-	-	-	-	-
Roma Tre (20)														
SUL	/	/	/	/	/	1	3	-	3	5	7	1	/	/
DUR	/	/	/	/	/	/	/	-	/	/	6	6	8	/
SUL-DUR	/	/	3	7	7	1	2	-	/	/	/	/	/	/
CST	/	/	/	/	/	7	7	6	-	-	-	-	-	-
Catania (70)														
SUL	/	/	/	/	/	/	2	-	19	23	6	3	12	5
DUR	/	/	/	/	/	/	/	-	3	5	29	18	15	/
SUL-DUR	/	4	18	20	8	5	4	-	4	2	/	/	/	5
CST	/	7	5	6	11	12	2	27	-	-	-	-	-	-

<u>Pavia</u>, isolates collected from the Microbiology Laboratory of the University of Pavia. <u>Gemelli</u>, isolates collected from the teaching "Gemelli" Hospital Rome. <u>PE/AQ</u>, isolates collected from Spirito Santo Hospital Pescara and the University of L'Aquila. <u>Roma Tre</u>, isolates collected from the Clinical Microbiology Laboratory of Roma Tre University. <u>Catania</u>, isolates collected from the Clinical Microbiology Laboratory of the University of Catania./= the number of isolates equal to zero. -, no values available. In the SUL-DUR combination, DUR was at a fixed concentration of 4 mg/L.

2.2. Whole-Genome Sequencing of SUL-DUR Resistant A. baumannii: Resistome and Virulome Characterization

Whole-genome sequencing of the eleven SUL–DUR resistant CRAb isolates was performed and these isolates were found to encode several antibiotic resistance genes (ARGs) (Table 3) and virulence-associated genes (VAGs) (Table 4). Among the eleven analyzed strains, all encoded for the class D β -lactamases OXA-20, OXA-58 and OXA-66, in addition to ADC-25, a chromosomally encoded class C β -lactamase. While the presence of these β -lactamases most likely confer resistance to β -lactam antibiotics such as carbapenems, durlobactam has been shown to effectively inhibit these enzymes, so are not a likely cause

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of the elevated SUL–DUR MICs. Genes that confer resistance to other classes of antibiotics were also detected including aminoglycoside resistance (aac(6')-Ib3 and aac(6')-Ib-cr) and fluoroquinolone resistance (mutations in gyrA (S81L) and parC (V104I, D105E) (Table 2). The Insertion Sequence (IS) IS26 and ISAba125 were also identified in all eleven CRAb, and the transposon Tn6018 was found in two isolates (CT24 and CT58). All of the SUL–DUR-resistant CRAb showed the same profile of virulence factors (Table 4); however, isolates CT57 and CT58 possessed, in addition, lpsB and lpx VAGs which confer resistance to CST. The eleven CRAb isolates showed the presence of AdeABC, AdeFGH, AdeIJK, abeS, abaQ and abaR multidrug efflux pumps. As shown in Table 4, several genes involved in the biofilm formation system were also identified. Resistance mediated by quorum sensing is represented by abaI and abaR genes. The pbpG, also known as PBP7, was also identified in all SUL–DUR-resistant CRAb (Table 4). The impact of these genes on SUL–DUR susceptibility is not known.

Table 3. Characterization of Sulbactam–Durlobactam-resistant A. baumannii.

Strain	Sequence	Ward		SUL-	SUL	DUR	CST	Resis	Mobile	
	Туре		Sample	DUR MIC (mg/L)	MIC (mg/L)	MIC (mg/L)	MIC (mg/L)	β- Lactamases	Other	Genetic Elements
A. baumannii CT20	2	transplant	BAL	8	128	128	0.125	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58}	aac(6')-Ib-cr aac(6')-Ib3 tetA(41)	IS26, ISAba125
A. baumannii CT57	2	ICU	BAL	8	128	64	64	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58}	aac(6')-Ib-cr aac(6')-Ib3 tetA(41)	Tn6018, IS26, ISAba125
A. baumannii CT58	2	ICU	wound	8	128	32	32	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58}	aac(6'-)Ib-cr aac(6')-Ib3 tetA(41)	Tn6018, IS26, ISAba125
A. baumannii CT68	2	ICU	blood	8	128	64	0.25	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58}	aac(6')-Ib-cr aac(6')-Ib3 sul1	IS26, IS <i>Aba</i> 125
A. baumannii CT24	2	ICU	blood	16	64	128	0.5	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58} bla _{OXA-66}	aac(6')-Ib-cr aac(6')-Ib3 qacE sul1 gyrA (S81L) parC(V104I, D105E)	IS26, ISAba125
A. baumannii CT25	2	ICU	catheter	16	128	64	1	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58} bla _{OXA-66}	aac(6')-Ib-cr aac(6')-Ib3 sul1	IS26, IS <i>Aba</i> 125
A. baumannii CT26	2	surgery	bile	>128	>128	64	0.5	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58} bla _{OXA-66}	aac(6')-Ib-cr aac(6')-Ib3 qacE sul1 gyrA (S81L) parC (V1041, D105E)	IS26, ISAba125
A. baumannii CT29	2	ICU	exudate	>128	>128	128	1	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58} bla _{OXA-66}	aac(6')-Ib-cr aac(6')-Ib3 qacE sul1 gyrA (S81L) parC (V104I, D105E)	IS26, ISAba125
A. baumannii CT30	20	ICU	catheter	>128	>128	32	1	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58} bla _{OXA-66}	aac(6')-Ib-cr aac(6')-Ib3 qacE sul1 gyrA (S81L) parC (V1041, D105E)	IS26, ISAba125

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Tab	ie 3.	Cont.

Strain	Casuamaa			SUL-	SUL	DUR	CST	Resi	Mobile	
	Sequence Type	Ward	Sample	DUR MIC (mg/L)	MIC (mg/L)	MIC (mg/L)	MIC (mg/L)	β- Lactamases	Other	Genetic Elements
A. baumannii CT31	20	ICU	pus	>128	>128	128	0.125	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58} bla _{OXA-66}	aac(6')-Ib-cr aac(6')-Ib3 qacE sul1 gyrA (581L) parC(V104I, D105E)	IS26, ISAba125
A. baumannii CT32	20	ICU	BAL	>128	>128	128	1	bla _{ADC-25} bla _{OXA-20} bla _{OXA-58} bla _{OXA-66}	aac(6')-Ib-cr aac(6')-Ib3 qacE sul1 gyrA (S81L) parC (V104I, D105E)	IS26, ISAba125

Table 4. Virulence factors encoded by the eleven *A. baumannii* isolates resistant to SUL–DUR.

SUL-DUR-Resistant <i>A. baumannii</i> (Strains No.: CT20, CT24, CT25, CT26, CT29, CT30, CT31, CT32, CT57, CT58, CT68)							
Virulence-Associated Genes	Virulence Factors						
adeA, adeC, adeF, adeG, adeH, adeI, adeK, adeL,	RND efflux pump AdeABC, AdeFGH						
adeN, adeJ, adeR	and <i>AdeIJK</i>						
abeS	SMR family of transporter efflux pumps						
abaQ, abaF	MFS transporters						
plc, plcD	Phospholipase						
lpsB (only in CT57 and CT58)	Lipopolysaccharide synthesis (mutations are involved in CST resistance)						
<i>lpxA</i> , <i>lpxB</i> , <i>lpxC</i> , <i>lpxD</i> , <i>lpxL</i> , <i>lpxM</i> (only in CT57	Biosynthesis of lipid A (mutations are involved						
and CT58)	in CST resistance)						
barA, barB							
basA, basB, basC, basD, basF, basG, basH, basI, basI							
bauA, bauB, bauC, bauD, bauE, bauF	Iron uptake: acinetobactin and heme utilization						
entE	1						
hemO							
bap, pgaA, pgaB, pgaC, pgaD, csuA, csuB, csuC,	Biofilm formation system and						
csuD, csuE, bfmR, bfmS	cell-cell adhesion						
abaI, abaR	Quorum sensing						
pbpG (or PBP7) and PBP3 ^{Q488K} and PBP3 ^{Y528H}	Penicillin-binding protein						
katA	A secondary catalase/peroxidase						

RND, resistant-nodulation division. SMR, small multidrug resistance. MFS, major facilitator superfamily.

2.3. Molecular Analysis of PBP-3 Gene

The amplification of the PBP-3 gene of the eleven SUL–DUR-resistant *A. baumannii* isolates gave an amplicon of about 1800 bp which was entirely sequenced. In all *A. baumannii* analyzed, the PBP3 showed the following amino acid substitutions: Q488K and Y528H.

3. Discussion

The production of carbapenem-hydrolysing β -lactamases is one of the most common mechanisms responsible for carbapenem resistance in *A. baumannii* [10]. Several carbapenemases have been identified in *A. baumannii*, in particular, serine β -lactamases, belonging to class D and metallo- β -lactamases (class B enzymes). Nevertheless, metallo- β -lactamases are very rare in this microorganism [10]. However, in addition to β -lactamases, other mechanisms of resistance to carbapenems, including overexpression of efflux pumps, the reduction or inactivation of the expression of porins and the modification in the expression or synthesis of new PBPs, are found in *A. baumannii* isolates [10]. In the 141 *A. baumannii* analyzed in the present study, class C and D β -lactamases such as OXA-23, OXA-58, OXA-66 (OXA-51-like enzyme), OXA-82 (OXA-51-like enzyme) and ADC-25 were previously identified [36–47]. The bla_{OXA} -types are, usually, flanked by one or two copies of

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the insertion sequences (i.e., ISAba1, ISAba125) which are located in opposite orientations. These ISAba insertion sequences enhance the expression of blaOXA genes and they give genetic plasticity to A. baumannii species [48]. Herein, we have demonstrated potent in vitro activity of the SUL–DUR combination against 92% of the CRAb clinical isolates collected from a range of geographical regions within Italy. Of note, SUL-DUR demonstrated antimicrobial activity against both OXA-23- and OXA-58-producing isolates. Moreover, all but two of the colistin-resistant isolates (more than 50% of total isolates) were susceptible to the SUL-DUR combination. Eleven isolates (all from the Microbiology Clinical Laboratory of Catania University) were resistant to SUL-DUR, with most of them belonging to ST2 (n = 8) and showing a MIC range of 8–>128 mg/L. Two of these isolates were also resistant to CST. The whole genome analysis of the eleven SUL–DUR-resistant CRAb showed the presence of several ARGs, including bla_{OXA-20} (bla_{OXA-58} like gene), bla_{OXA-58}, bla_{ADC-25}, aac(6')Ib-cr, aac(6')-Ib3, and tetA(41), a tetracycline efflux pump protein closely related to Tet(39) often found in Acinetobacter spp. [49]. Multiple VAGs were also found in these isolates. The multidrug efflux systems (RND, SMR, MFS families) are associated with multiple resistance mechanisms which are capable of extruding a broad range of structurally unrelated compounds [50–52]. The contribution of these ARGs and VAGs to the SUL-DUR-resistant phenotype seen in these isolates is not known. However, in the eleven SUL-DUR-resistant A. baumannii we found Q488K and Y528H mutations in PBP3. To date, reports of SUL-DUR resistance have been rare and resistance is usually attributed to the presence of metallo-β-lactamases, which DUR does not inhibit, or to mutations near the active site of PBP3, the target of sulbactam [24-26]. Few therapeutic choices are available to treat CRAb isolates [14,16,53]. CRAb pneumonia is a major clinical issue with unmet therapeutic needs; in fact, both colistin and tigecycline did not reach a satisfactory epithelial lining fluid concentration and cefiderocol showed disappointing clinical outcomes [54]. DUR displayed an acceptable ratio of epithelial lining fluid to plasma concentrations of 0.37 while SUL reached a 0.5 ratio [34,55]. Another important clinical issue to consider is that the SUL-DUR combination is expected to have a lower degree of nephrotoxicity compared to CST (ATTACK Trial. Available online: https://investors.entasistx.com/news-releases/ news-release-details/entasis-therapeutics-announces-positive-topline-results, accessed on 2 August 2022), and in general be more safe. Taking into account the significant MIC reduction reached upon adding DUR to SUL and the promising clinical data from the phase 3 clinical trial comparing the safety and efficacy of SUL-DUR to CST for the treatment of infections caused by CRAb (SUL–DUR mortality 19%, CST mortality 32%, 95% CI: -30.0, 3.5), if approved, SUL–DUR may be an important option for CRAb treatment regimens. Further studies are needed to elucidate the molecular mechanisms responsible for resistance to SUL-DUR and to explore its therapeutic potential. It will also be necessary to combine in vitro findings with additional pharmacokinetic and pharmacodynamic data in order to provide more meaningful predictions of the in vivo efficacy of SUL-DUR combination in clinical practice.

4. Materials and Methods

4.1. Antibiotics and Inhibitors

SUL and DUR (ETX2514) were kindly provided by Dr. Alita A. Miller, Entasis Therapeutics, Waltham, MA, USA.

4.2. Bacterial Strains Selection

A total of 141 non duplicate CRAb strains, which were previously characterized for their mechanisms of resistance, were included in this study [36–47]. In particular, we retrospectively selected 64 XDR and 77 PDR previously characterized CRAb clinical isolates collected in six centers from Italy. Isolates were selected on the basis of this extensive resistance although resistance determinants were different (mostly including OXA-type enzymes, as reported in related publications). Most of the isolates (121 out of 141) were collected from five clinical microbiology laboratories distributed throughout northern,

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central and southern Italy. Specifically, 16 A. baumannii were collected from the Microbiology Laboratory of the University of Pavia (Northern Italy) during 2018, 26 isolates were collected from the teaching "Gemelli" Hospital Rome (central Italy) between 2020 and 2022, 8 isolates were collected from Spirito Santo Hospital Pescara (Central Italy) in 2020–2021, 1 isolate was from the University of L'Aquila (Central Italy) and 70 isolates were collected from the Clinical Microbiology Laboratory of the University of Catania (Southern Italy) between 2008 and 2018. In addition, 20 A. baumannii were kindly given by Professor Visca, Clinical Microbiology Laboratory of Roma Tre University (Central Italy). These strains were collected in 2004–2014 from different countries during the project "Carbapenem-resistant Acinetobacter baumannii: whole-genomic and phenomic investigation of the traits that favored the predominance and shift to OXA-23-producing IC2 isolates"; funded by ESCMID in 2017. The antimicrobial susceptibility of CRAb isolates was previously assessed by participating centers using commercial systems in the context of normal clinical routine. Tested antibiotics were imipenem, meropenem, gentamicin, ciprofloxacin and colistin. All strains were collected from different wards including intensive care units, infectious diseases units, neurosurgery, pneumology, thoracic surgery and internal medicine. All A. baumannii were isolated from clinical sources, including sputum, blood, urine, wounds, peritoneal fluid, liquor and stool. The A. baumannii isolates belonged to the following sequence types: ST2 (n = 121), ST1 (n = 6), ST4 (n = 1), ST20 (n = 5), ST78 (n = 2), ST81 (n = 1), ST95 (n = 1), ST109 (n = 1), ST196 (n = 1) and ST197 (n = 1). In these A. baumannii strains, the carbapenem resistance was mainly mediated by the presence of OXA-23 (80 isolates), OXA-58 (48 isolates), OXA-66 (4 isolates) and OXA-82 (4 isolates). The simultaneous presence of OXA-23 and OXA-58 was found in 11 isolates and, in addition, ADC-25, a chromosomal AmpC enzyme, was also identified [36–47].

MDR isolates were defined as those with acquired non-susceptibility to at least one agent in three or more antimicrobial categories. XDR isolates were defined as those with acquired non-susceptibility to all antibiotics, except for one or two. PDR isolates were defined as those with acquired non-susceptibility to all antibiotics.

4.3. Bacterial Strains Identification

A. baumannii isolates were collected by standard methods, followed by isolation in pure culture on MacConkey agar plates, identified by the Vitek 2 system (bioMerieux, Marcy l'Etoile, France) and stored in Brain Hearth Infusion broth with 15% glycerol and frozen at -80 °C.

4.4. MIC Determination

The MIC experiments were performed by conventional broth microdilution procedures in Mueller Hinton broth supplemented with calcium and magnesium to physiological concentrations (CAMHB), using an inoculum of 5×10^5 CFU/mL according to the Clinical and Laboratory Standards Institute (CLSI) [56]. One hundred and forty-one non-duplicate *A. baumannii* isolates were tested against DUR alone as well as SUL alone, plus SUL–DUR and CST. For SUL, a susceptibility breakpoint of 4 mg/L was used, based on the CLSI ampicillin–sulbactam susceptible breakpoint of 8/4 mg/L for *Acinetobacter spp* [56]. SUL–DUR MICs were performed as 2-fold dilutions of SUL with DUR at a fixed concentration of 4 mg/L [56]. MICs were interpreted using CLSI breakpoints where available. Concurrent quality control (QC) procedures were performed by testing *Escherichia coli* ATCC 25922, examined for each MIC run. Following 18 to 20 h of aerobic incubation at 37 °C, the microplates were examined for growth. The determination of all MICs was performed in three separate sets of experiments.

4.5. Whole-Genome Sequencing

Total nucleic acid was extracted using MagMax Microbiome Ultra Nucleic Acid Isolation kit (Applied Biosystems and ThermoFisher Scientific, Monza, Italy). Genomic libraries were prepared using Swift 2S Turbo DNA Library kit (Swift Biosciences, Ann Arbor, MI,

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USA) as previously reported [57,58]. WGS was performed on an Illumina MiSeq using v3 reagent kits generating 2 × 300 bp paired-end reads (Illumina, San Diego, CA, USA). DRAGEN FastQC + MultiQC v3.9.5 (https://basespace.illumina.com/apps/10562553 /DRAGEN-FastQC-MultiQC, accessed on 24 May 2022) were used for quality control and sequences filtering. Paired-end reads were assembled with Velvet de novo Assembly v1.0.0 (https://basespace.illumina.com/apps/8556549/Velvet-de-novo-Assembly, accessed on 5 June 2022). Multi-Locus Sequence Typing (MLST) on assembled *A. baumannii* genomes was performed according to the Pasteur scheme. ResFinder4.1 and MobileElementFinder 1.0.3 were used to detect acquired antimicrobial resistance genes and mobile genetic elements, respectively. ResFinder and MobileElementFinder 1.0.3 databases were synchronized with databases from Center for Genomic Epidemiology (http://www.genomicepidemiology.org/, accessed on 10 June 2022). Virulence Factor Database (VFDB) was used for the detection of virulence genes (http://www.mgc.ac.cn/VFs/, accessed on 2 August 2022).

4.6. PBP-3 Amplification and Sequencing

The amplification of the PBP-3 gene was performed in PCR using the total genome of the SUL–DUR-resistant *A. baumannii* (CT20, CT24, CT25, CT26, CT29, CT30, CT31, CT32, CT57, CT58, CT68) and the following external primers: PBP-3_F 5'TTACCTGCGAATAGGATTTTCTG and PBP-3_R 5' ATGTGGCGGTTTTATCTGCT. The amplicons obtained were purified and directly sequenced on both strands by using a BigDye Sequencing Reaction Kit and an ABI PRISM 3500 capillary automated sequencer (Applied Biosystem, Monza, Italy).

5. Conclusions

In the present study, SUL–DUR demonstrated good in vitro antimicrobial activity against XDR and PDR *A. baumanni* clinical isolates, collected from different regions across Italy. These data confirmed the results from recent studies showing good activity of the SUL–DUR combination against MDR, XDR and PDR *A. baumannii* [59]. To the best our knowledge, this study also represents the first report on SUL–DUR activity against a large number of carbapenem-resistant, and largely colistin-resistant, *A. baumannii* isolates from Italy.

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