



ReFORMÚLA**T**E

En busca del tesoro

“La evolución de las resistencias”



Dr. Rafael Cantón
Hospital Universitario Ramón y Cajal
SERVICIO DE MICROBIOLOGÍA Y PARASITOLOGÍA



@RafaMCanton



@microRyC



Departamento de
Microbiología y
Parasitología
Universidad
Complutense. Madrid



La evolución de las resistencias

Disclosures

■ Participation in educational programs

- FastInov
- Roche
- MSD
- Shionogi
- Pfizer

■ Participation in research studies

- BioMerieux
- Cepheid
- FastInov
- Quantamatrix
- MSD
- Resistell
- Shionogi

■ Evaluation of clinical trials

- MSD
- Pfizer



European Society of Clinical Microbiology and Infectious Diseases

Acknowledgements



ciberinfec isciii

Antimicrobial resistance: a microbiological view

Consequence of “genetic capitalisms”

Baquero et al. ASM News 2003; 69: 547-51; Cantón et al. Curr Opin Infect Dis 2003; 16:315-25;
Canton, Ruiz-Garbajosa Curr Opin Pharmacol 2011; 11:477-85

Association with *high-risk clones*

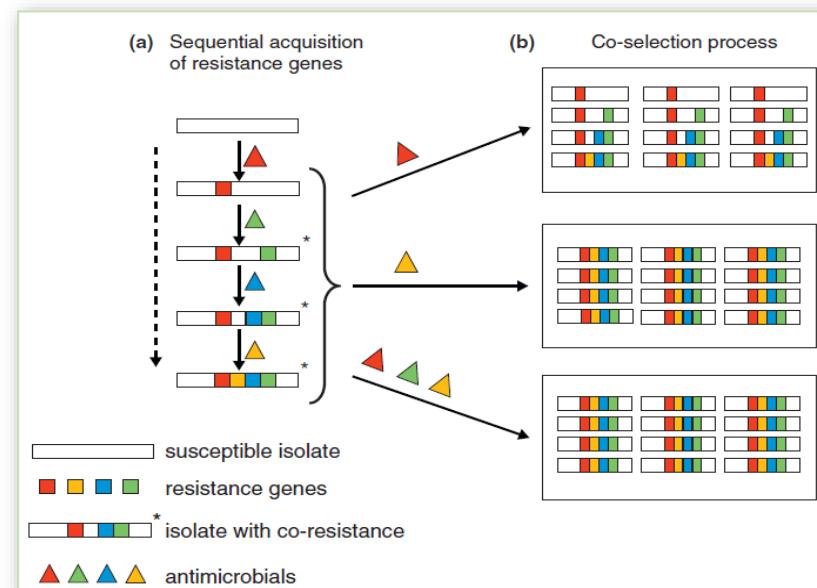
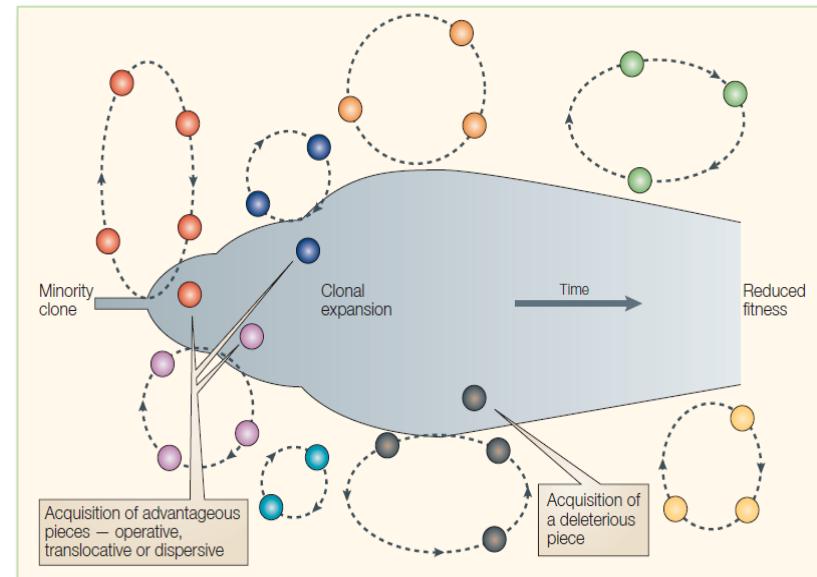
- Efficiently colonize human hosts during long periods of time
- Ability to be transmitted with high efficiency among patients
- Ability to produce severe or invasive infections
- Major role to spread resistance mechanisms of critical importance

TROCAR FP7 Health EU project (Baqueiro F); Woodford et al. FEMS Microbiol Rev 2011; 35:736-55;
Cantón R, Ruiz-Garbajosa P. Curr Opin Pharmacol 2011; 11:477-85;
Cantón R, et al. Curr Opin Crit Care. 2020;26(5):433-441

Consequence of selection and co-selection processes

- Different antimicrobials might select the same resistant bacteria
- A single antimicrobial might select different resistant bacteria

Baqueiro F & Cantón R. Evolutionary Biology of Drug Resistance. In: Antimicrobial Drug Resistance. Lerner SA (ed). 2nd ed. 2017



High risk clones and antimicrobial resistance

Species	Clon	Mechanism of antimicrobial resistance	Coresistance
<i>Escherichia coli</i>	ST131	ESBL (CTX-M-15, -14, -27)	Fluoroquinolones [topoisomerase mutations, <i>qnr</i> , <i>aac(6')</i> -Ib-cr...]; plasmidic AmpC beta-lactamases, carbapenemases; colistin resistance (<i>mcr-1</i>)
<i>Klebsiella pneumoniae</i>	ST11	ESBL (CTX-M-15, ...)	Fluoroquinolones [topoisomerase mutations, <i>qnr</i> , <i>aac(6')</i> -Ib-cr...]; plasmidic AmpC beta-lactamases (DHA-1), aminoglycoside resistance (ArmA, RmtB methylases)
	ST15	Carbapenemases (KPC, VIM, NDM, OXA-48)	
	ST101	VIM, NDM, OXA-48	
	ST147		
	ST258	Carbapenemases (KPC)	Colistin resistance (mutations in <i>pmrB</i>), ceftazidime-avibactam resistance
	ST307	Carbapenemases (KPC-like, NDM)	Ceftazidime-avibactam resistance
<i>Pseudomonas aeruginosa</i>	ST405	Carbapenemases (OXA-48)	ESBL (CTX-M-15)
	ST101	Multiresistance	Carbapenemases (VIM-2, GES-7, VEB-1, IMP-1, KPC-2, PER-1)
	ST175		
	ST235		
<i>Acinetobacter baumannii</i>	ST244		
	ST2	Carbapenemases (OXA-23)	Carbapenemases (OXA-24, OXA-58, NDM-1); aminoglycosides [AAC(3')-Ia, AADA, ANT(2')-I, APH(3')-VI, ... and methylases (ArmA)]

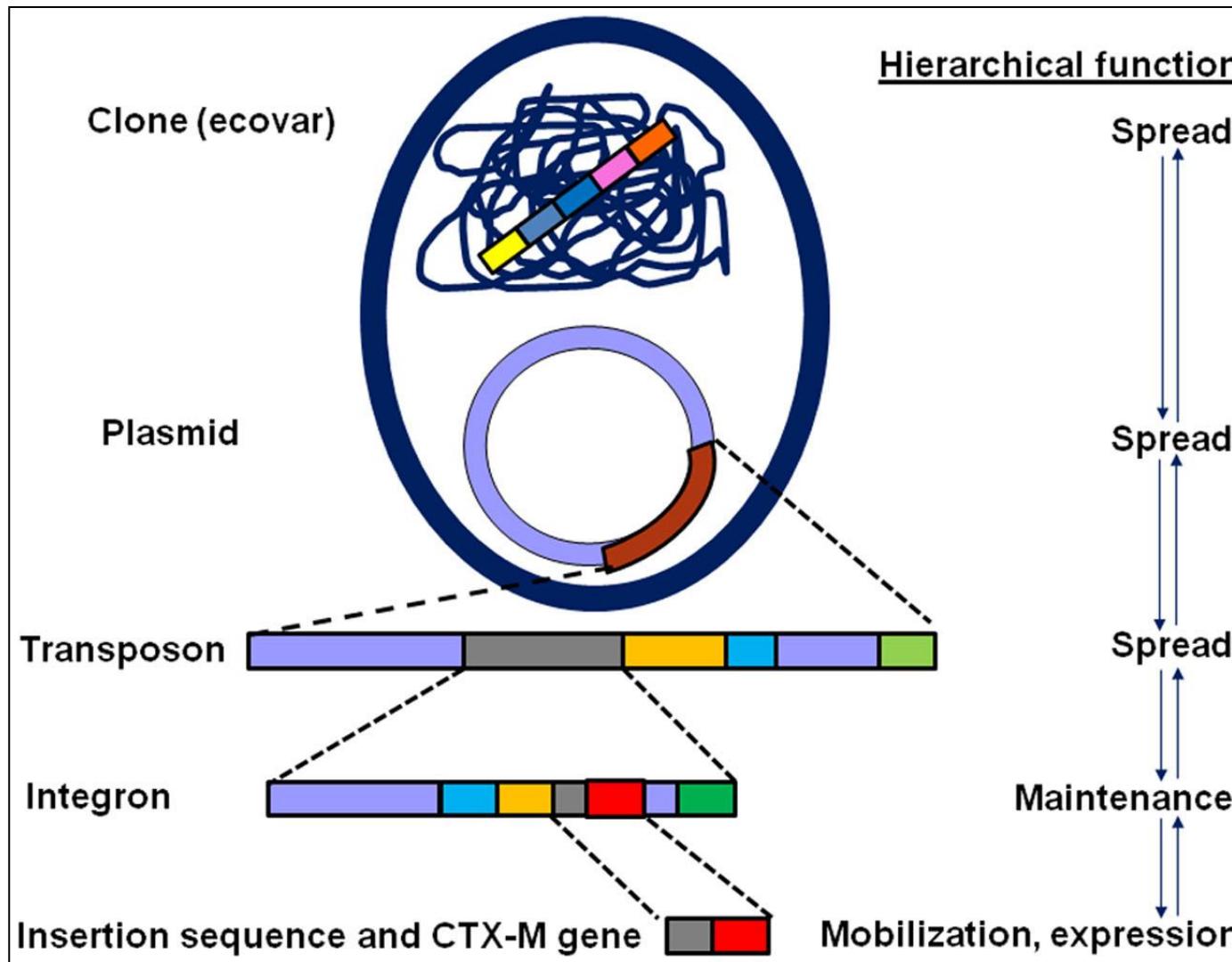
CTX-M, Active on cefotaxime, first isolated at Munich; ESBL, extended-spectrum beta-lactamases; GES, Guiana-extended spectrum; IMP, active on imipenem; KPC, *Klebsiella pneumoniae* carbapenemase; NDM, New Dehli metallo-beta-lactamase; OXA, Active on oxacillin; PER, *Pseudomonas* extended resistant; VEB, Vietnamese extended-spectrum β-lactamase; VIM, Verona integron encoded metallo-beta-lactamases.

High-risk clones:

Highly specialized genetic populations or subpopulations with enhanced ability to **colonize, spread and persist** in particular niches after having **acquired a diversity of adaptative traits** that increase their **epidemicity and/or pathogenic potential, including antibiotic resistance**

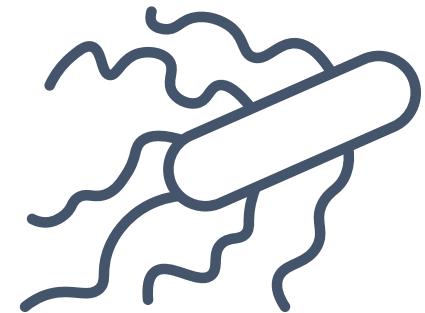
Baquero F, Coque TM. Multilevel population genetics in antibiotic resistance. FEMS Microbiol Rev. 2011;35:705-6

Antibiotic resistance: genetic capitalisms and *high-risk clones*



ST131 *Escherichia coli* high-risk clone

- Classified as an **extra-intestinal pathogenic *E. coli* (ExPEC)**
- Belongs to **phylogroup B2** and are **serotype O16:H5 or O25b:H4**
- **World wide distributed**, most frequently isolated in **patients with urinary tract infections (UTI) and bacteremia emanating from the urinary tract**



- Initially described late 80', most commonly associated with community-onset healthcare
- Involved in the spread of **multi-drug resistance**

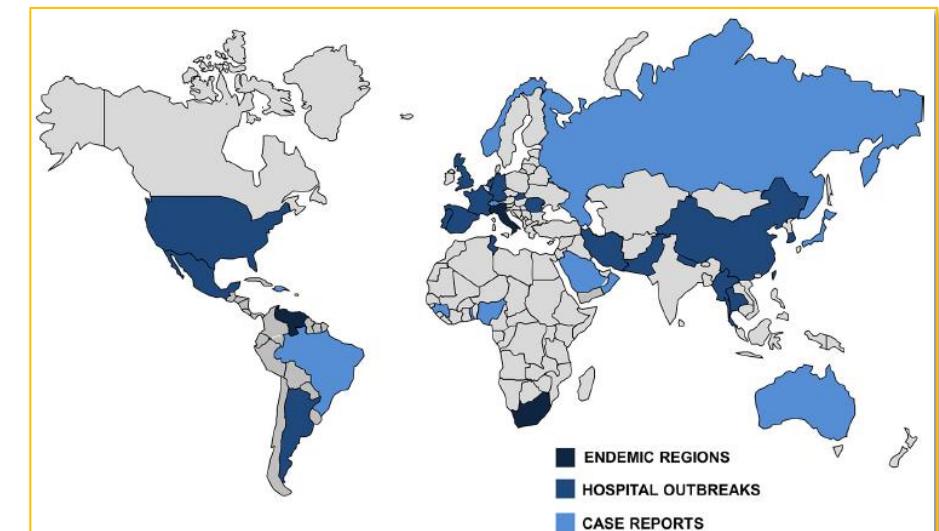
1980s - emergence of ciprofloxacin resistance
 - 70% of total ESBL-producing isolates (IncF plasmids)
 - 80% of total fluoroquinolone resistant isolates
 - high co-existence (>50%) of ESBL and fluoroquinolone resistance

↓
2020s - emergence and spread of carbapenemase producers

- Described causing **community acquired uncomplicated urinary tract and nosocomial infections**

ST307 *Klebsiella pneumoniae* high-risk clone

- 1990s Emerged in Europe during the early to mid-1990s
 - linked with *gyrA* S831 and *parC* S810 mutations (QRDR region) devoting **quinolone resistance**
- 2000s **3rd gen. cephalosporin resistance** (FIB-like plasmids with *bla*_{CTX-M-15})
 - associated with aminoglycoside [*strA*, *strB*, *aac(3)-Ila*, *aac(6')-Ib-cr*], quinolone [*qnrB1*, *oqxAB*] and other resistances genes [*sul2*, *dfrA14*, *catB*, *fosA*]
- 2010s **Carbapenem resistance** due to OXA-48, OXA-181, KPC-2, KPC-3, VIM-1, NDM-1 carbapenemases
Colistin resistance associated with *mcr-1*
Ceftazidime-avibactam resistance due to KPC mutations
- Widely distributed and currently endemic in Italy, Colombia, Argentina, United States, Spain, China, ...
- High ability to colonized
- Enhanced pathogenicity



Antimicrobial resistance: *the clinical view*

Term	Definition	Comment
Multi-drug resistant (MDR)	Non-susceptibility to at least one agent in three or more antimicrobial categories*	<ul style="list-style-type: none">• R to multiple antimicrobial agents (≥ 3), classes or subclasses• Includes XDR and PDR• Definition based on in-vitro susceptibility data with the aim to alert clinicians when treating patients and infection control
Extremely drug resistant (XDR)	Non-susceptibility to at least one agent in all but two or fewer antimicrobial categories*	<ul style="list-style-type: none">• R to all, or almost all, approved antimicrobial agents
Pan-drug resistant (PDR)	Non-susceptibility to all agents in all antimicrobial categories *	<ul style="list-style-type: none">• Organisms resistant to:<ul style="list-style-type: none">- almost all commercially available antimicrobials- all antimicrobials routinely tested- all antimicrobial available for empirical treatment

*therapeutic categories (i.e., aminoglycosides, fluoroquinolones, cephalosporins, carbapenems, ...)



Magiorakos et al. Clin Microbiol Infect
2012; 18:268-81

Multi-drug resistant (MDR) versus difficult to treat resistant (DTR) pathogens

Multi-drug resistant (MDR)

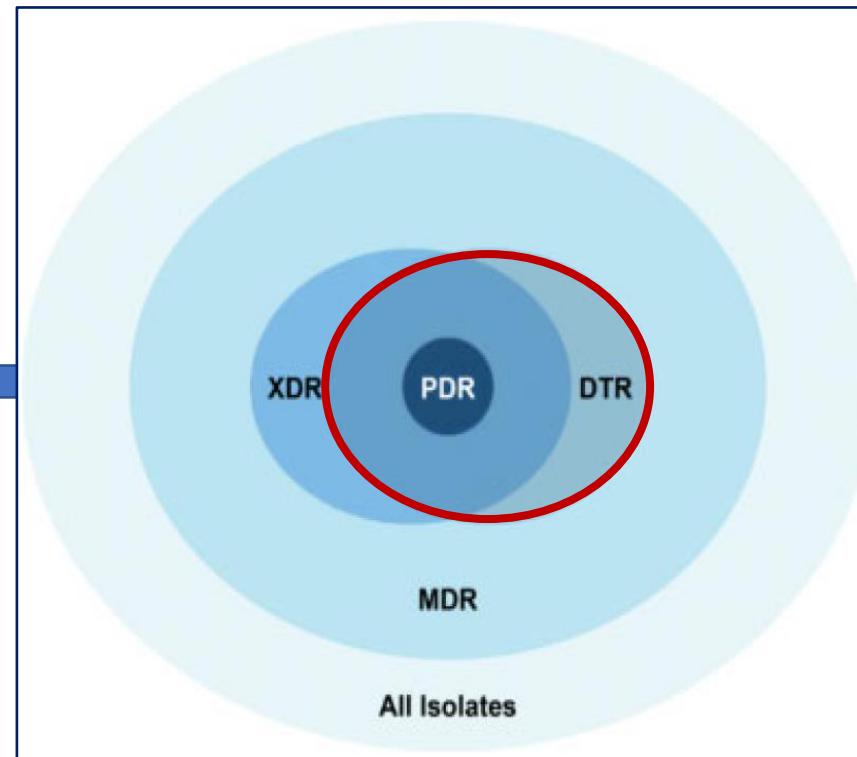
Non-susceptible to at least one antimicrobial in three or more antimicrobial categories

Extensive-drug resistant (XDR)

Non-susceptible to at least one antimicrobial in all but two or fewer antimicrobial categories

Pan-drug resistant (PDR)

Non-susceptible to all antimicrobial agents



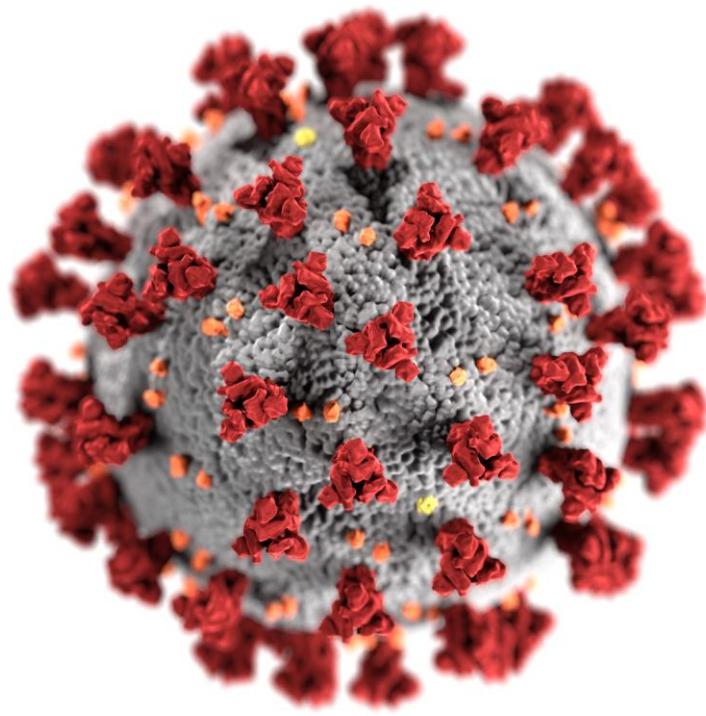
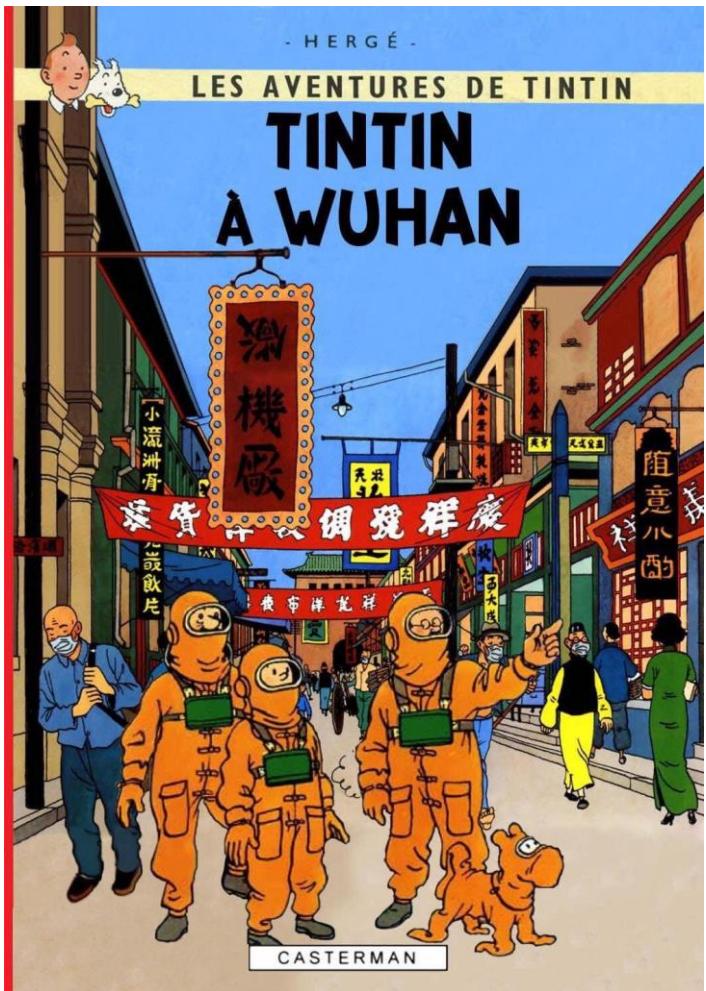
Difficult to treat resistant (DTR) pathogens

Resistant to all first-line high efficacy, low-toxicity agents, but susceptible to 'reserve agents', including colistin, aminoglycosides and tigecycline

ESKAPE microorganisms

Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter spp

SARS-CoV-2 – COVID-19



SARS-CoV-2

Total cases*
641.069.082

Total deaths*
6.629.849

COVID-19 – coinfections/superinfections and excess of antimicrobial use

Bacterial co-infection and secondary infection in patients with COVID-19: a living rapid review and meta-analysis

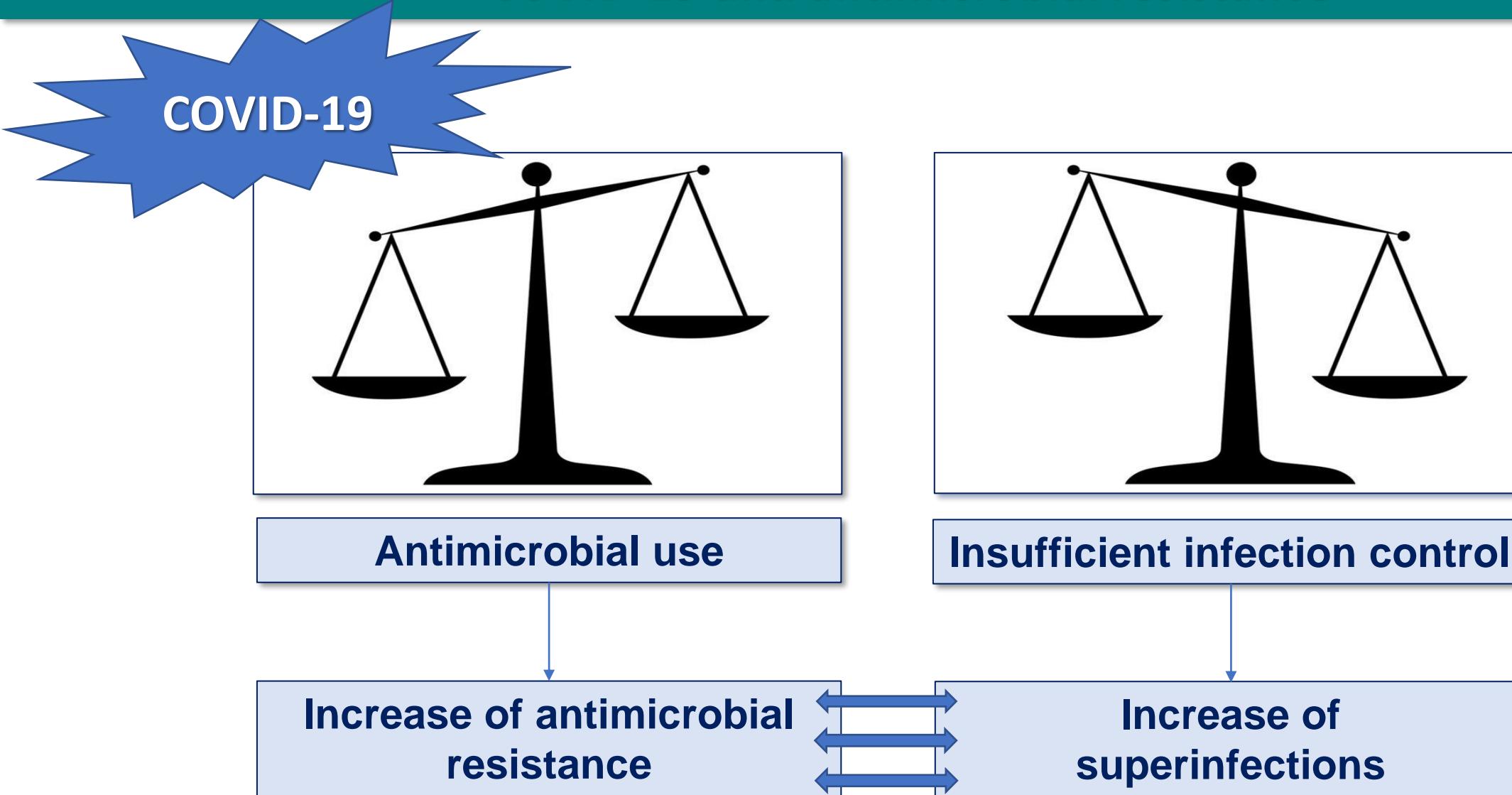
Bradley J. Langford ^{1,2,*}, Miranda So ^{3,4,5}, Sumit Raybardhan ⁶, Valerie Leung ^{1,7},
Duncan Westwood ⁸, Derek R. MacFadden ⁹, Jean-Paul R. Soucy ¹⁰, Nick Daneman ^{1,4,8,11}

Clinical Microbiology and Infection 26 (2020) 1622–1629

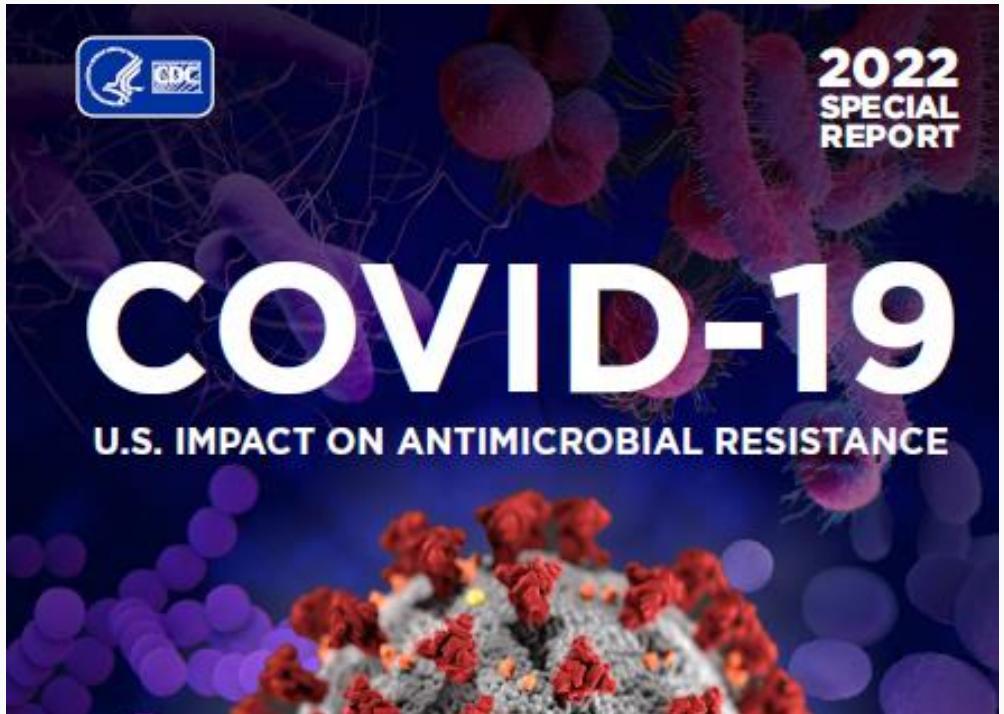
Indicator	Proportion of patients (95% CI)
Bacterial coinfection (at admission)	3.5 (0.4-6.7)
Secondary infection (during admission)	14.3 (9.6-18.9)
Overall infections	6.9 (4.3-9.5)
Antibiotic use	71.9 (56.1-87.7)



COVID-19 and antimicrobial resistance



Antibiotic resistance and COVID-19



<https://www.cdc.gov/drugresistance/pdf/covid19-impact-report-508.pdf>



Available data show an alarming increase in resistant infections starting during hospitalization, growing at least 15% from 2019 to 2020.

- Carbapenem-resistant *Acinetobacter* ($\uparrow 78\%$)
- Antifungal-resistant *Candida auris* ($\uparrow 60\%$)*
- Carbapenem-resistant Enterobacterales ($\uparrow 35\%$)
- Antifungal-resistant *Candida* ($\uparrow 26\%$)
- ESBL-producing Enterobacterales ($\uparrow 32\%$)
- Vancomycin-resistant *Enterococcus* ($\uparrow 14\%$)
- Multidrug-resistant *P. aeruginosa* ($\uparrow 32\%$)
- Methicillin-resistant *Staphylococcus aureus* ($\uparrow 13\%$)

**Candida auris* was not included in the hospital-onset rate calculation of 15%.

Multi-drug resistant microorganisms

WHO priority list of pathogens to guide research and development of new antibiotics

Priority 1: CRITICAL[#]

Acinetobacter baumannii, carbapenem-resistant

Pseudomonas aeruginosa, carbapenem-resistant

*Enterobacteriaceae**, carbapenem-resistant, 3rd generation cephalosporin-resistant



Tacconelli and Magrini, 25 Feb 2017



Priority 2: HIGH

Enterococcus faecium, vancomycin-resistant

Staphylococcus aureus, methicillin-resistant, vancomycin intermediate and resistant

Helicobacter pylori, clarithromycin-resistant

Campylobacter, fluoroquinolone-resistant

Salmonella spp., fluoroquinolone-resistant

Neisseria gonorrhoeae, 3rd generation cephalosporin-resistant, fluoroquinolone-resistant

Priority 3: MEDIUM

Streptococcus pneumoniae, penicillin-non-susceptible

Haemophilus influenzae, ampicillin-resistant

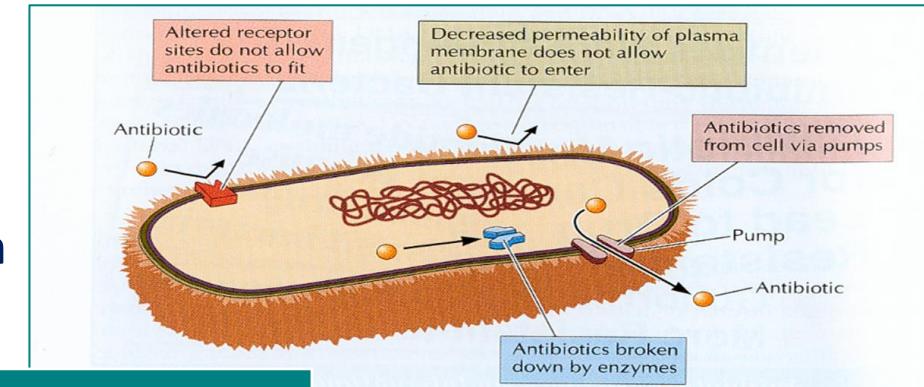
Shigella spp., fluoroquinolone-resistant

Carbapenem resistant microorganisms

Relative contribution of different resistance mechanism in carbapenem resistance in different pathogens

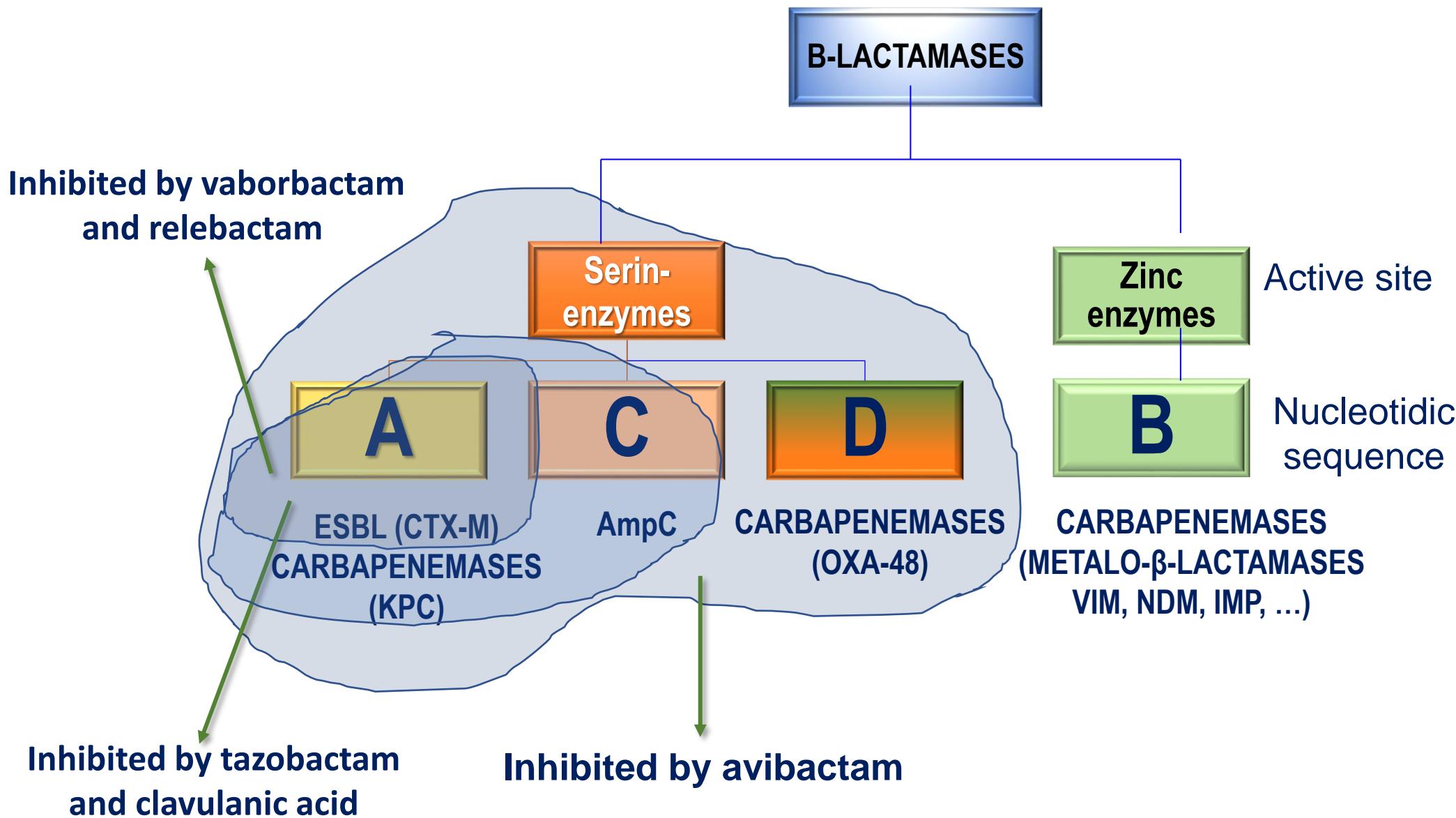
Microorganisms	Porin deficiency	Porin deficiency + ESBL	PBP modifications	Eflux pumps overexpression	Carbapenemases
Enterobacterales		✓			✓✓✓
<i>Pseudomonas aeruginosa</i>	✓✓		✓	✓✓	✓✓
<i>Acinetobacter baumannii</i>	✓		✓	✓	✓✓✓
<i>Stenotrophomonas maltophilia</i>	✓			✓✓	✓✓✓

ESBL: extended spectrum β-lactamase; CP: carbapenemase



Information obtained from Eichenberger EM, Thaden JT. *Antibiotics* 2019 Apr 6;8(2):37; Gil-Gil T, et al. *Anti Infect Ther* 2020; 18:335-47; Glen KA, Lamont IL. *Pathogens* 2021 Dec 18;10(12):1638; Mancuso G, et al. *Pathogens* 2021 Oct 12;10(10):1310; Kyriakidis I et al. *Pathogens*. 2021 Mar 19;10(3):373; Lepe JA, Martínez-Martínez L. *Med Intensiva* 2022; 46:392-402; Canton R et al. *Expert Rev Anti Infect Ther* 2022; 20:1077-94

Carbapenemases and β -lactamase inhibitors



Carbapenemases and β -lactamase inhibitors

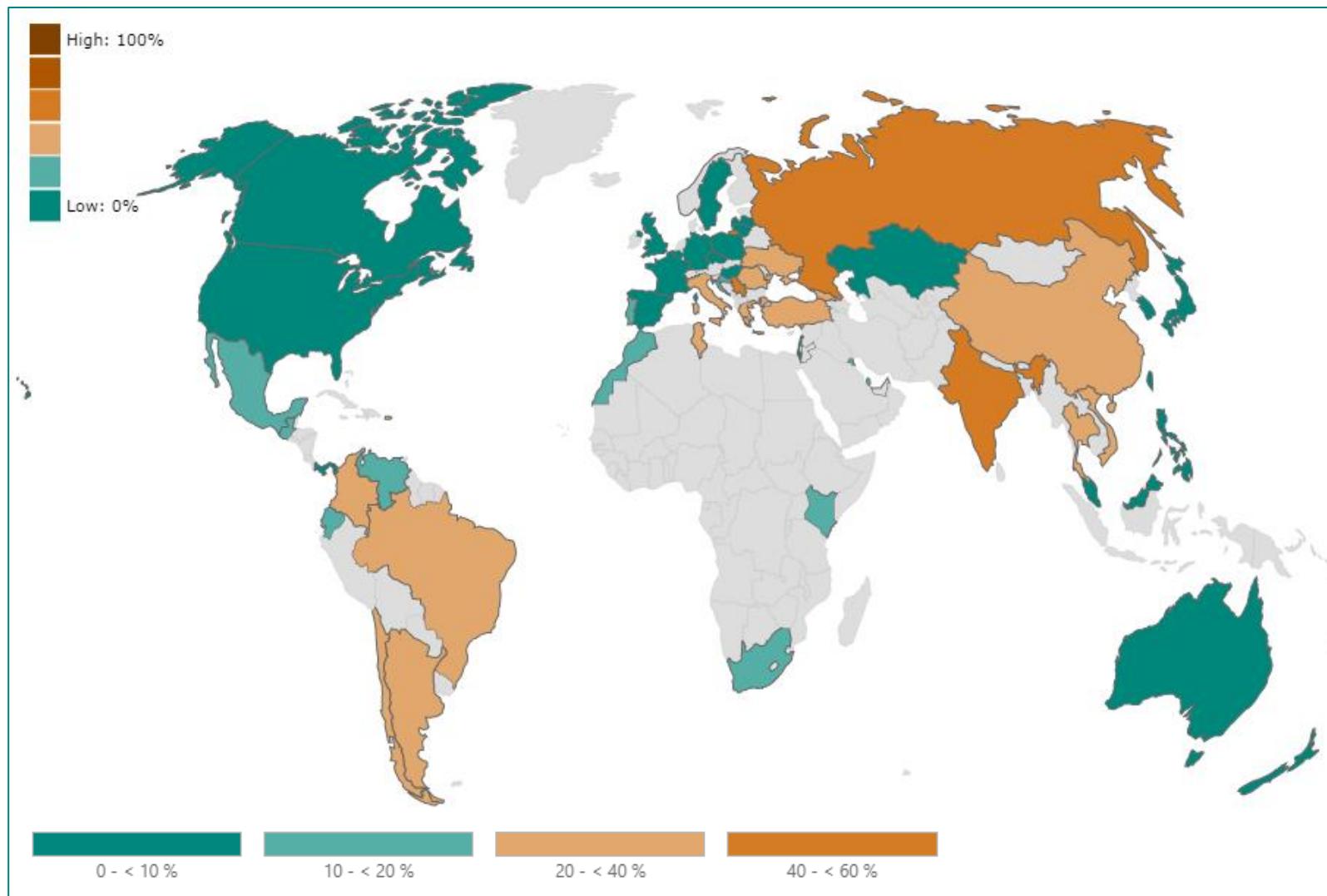
- Inhibit the enzymatic action of β -lactamases
- Marketed in association with β -lactam antibiotics depending on the type of enzyme to be inhibited and their pharmacokinetics
- In general, they act as suicide inhibitors:
 - β -lactamases hydrolyse the inhibitors leaving the β -lactam to act
- There is no universal β -lactamase inhibitor
- Used in the laboratory to recognize the different enzymes

β -lactamase inhibitor	ESBL	A CP (KPC)	C AmpC	ESBL	D CP (OXA-48)	B CP (VIM, NDM)
Clavulanic ac.	+++	-	-	-	-	-
Sulbactam	++	-	-	-	-	-
Tazobactam	+++	-	+ / -	-	-	-
Avibactam	+++	+++	++	++ / -	++	-
Vaborbactam	+++	+++	++	-	-	-
Relebactam	+++	+++	++	-	-	-
ANT431	-	-	-	-	-	++
Taniborbactam	+++	+++	++	+++	+++	++/+

ESBL: extended spectrum β -lactamase; CP: carbapenemase

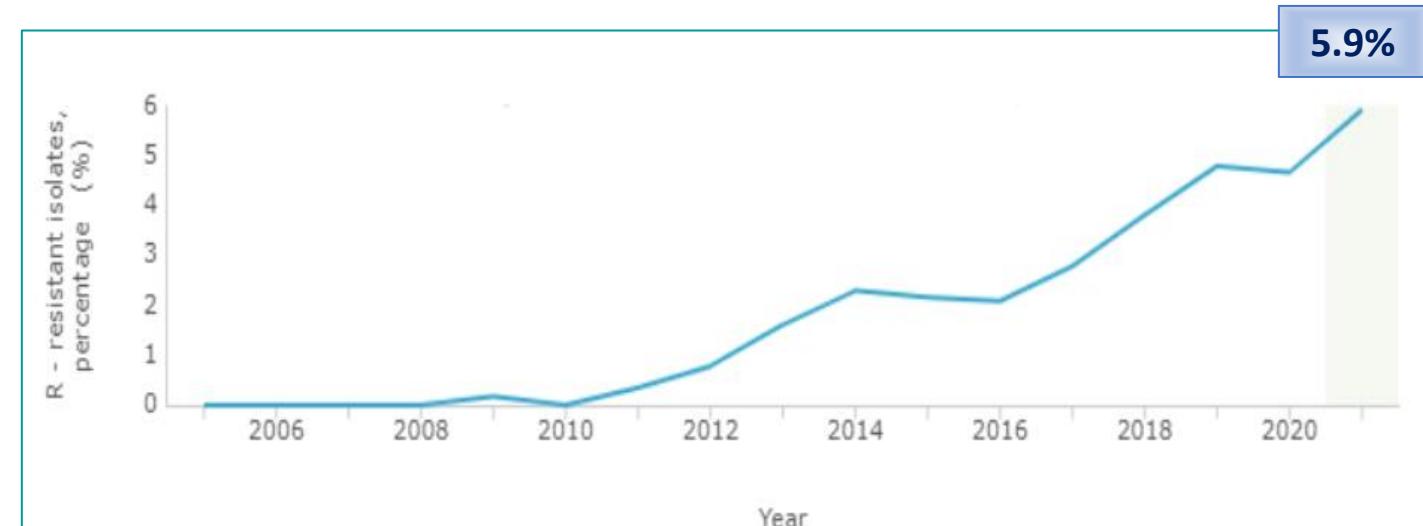
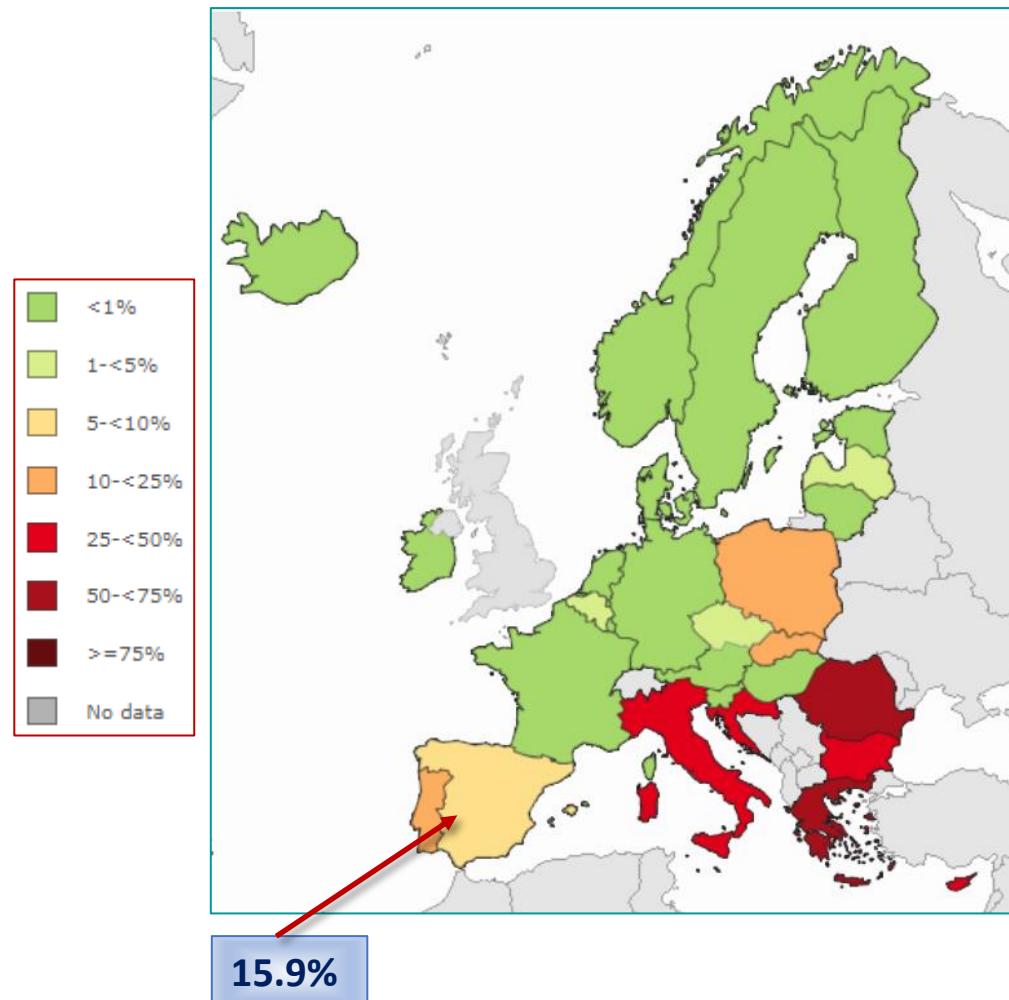
Carbapenem (meropenem) resistant *K. pneumoniae* – SMART database

Non-susceptible heatmap for meropenem resistance in *K. pneumoniae* (n = 10015) in 2019. CLSI criteria



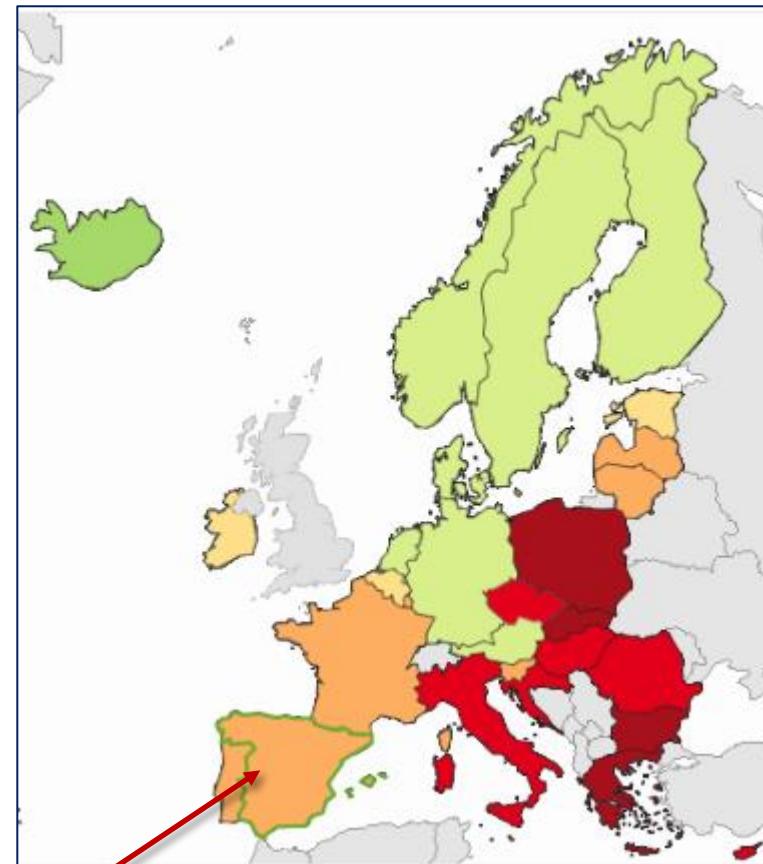


% of carbapenem resistant isolates

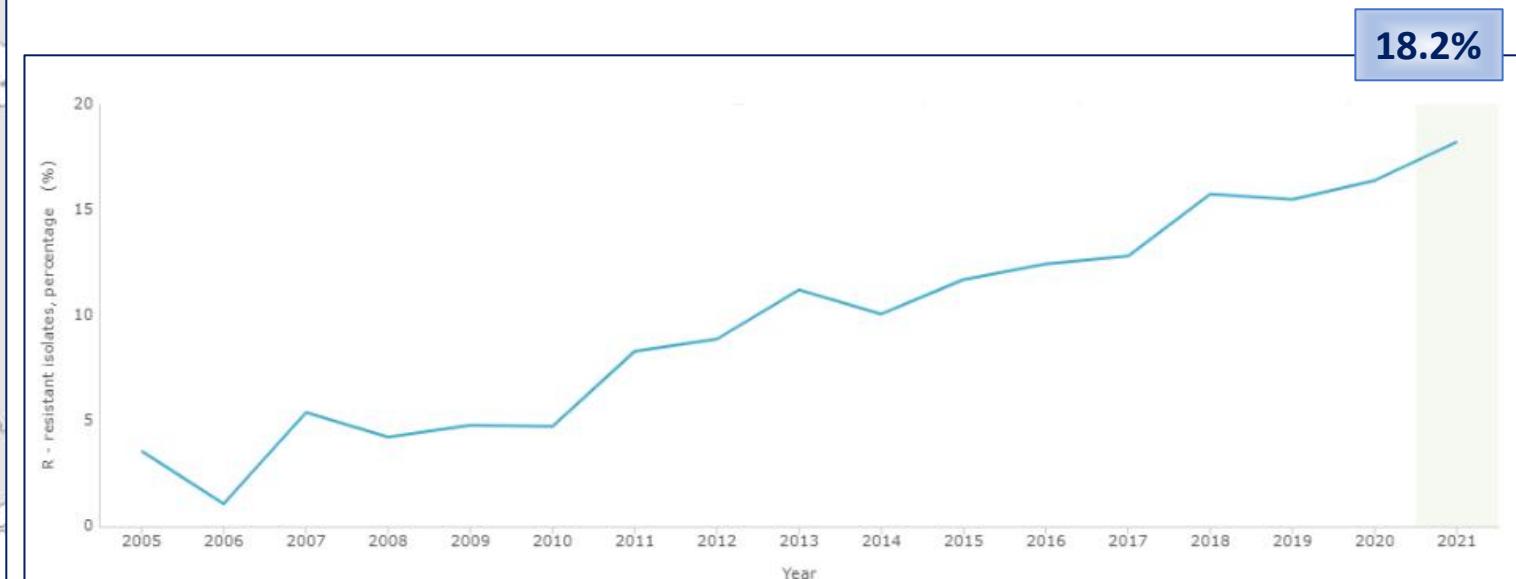


% of MDR* isolates

(R ≥3 antimicrobials: piper/tazob, ceftazidime, fluoroquinolones, aminoglycosides and/or carbapenems)



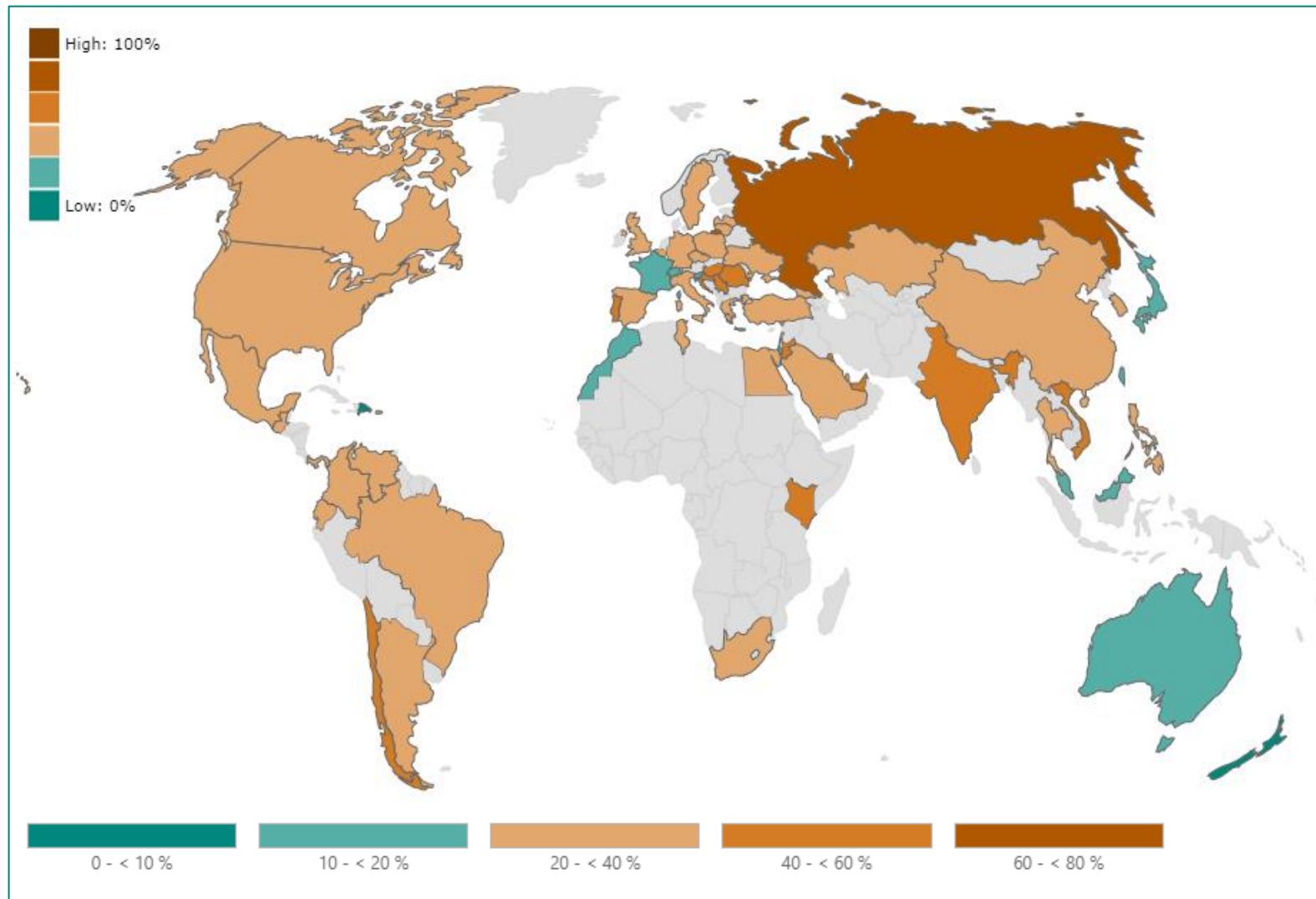
18.2%



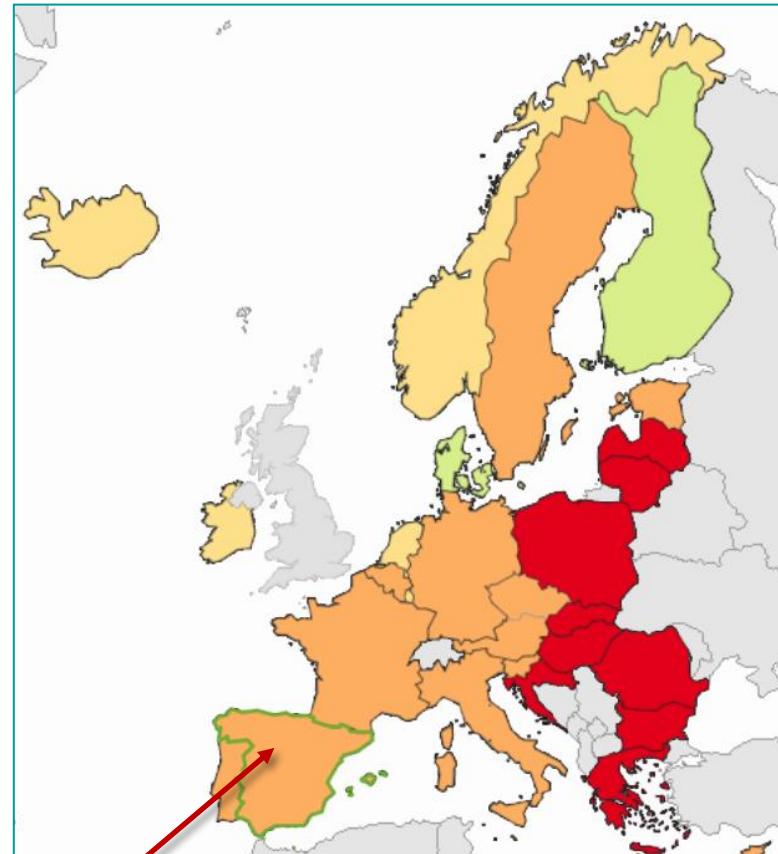
18.2%

Carbapenem (meropenem) resistant *P. aeruginosa* – SMART database

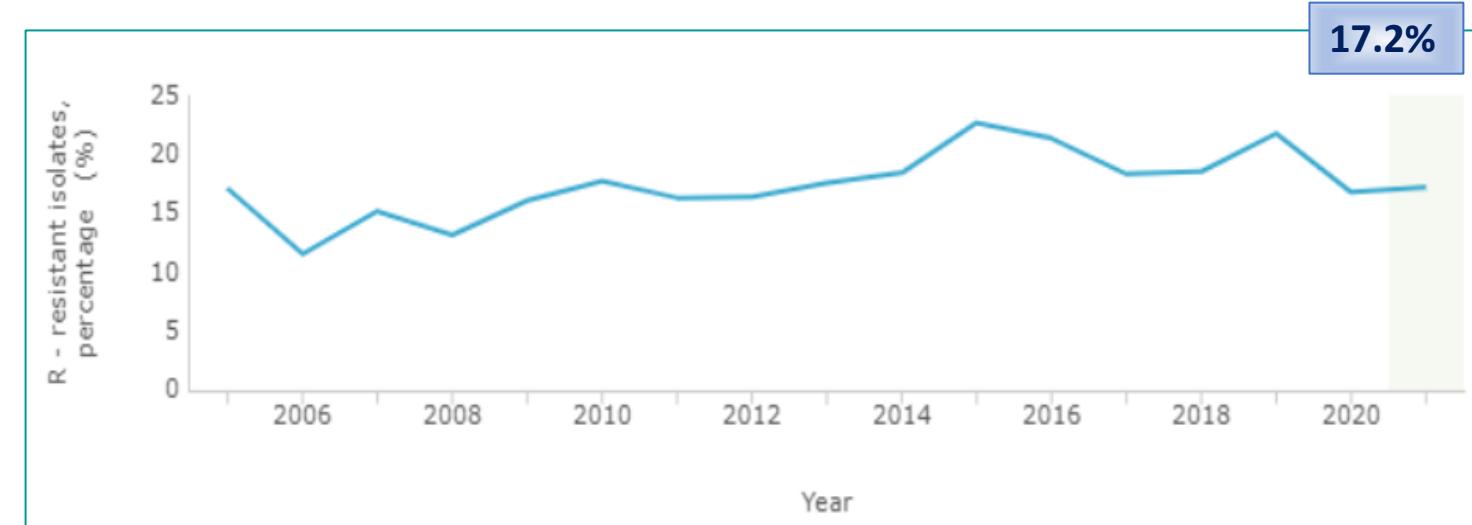
Non-susceptible heatmap for meropenem resistance in *P. aeruginosa* (n = 10015) in 2019. CLSI criteria



% of carbapenem resistant isolates

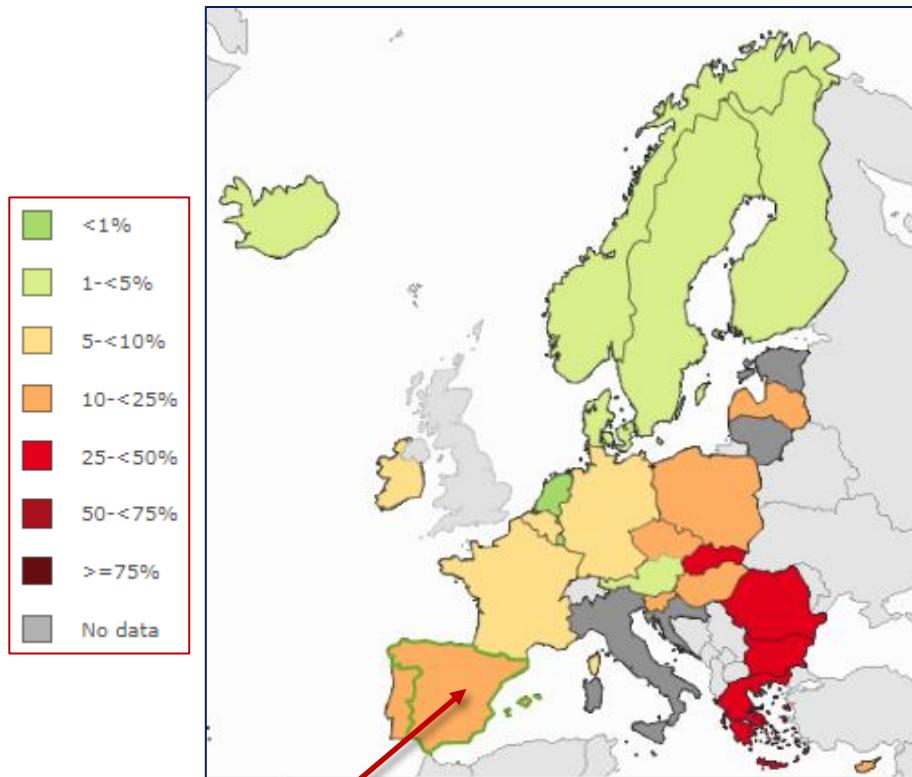


17.2%

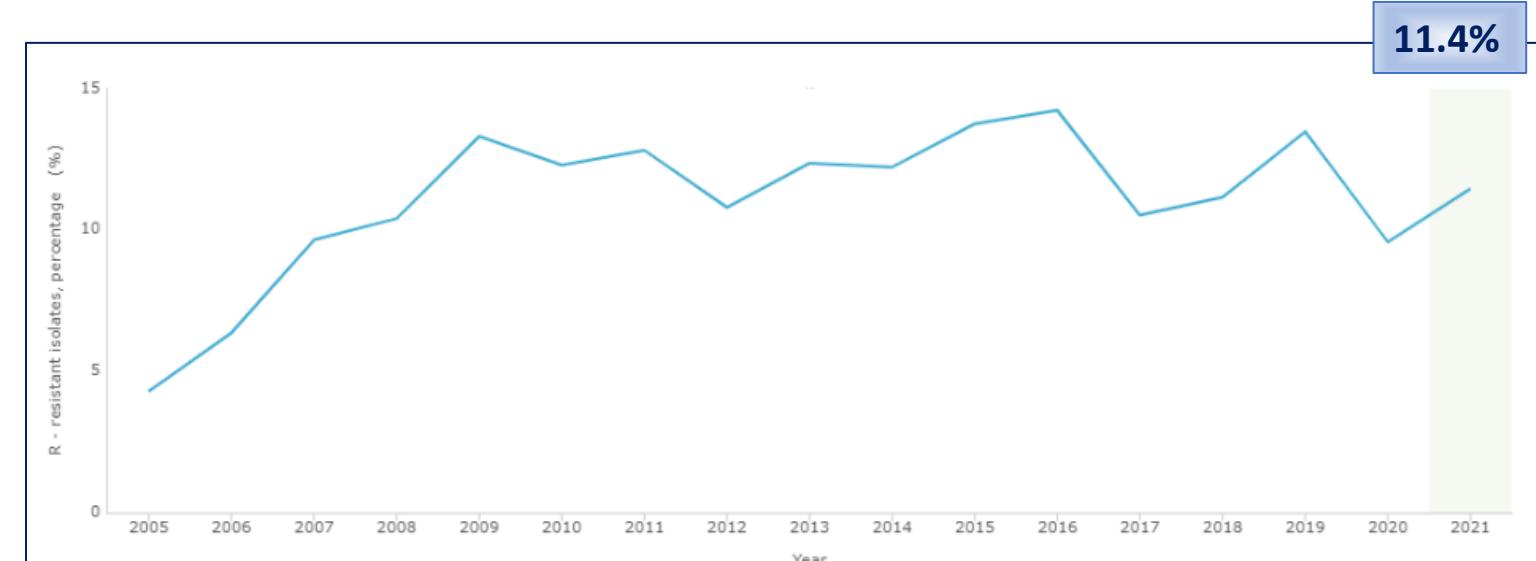


% of MDR* isolates

(R ≥3 antimicrobials: piper/tazob, ceftazidime, fluoroquinolones, aminoglycosides and/or carbapenems)

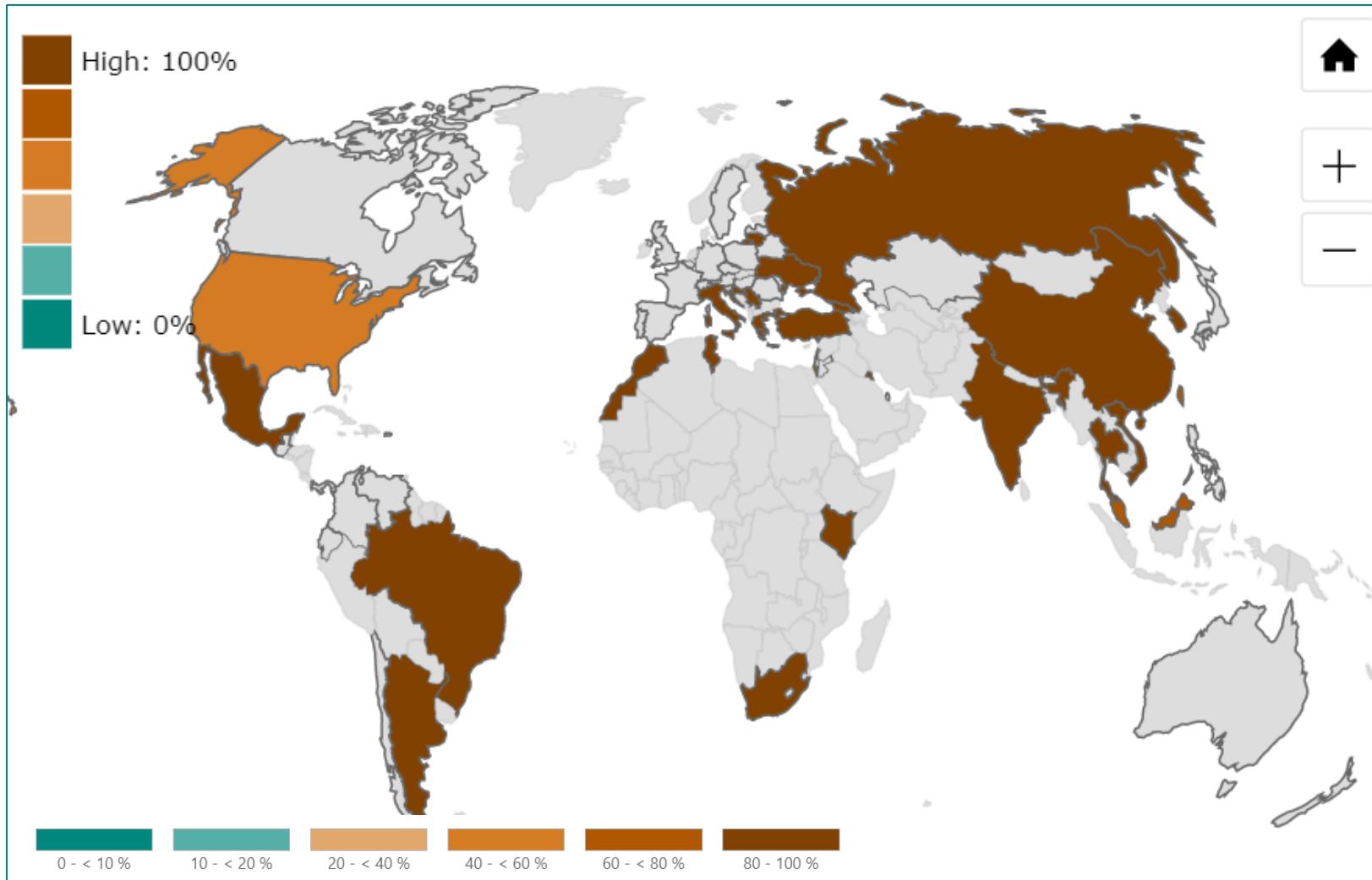


11.4%

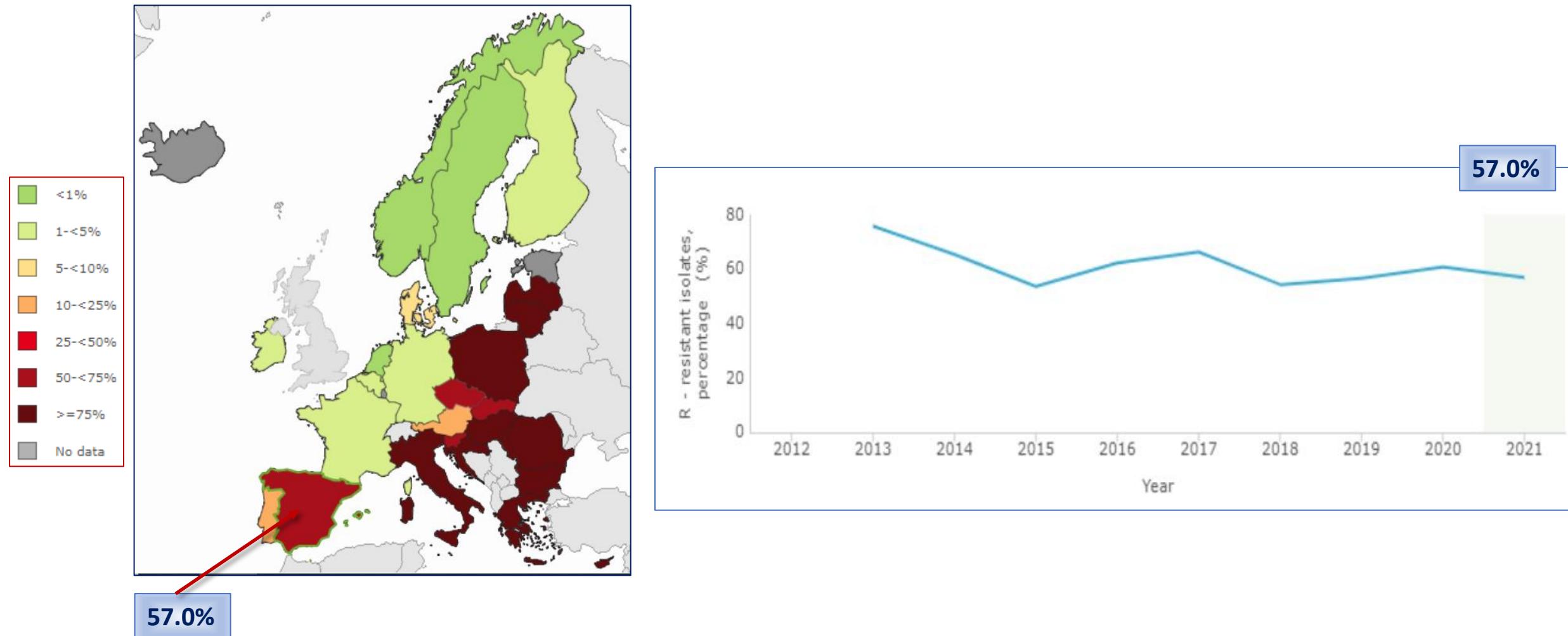


Carbapenem (meropenem) resistant *A. baumannii* – SMART database

Non-susceptible heatmap for meropenem resistance in *A. baumannii* (n = 2553) in 2019. CLSI criteria

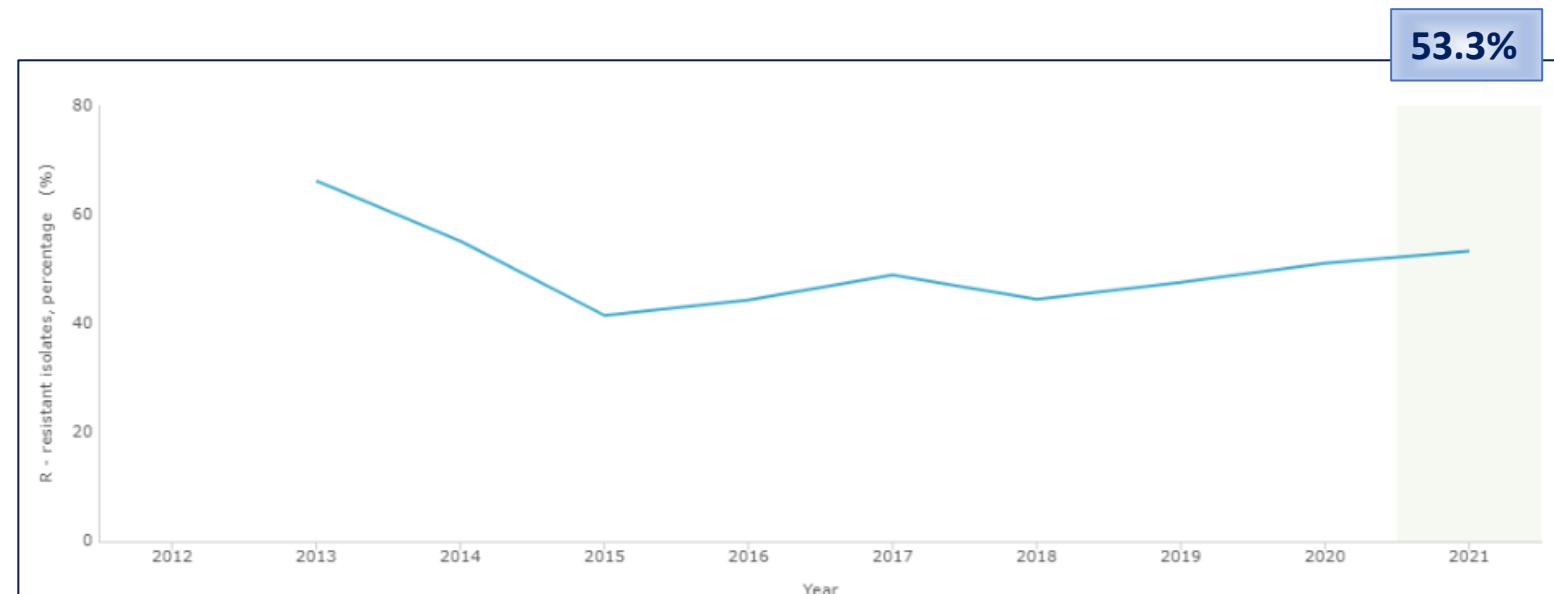
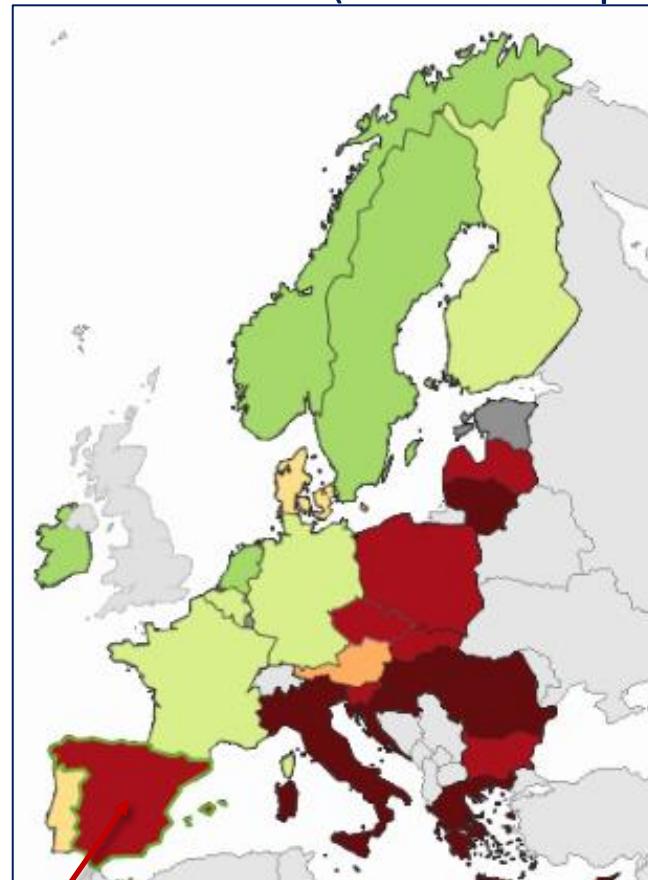


% of carbapenem resistant isolates



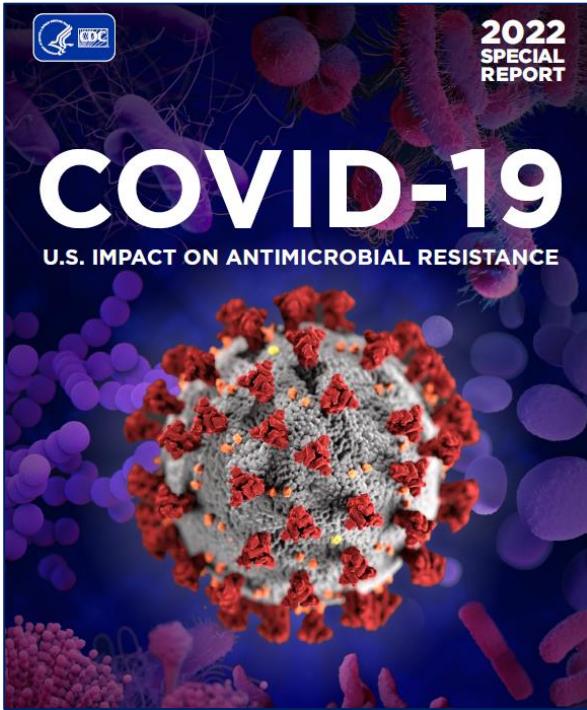
% of MDR* isolates

(R ≥3 fluoroquinolones, aminoglycosides and/or carbapenems)

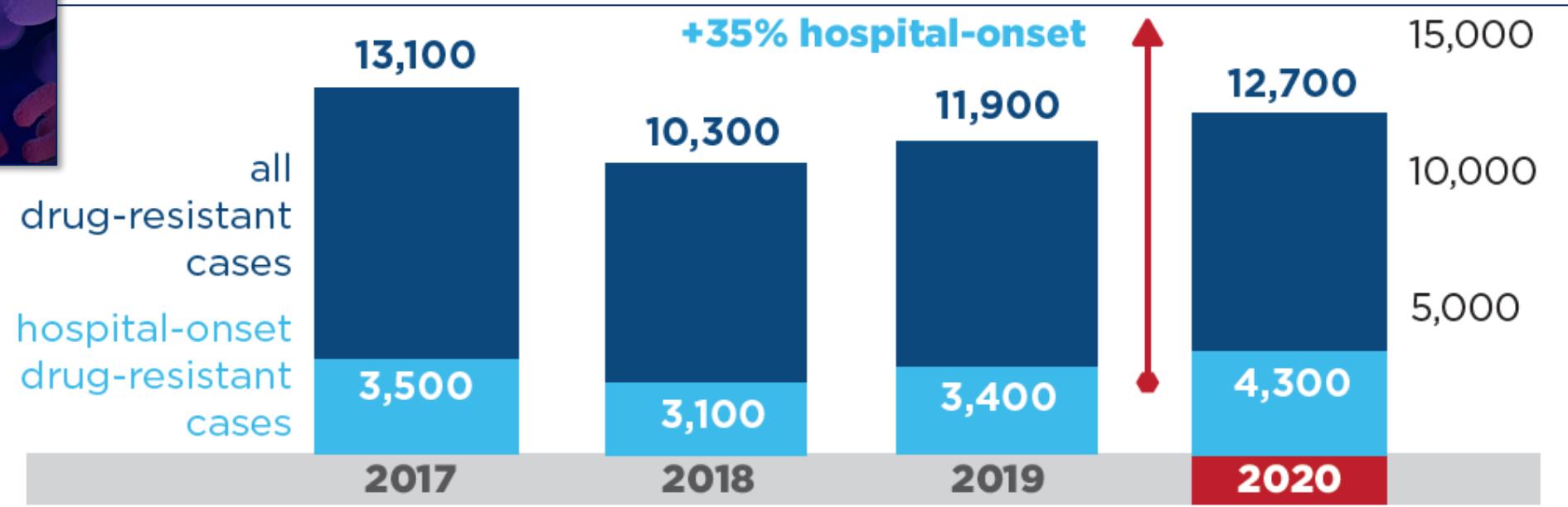


53.3%

Carbapenem resistant Enterobacterales (CRE)



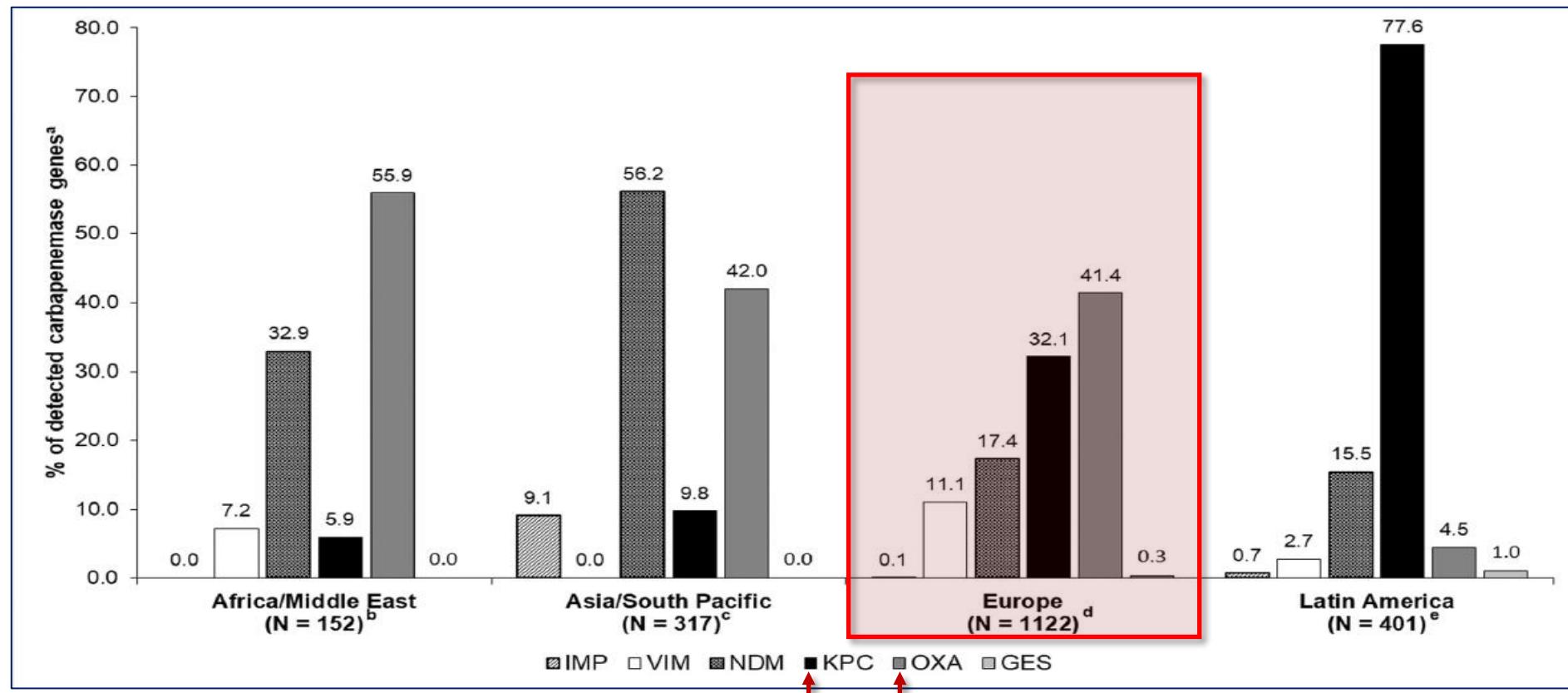
- The rate of CRE cases declined significantly from 2017 to 2018, but began to rise again in 2019 and continued into 2020 (\uparrow 35% hospital-onset) due to challenges created by the pandemic



Data from 2018–2020 are preliminary.

Carbapenemase distribution in Enterobacterales: pre-COVID-19 pandemic

Carbapenemase genes (%) in carbapenemase-producing Enterobacterales isolates
(Atlas program 2016-2018)





Carbapenemase-producing *Enterobacteriales* infections in COVID-19 patients

Infect Dis (Lond) 2022; 54:36-45

Vicente Pintado^a , Patricia Ruiz-Garbajosa^b , Rosa Escudero-Sánchez^a, Francesca Gioia^a, Sabina Herrera^a, Pilar Vizcarra^a , Jesús Fortún^a, Javier Cobo^a, Pilar Martín-Dávila^a, María Isabel Morosini^b, Rafael Cantón^b and Santiago Moreno^a



- **More frequent CPE infections** in COVID-19 patients (1.1 vs. 0.5%, p=0.005).
- COVID-19 patients were younger, had lower frequency of underlying diseases (p=0.01), and lower median Charlson score (p=0.002) than controls
- **Predisposing factors:** antimicrobial use, mechanical ventilation, ICU admission (p<0.05).
- More frequent
 - hospital acquired infections (UTI, 47.9%; pneumonia, 23.3%) diagnosed at the ICU (p<.001)
 - severe sepsis or shock (p=0.01) with higher median SOFA score (p<0.04)
 - overall 30-d mortality rate 30% vs 16.7% (p=0.25).
- CPE: *K. pneumoniae* (80.8%), *S. marcescens* (11%) and *E. cloacae* (4.1%)
- **Carbapenemases:** KPC 56.2% OXA-48 26% and VIM 17.8%



Impact of COVID-19 on antimicrobial resistance



Journal of
Clinical Medicine

J. Clin. Med. 2021, 10, 2067. <https://doi.org/10.3390/jcm10102067>



Review

Carbapenem-Resistant *Klebsiella pneumoniae* Infections in ICU COVID-19 Patients—A Scoping Review

Wioletta Mędrzycka-Dąbrowska ^{1,*}, Sandra Lange ², Katarzyna Zorena ³, Sebastian Dąbrowski ⁴, Dorota Ozga ⁵ and Lucyna Tomaszek ⁶



antibiotics

Antibiotics 2021, 10, 561. <https://doi.org/10.3390/antibiotics10050561>



Case Report

Carbapenem-Resistant *Klebsiella pneumoniae* Associated with COVID-19

Irina Magdalena Dumitru ^{1,2,3,*}, Mirela Dumitrascu ¹, Nicoleta Dorina Vlad ^{1,3}, Roxana Carmen Cernat ^{1,2}, Carmen Ilie-Serban ¹, Aurelia Hangari ^{1,2}, Raluca Elena Slujitoru ¹, Aura Gherghina ¹, Corina Mitroi-Maxim ¹, Liedan Curtali ¹, Dalia Sorina Carp ¹, Anca Dumitrescu ¹, Romelia Mitan ¹, Rodica Lesanu ¹ and Sorin Rugina ^{1,2,3,4,5}



Journal of
Clinical Medicine

J. Clin. Med. 2020, 9, 2744; doi:10.3390/jcm9092744



Article

Antimicrobial Stewardship Program, COVID-19, and Infection Control: Spread of Carbapenem-Resistant *Klebsiella pneumoniae* Colonization in ICU COVID-19 Patients. What Did Not Work?

Beatrice Tiri ¹, Emanuela Sensi ², Viola Marsiliani ², Mizar Cantarini ², Giulia Priante ³, Carlo Vernelli ³, Lucia Assunta Martella ³, Monya Costantini ⁴, Alessandro Mariottini ⁵, Paolo Andreani ⁵, Paolo Bruzzone ⁶, Fabio Suadoni ⁷, Marsilio Francucci ⁸, Roberto Cirocchi ⁹ and Stefano Cappanera ^{1,*}



antibiotics

Antibiotics 2021, 10, 1127. <https://doi.org/10.3390/antibiotics10091127>



Article

A Study in a Regional Hospital of a Mid-Sized Spanish City Indicates a Major Increase in Infection/Colonization by Carbapenem-Resistant Bacteria, Coinciding with the COVID-19 Pandemic

Estefanía Cano-Martín ¹, Inés Portillo-Calderón ², Patricia Pérez-Palacios ², José María Navarro-Marí ³, María Amelia Fernández-Sierra ¹ and José Gutiérrez-Fernández ^{3,4,*}

Infection and Drug Resistance

Dovepress
open access to scientific and medical research

Open Access Full Text Infection and Drug Resistance 2021;14:1855–1863

ORIGINAL RESEARCH

Shift in the Dominant Sequence Type of Carbapenem-Resistant *Klebsiella pneumoniae* Bloodstream Infection from ST11 to ST15 at a Medical Center in Northeast China, 2015–2020

J Antimicrob Chemother
doi:10.1093/jac/dkaa466

Journal of
Antimicrobial
Chemotherapy

Carbapenemase-producing Enterobacteriales causing secondary infections during the COVID-19 crisis at a New York City hospital

Angela Gomez-Simmonds ¹, Medini K. Annavajhala ¹, Thomas H. McConville ¹, Donald E. Dietz ¹, Sherif M. Shoucri ¹, Justin C. Laracy ¹, Felix D. Rozenberg ¹, Brian Nelson ¹, William G. Greendyke ¹, E. Yoko Furuya ¹, Susan Whittier ² and Anne-Catrin Uhlemann ^{1,*}

Journal Pre-proof

Outbreak of ceftazidime-avibactam resistant KPC-producing *Klebsiella pneumoniae* in a COVID-19 Intensive Care Unit, Italy: urgent need for updating diagnostic protocols of surveillance cultures J Hosp Infect. 2022 Feb 6:S0195-6701(22)00038-X.

Gabriele Bianco ¹, Matteo Boattini ^{1,2}, Alessandro Bondi ^{1,2}, Sara Comini ^{1,2}, Teresa Zaccaria ¹, Rossana Cavallo ^{1,2}, Cristina Costa ^{1,2}

■ Changing epidemiology during COVID-19

Increased prevalence of

- carbapenemase producing *K. pneumoniae* high-risk clones
- KPC carbapenemases, including KPC-variants

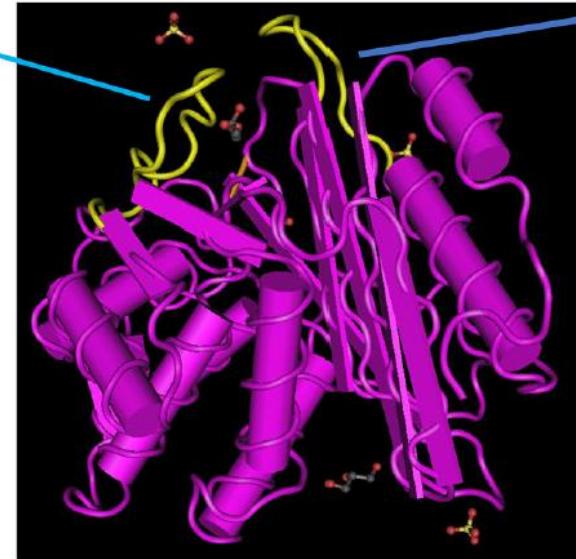
Emergence of KPC-variants ceftazidime/avibactam resistant

Multiple evolutionary trajectories conferring resistance to ceftazidime/avibactam due to amino acid substitutions, insertions, and deletions in the Ω-loop of KPC-3 β-lactamase

KPC-31 GDTTFRLDRW--ELELNSAIPGDARYTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDD-----KYSEAVIAAAAARLALEGGLGVNGQ
KPC-70 GDTTFRLDRW--ELELNSAIPGDARYTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYARAPNKDD-----KYSEAVIAAAAARLALEGGLGVNGQ
KPC-49 GDTTFRLDRWSW--ELELNSAIPGDARDTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDD-----KYSEAVIAAAAARLALEGGLGVNGQ
KPC-39 GDTTFRLDRW--ELELNSTIPGDARDTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDD-----KYSEAVIAAAAARLALEGGLGVNGQ
KPC-66 GDTTFRLDRW--EL--NSAIPGDARDTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDD-----KYSEAVIAAAAARLALEGGLGVNGQ
KPC-69 GDTTFRLDRWGLELELNSAIPGDARDTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDD-----KYSEAVIAAAAARLALEGGLGVNGQ
KPC-68 GDTTFRLDRW--ELELNSAIPGDARDTSSSSPRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDD-----KYSEAVIAAAAARLALEGGLGVNGQ
KPC-67 GDTTFRLDRW--ELELNSAIPGDARDTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKKDKDDKYSEAVIAAAAARLALEGGLGVNGQ
KPC-29 GDTTFRLDRW--ELELNSAIPGDARDTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKDD--KYSEAVIAAAAARLALEGGLGVNGQ
KPC-3 GDTTFRLDRW--ELELNSAIPGDARDTSS--PRAVTESLQKLTLSGALAAFPQRQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDD-----KYSEAVIAAAAARLALEGGLGVNGQ

Ω-LOOP

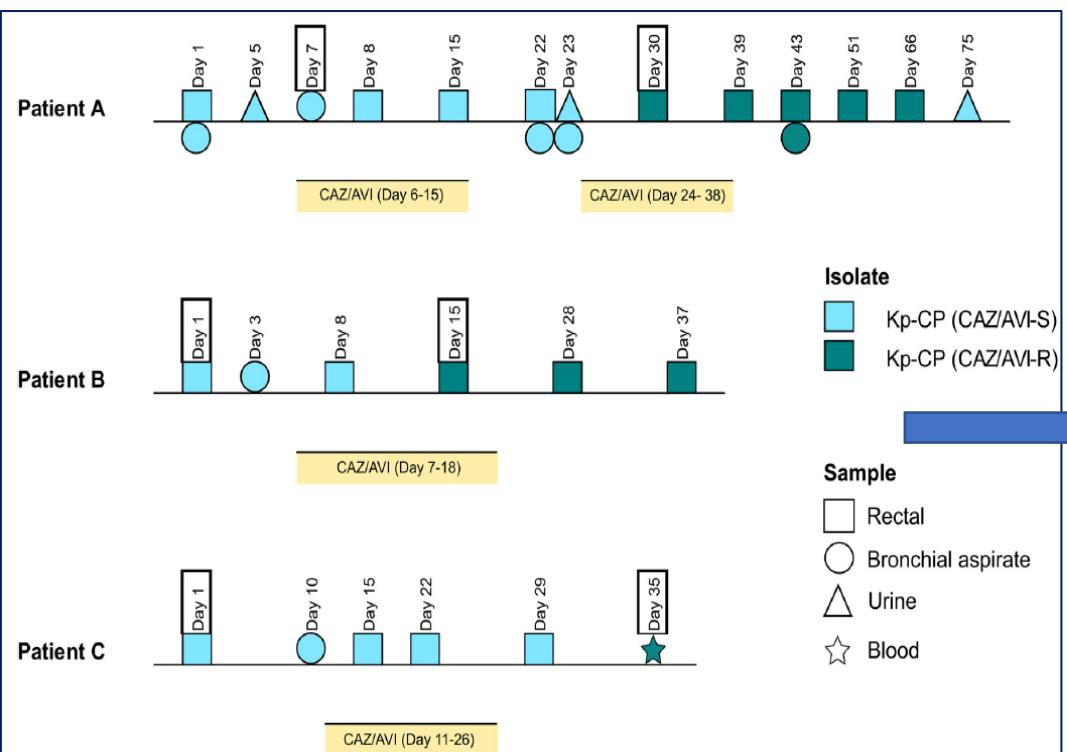
270-LOOP



Emergence of KPC-variants with resistance to new antimicrobials

Impact of Ceftazidime-Avibactam Treatment in the Emergence of Novel KPC Variants in the ST307-*Klebsiella pneumoniae* High-Risk Clone and Consequences for Their Routine Detection

Marta Hernández-García,^{a,b,c} Juan Antonio Castillo-Polo,^{a,c} Desirée Gijón Cordero,^{a,c} Blanca Pérez-Viso,^{a,c} María García-Castillo,^{a,c} Javier Saez de la Fuente,^d María Isabel Morosini,^{a,c} Rafael Cantón,^{a,b,c} Patricia Ruiz-Garbajosa^{a,b,c}



Patient	Sample	KPC	CAZ-AVI	IMP	IMP-REL	MER	MER-VAB	FDC
1	1-1	KPC-3	2/4*	16	0.25/4	8	≤.006/4	0.5
	1-2	KPC-46	32/4	≤1	0.25/4	≤.12	≤.006/4	1
2	2-1	KPC-3	2/4	16	0.5/4	>16	≤.006/4	1
	2-2	KPC-66	8/4	≤1	0.25/4	≤.12	≤.006/4	2
3	3-1	KPC-3	1/4	16	0.25/4	>16	≤.006/4	1
	3-2	KPC-92	8/4	≤1	0.25/4	≤.12	≤.006/4	2

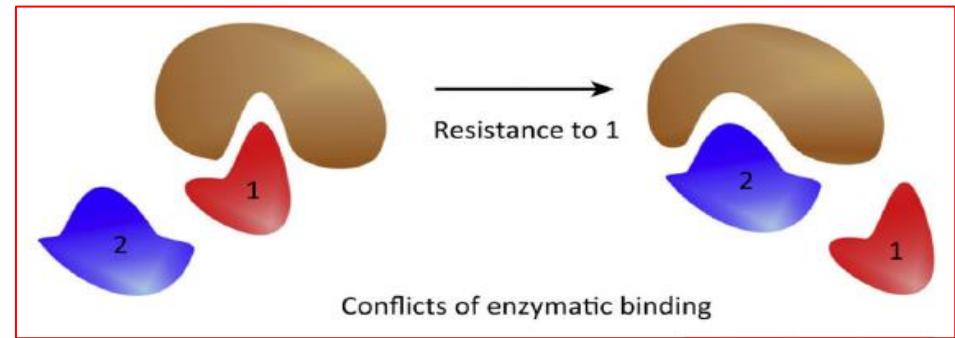
*MIC (mg/L); CAZ-AVI = ceftazidime-avibactam; IMP= imipenem; IMP-REL = imipenem-relebactam; MER = meropenem; MER-VAB = meropenem-vaborbactam; FDC = cefiderocol

Susceptibility to imipenem/relebactam and meropenem/vaborbactam due to collateral sensitivity and/or relebactam and vaborbactam inhibitory activity

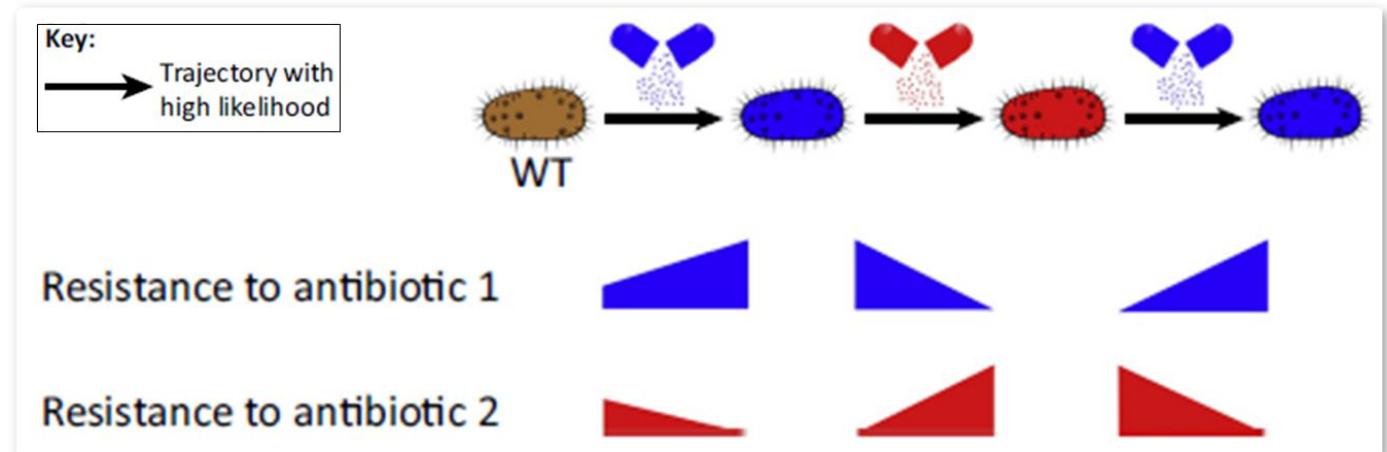
Collateral sensitivity

Collateral sensitivity:

Phenomenon in which an organism that has developed resistance to one drug displays increased sensitivity to a second drug



- Frequently occurs during the **evolution of antibiotic resistance**
- Associated with
 - mutational resistance, including target or enzymatic mutations and those affecting drug uptake and efflux
 - gene expression
- Future clinical applications:
 - drug combinations and cycling strategies





First Report of New Delhi Metallo- β -Lactamase-6 (NDM-6) in a Clinical *Acinetobacter baumannii* Isolate From Northern Spain

Kyriaki Xanthopoulou^{1,2†}, Mikel Urrutikoetxea-Gutiérrez^{3†}, Matxalen Vidal-García³, José-Luis Diaz de Tuesta del Arco³, Sandra Sánchez-Urtaza⁴, Julia Wille^{1,2}, Harald Seifert^{1,2}, Paul G. Higgins^{1,2} and Lucía Gallego^{4*}

New Microbe and New Infect 2020; 34: 100660

Detection of two simultaneous outbreaks of *Klebsiella pneumoniae* coproducing OXA-48 and NDM-1 carbapenemases in a tertiary-care hospital in Valencia, Spain

B. Fuster¹, N. Tormo¹, C. Salvador¹ and C. Gimeno^{1,2}

J Antimicrob Chemother 2019; 74: 3489–3496
doi:10.1093/jac/dkz366 Advance Access publication 3 September 2019

Journal of
Antimicrobial
Chemotherapy

Emergence of NDM-producing *Klebsiella pneumoniae* and *Escherichia coli* in Spain: phylogeny, resistome, virulence and plasmids encoding bla_{NDM}-like genes as determined by WGS

María Pérez-Vázquez^{1,2*}, Pedro Guillermo Ruiz-Carrascoso^{2,4}, Jo Belén Aracil^{1,2}, David Sáez^{1,2}, No Robert A. Kingsley^{8,9}, Gordon Doug

International Journal of Antimicrobial Agents 59 (2022) 106551

Contents lists available at ScienceDirect

International Journal of Antimicrobial Agents

journal homepage: www.elsevier.com/locate/ijantimicag

Molecular characterisation of an outbreak of NDM-7-producing *Klebsiella pneumoniae* reveals ST11 clone expansion combined with interclonal plasmid dissemination

Jesús Machuca^{a,*}, Lorena Lopez-Cerero^{a,b,c,d}, Manuel Rodríguez-Maresca^e, Felipe Fernández-Cuenca^{a,b,c}, Inmaculada López-Hernández^{a,b,c}, Mercedes Delgado-Valverde^{a,b,c}, Waldo Sanchez-Yebra^e, Álvaro Pascual^{a,b,c,d}



Contents lists available at ScienceDirect

International Journal of Antimicrobial Agents

journal homepage: www.elsevier.com/locate/ijantimicag

Molecular characterisation of an outbreak of NDM-7-producing *Klebsiella pneumoniae* reveals ST11 clone expansion combined with interclonal plasmid dissemination

Jesús Machuca^{a,*}, Lorena Lopez-Cerero^{a,b,c,d}, Manuel Rodríguez-Maresca^e, Felipe Fernández-Cuenca^{a,b,c}, Inmaculada López-Hernández^{a,b,c}, Mercedes Delgado-Valverde^{a,b,c}, Waldo Sanchez-Yebra^e, Álvaro Pascual^{a,b,c,d}

Journal of
Antimicrobial
Chemotherapy

J Antimicrob Chemother 2021; 76: 345–354
doi:10.1093/jac/dkaa459 Advance Access publication 17 November 2020

Dissemination of NDM-producing *Klebsiella pneumoniae* and *Escherichia coli* high-risk clones in Catalan healthcare institutions

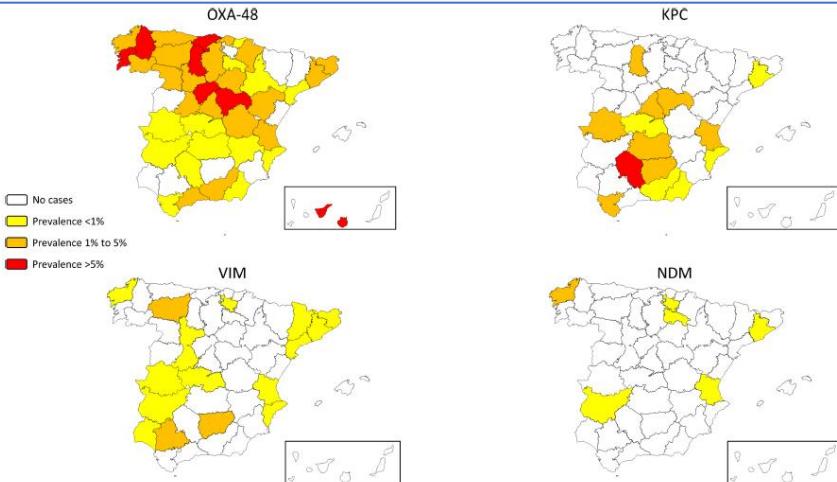
Marta Marí-Almirall^{1†}, Clara Cosgaya^{1†}, Cristina Pitart^{2†}, Joaquim Viñes^{3,4}, Laura Muñoz¹, Irene Campo², Anna Cuscó⁴, Laura Rodríguez-Serna⁵, Gemma Santana⁵, Ana Del Río⁶, Olga Francino³, Pilar Ciruela^{7,8}, Isabel Pujol^{9,10}, Frederic Ballester¹¹, Francesc Marco^{1,2}, José Anton Martínez⁶, Álex Soriano^{ID 6}, Jordi Vila^{ID 1,2} and Ignasi Roca^{ID 1*}. Half of the members of the CAT Study Group

**Emergence and dispersion
of NDM-producing high-risk clones,
including health-care
extrahospitalary settings**

CARB-ES-19 Multicenter Study of Carbapenemase-Producing *Klebsiella pneumoniae* and *Escherichia coli* From All Spanish Provinces Reveals Interregional Spread of High-Risk Clones Such as ST307/OXA-48 and ST512/KPC-3

Javier E. Cañada-García^{1†}, Zaira Moure^{1†}, Pedro J. Sola-Campoy¹, Mercedes Delgado-Valverde^{2,3}, María E. Cano⁴, Desirée Gijón^{3,5}, Mónica González^{3,6}, Irene Gracia-Ahufinger^{3,7}, Nieves Larrosa^{3,8}, Xavier Mulet^{3,9}, Cristina Pitart¹⁰, Alba Rivera¹¹, Germán Bou^{3,6}, Jorge Calvo^{3,4}, Rafael Cantón^{3,5}, Juan José González-López^{3,8}, Luis Martínez-Martínez^{3,7,12}, Ferran Navarro¹¹, Antonio Oliver^{3,9}, Zaira R. Palacios-Baena^{2,3,13}, Álvaro Pascual^{2,3,13}, Guillermo Ruiz-Carrascoso¹⁴, Jordi Vila^{3,10}, Belén Aracil^{1,3}, María Pérez-Vázquez^{1,3†}, Jesús Oteo-Iglesias^{1,3,4‡} and the GEMARA/GEIRAS-SEIMC/REIPI CARB-ES-19 Study Group[§]

Prevalence of carbapenemase-producing *K. pneumoniae* according to carbapenemase groups



Enterobacterales with several carbapenemases

- 377 *K. pneumoniae* isolates (Feb-May 2019)

<i>bla</i> _{OXA-48}	69.8%
<i>bla</i> _{KPC-3}	16.4%
<i>bla</i> _{VIM-1}	7.4%
<i>bla</i> _{NDM-1}	3.2%
Others	5.5%

8 isolates (2.1%) with two carbapenemases

2 OXA-48 + VIM-1
2 OXA-48 + KPC
1 OXA-48 + NDM-1
1 VIM-1 + NDM-1
1 NDM-1 + GES-2
1 VIM-1 + NDM-3

Antibiotic susceptibility of 377 carbapenemase-producing *K. pneumoniae* isolates

Antibiotic	Susceptibility (%)		
	OXA-48-group-producing isolates (n = 262)	KPC-group-producing isolates (n = 72)	MBL-group-producing isolates (n = 37)
Cefiderocol*	95.8	86.1	94.6
Plazomicin*	93.5	98.6	86.5
Colistin	92.4	81.9	91.9
Meropenem/vaborbactam*	89.3	100	73
Ceftazidime/avibactam	95.4	90.3	0
Imipenem/relebactam*	75.2	100	56.7
Amikacin	86.6	33.3	56.8
Imipenem	68.3	13.9	43.2
Meropenem	64.9	13.9	45.9
Gentamicin	47.3	48.6	32.4
Trimethoprim/sulfamethoxazole	34.7	6.9	13.5
Tobramycin	32.8	9.7	8.1
Aztreonam	17.6	0	27
Cefepime*	16.8	0	0
Ceftazidime	15.3	0	0
Ceftolozane/tazobactam	14.1	0	0
Cefotaxime	8.4	0	0
Ciprofloxacin	7.6	1.4	0
Ertapenem	2.3	0	16.2

Cefiderocol: resistance mechanism

Microorganisms	Cefiderocol MIC (MIC or range) (mg/L)	Resistance mechanism	Country (Year of publication)
<i>K. pneumoniae</i>	16 - >32	Mutation of two-component regulation system (BaeSR and OmpR/EnvZ). Mutation of <i>exbD</i> (accessory protein related to iron transport)	Japan (2020)
<i>K. pneumoniae</i>	4 - >32	KPC β-lactamase mutants	France (2021)
<i>E. coli</i>			
<i>E. cloacae</i>			
<i>K. pneumoniae</i>	8	KPC β-lactamase mutant (KPC-31)	Italy (2021)
<i>E. cloacae</i>	>16	AmpC R2 loop deletion	USA (2020)
<i>E. cloacae</i>	≥256	Mutations in <i>cirA</i> gene	Germany (2021)
<i>P. aeruginosa</i>	8	Mutations in <i>pirA</i> and deletion in <i>piuA</i>	USA (2021)
<i>A. baumannii</i>	>4	PER and NDM β-lactamase	Russia, Turkey and USA (2020)
<i>B. multivorans</i>		Disruption of iron transport genes (<i>piuA</i> , <i>pirA</i> and <i>fiuA</i>)	
<i>P. aeruginosa</i>			
<i>S. maltophilia</i>			
<i>A.baumannii</i>	≥32	Loss of <i>pirA</i> and <i>piuA</i>	USA (2020)

Resistance mechanism to new compounds: beta-lactamases

Impact of different beta-lactamases in the susceptibility of new beta-lactams

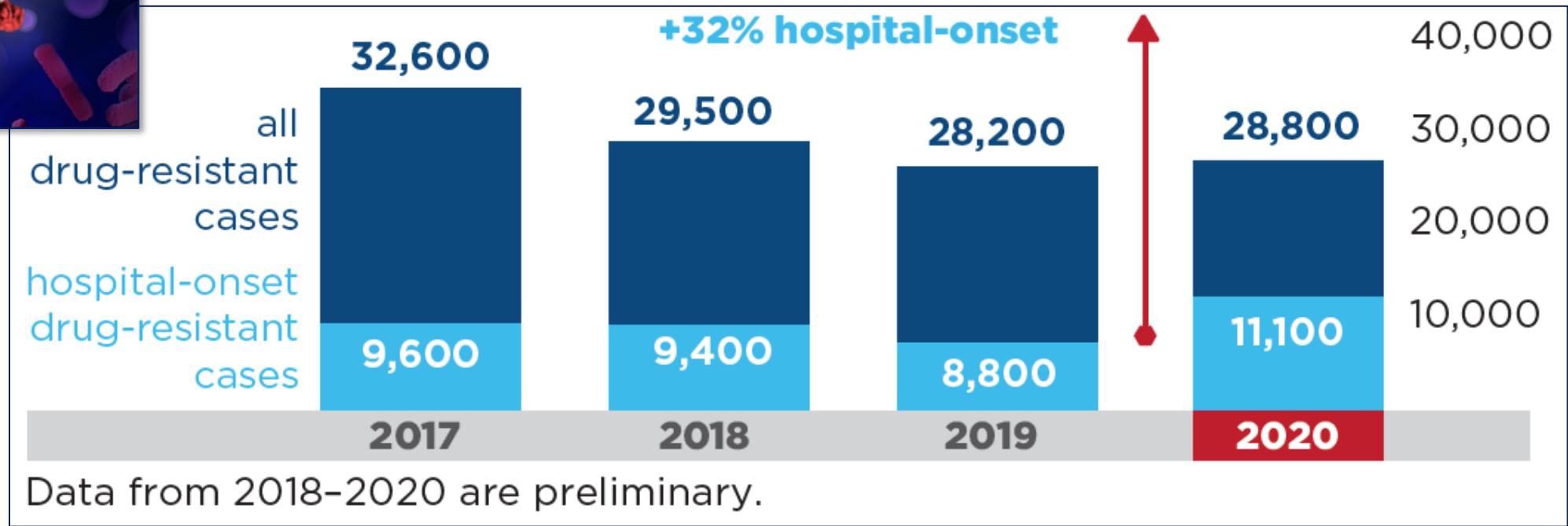
Microorganisms	Enzyme	C/T	CAZ-AVI	IMP-REL	MER-VAB	FCD
<i>E. coli</i> TOP10	-	0.25*	≤0.125	0.25	0.03	≤0.125
	SHV-12	32	0.5	0.25	0.03	4
	CTX-M-33	4	0.25	0.5	0.03	≤0.125
	GES-1	8	0.25	0.25	0.03	≤0.125
	GES-6	32	2	0.5	0.03	≤0.125
	BEL-2	8	1	0.25	0.03	0.5
	PER-1	64	16	0.5	0.03	4
	GIM-1	16	16	4	0.25	≤0.125
	DIM-1	64	16	2	0.25	≤0.125

*MIC, mg/L

Multi-drug resistant *Pseudomonas aeruginosa*

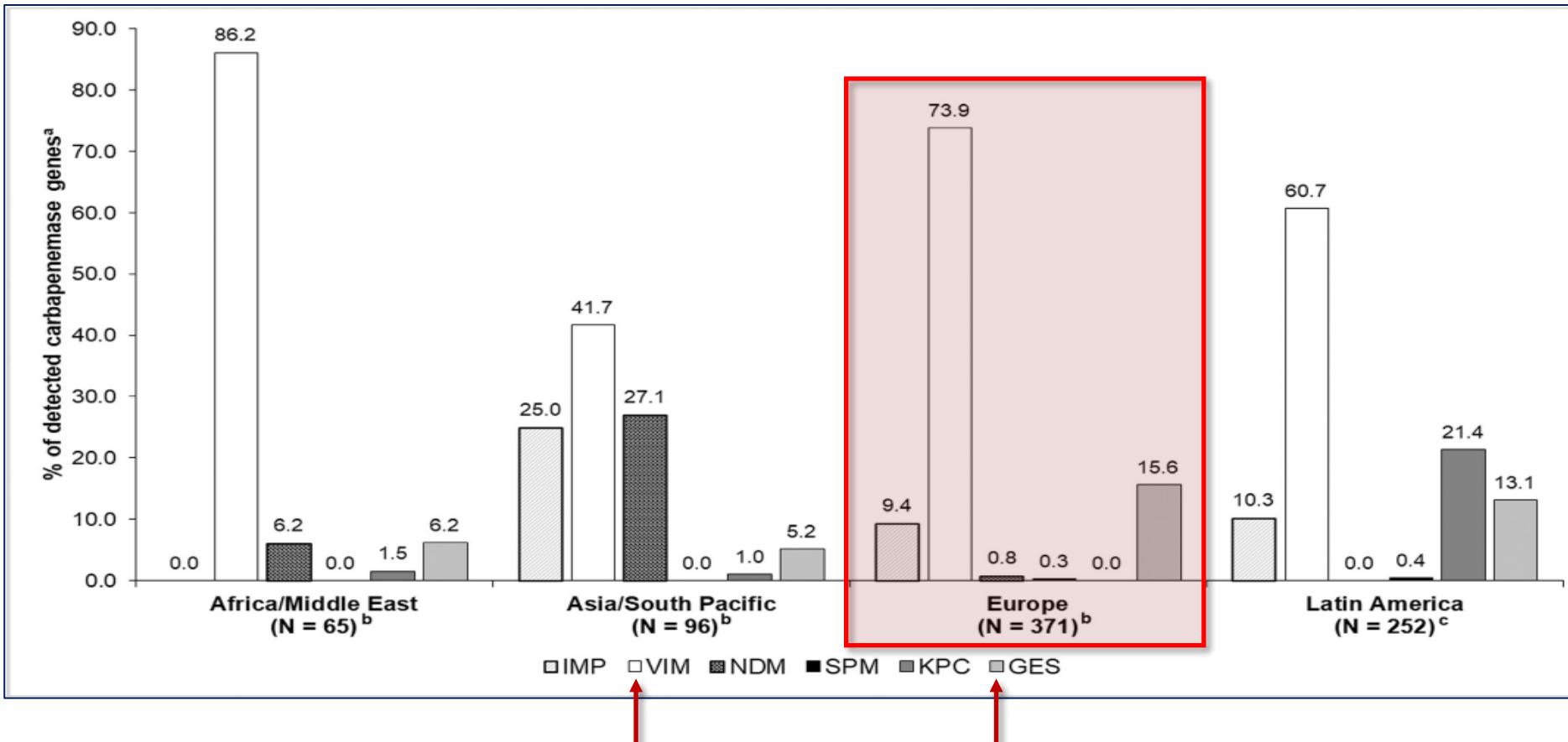


- The increase of MDR *P. aeruginosa* in 2020 was driven by hospital-onset cases potentially due to longer hospitalizations and secondary bacterial infections associated with COVID-19 infections



Carbapenemase distribution in *P. aeruginosa*: pre-COVID-19 pandemic

Carbapenemase genes (%) in carbapenemase-producing *P. aeruginosa* isolates (Atlas program 2016-2018)



Multi-drug resistant *Pseudomonas aeruginosa* in Spain and Portugal

2020 Oct 25:dkaa430. doi:10.1093/jac/dkaa430

J Antimicrob Chemother
doi:10.1093/jac/dkaa430

Journal of
Antimicrobial
Chemotherapy

Distinct epidemiology and resistance mechanisms affecting ceftolozane/tazobactam in *Pseudomonas aeruginosa* isolates recovered from ICU patients in Spain and Portugal depicted by WGS

Marta Hernández-García  ¹, María García-Castillo¹, Sergio García-Fernández¹, José Melo-Crist Margarida F. Pinto³, Elsa Gonçalves⁴, Valquíria Alves⁵, Ana Raquel Vieira⁶, Elmano Ramalheira⁷, Luís José Diogo⁹, Rui Ferreira¹⁰, Tânia Silva¹¹, Catarina Chaves¹², Germán Bou¹³, Emilia Cercenado Mercedes Delgado-Valverde  ¹⁵, Antonio Oliver¹⁶, Cristina Pitart¹⁷, Jesús Rodríguez-Lozano¹⁸, Nuria Joao Romano²⁰, Leonor Pássaro²⁰, Laura Paixão²⁰, Diego López-Mendoza²¹, Jazmín Diaz-Reganón Rafael Cantón  ^{1*} on behalf of the STEP and SUPERIOR study groupst

■ *P. aeruginosa* from ICU patients:

- 396 Portugal (2017-2018)
- 80 Spain (2016-2017)

■ Whole genome sequencing

■ Inter-hospital clonal dissemination

- Portugal CC235, CC244, CC348, C253
- Spain CC175, CC309

■ Different carbapenemase epidemiology



P. aeruginosa isolates from IAI, UTI and LRTI in ICU patients admitted to 11 Portuguese (STEP) and 8 Spanish (SUPERIOR) hospitals

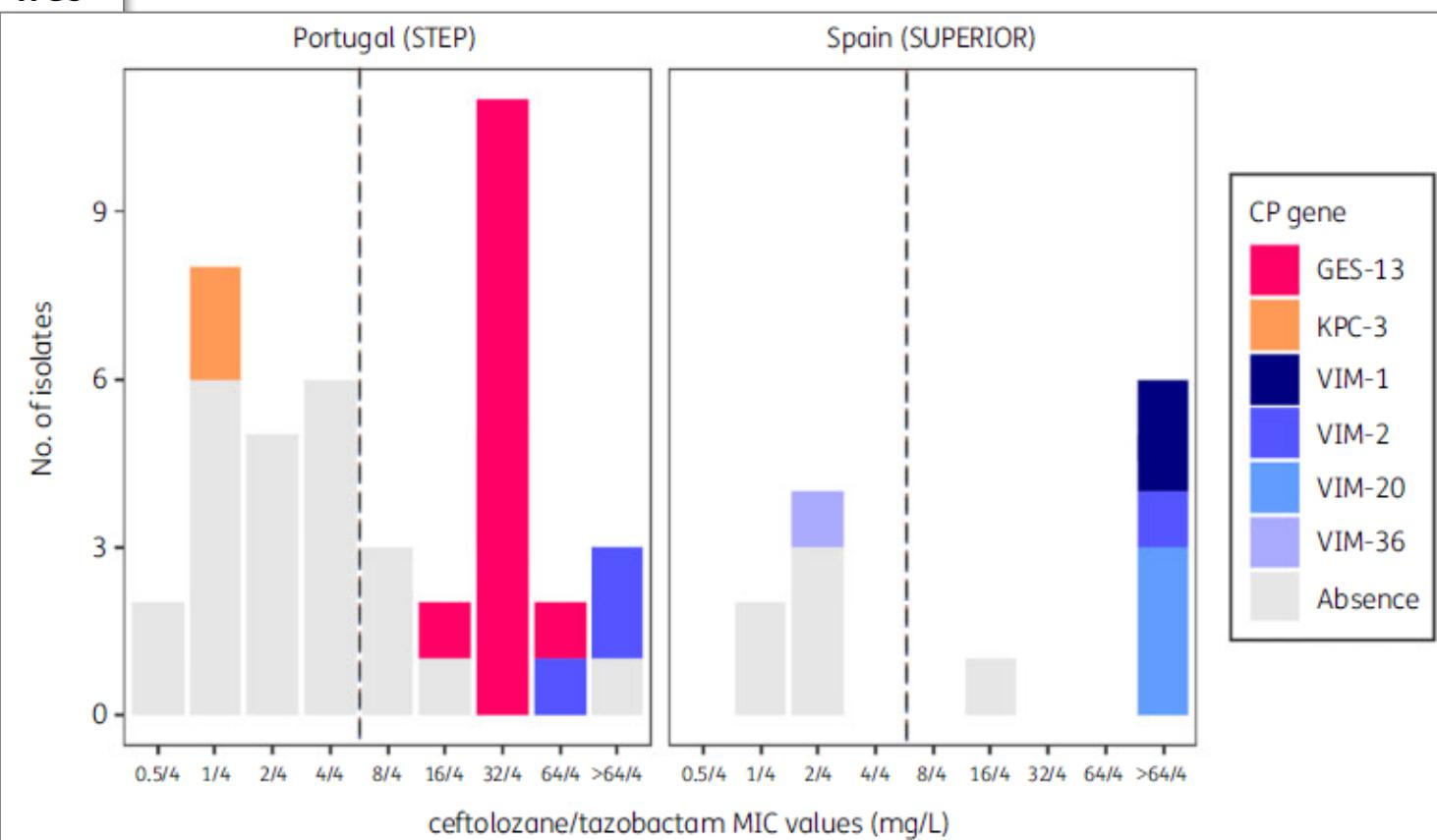


Figure 3. Distribution of *P. aeruginosa* isolates according to different ceftolozane/tazobactam MIC values, the origin country (Portugal, STEP study; Spain, SUPERIOR study) and the detection of carbapenemase-encoding genes by WGS.^{14,15} Dotted line represents the ceftolozane/tazobactam EUCAST 2020 breakpoint ($S \leq 4$ mg/L; $R > 4$ mg/L). CP, carbapenemase. This figure appears in colour in the online version of JAC and in black and white in the printed version of JAC.

Carbapenem resistance and carbapenemases in *P. aeruginosa*

Betalactam agent	MIC breakpoints (mg/L)		Wild type	AmpC derepressed	Porin deficiency (OprD ⁻)	Efflux pump (MexAB-OprM)	Metallo-β-lactamase (VIM-2)	Carbapenemase (GES-5) (MIC category)
	S ≤	R >	MIC (category)	MIC (category)	MIC (category)	MIC (category)	MIC (category)	MIC (category)
Piperacillin-tazobactam	0.001 ¹	16 ¹	4 (I)	>64 (R)	8 (I)	>64 (R)	>64 (R)	>64 (R)
Ceftazidime	0.001	8	1 (I)	>32 (R)	2 (I)	2 (I)	>32 (R)	>32 (R)
Cefepime	0.001	8	2 (I)	>16 (R)	4 (I)	4 (I)	>16 (R)	>16 (R)
Aztreonam	0.001	16	4 (I)	>16 (R)	8 (I)	8 (I)	4 (I)	>16 (R)
Ceftazidime-avibactam	8 ¹	8 ¹	1 (S)	1 (S)	2 (S)	2 (S)	>32 (R)	4 (S)
Ceftolozane-tazobactam	4 ¹	4 ¹	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	>16 (R)	>16 (R)
Imipenem	0.001	4	0.5 (I)	1 (I)	>8 (R)	1 (I)	>8 (R)	>8 (R)
Imipenem-relebactam	2 ¹	2 ¹	0.25 (S)	0.5 (S)	8 (R)	0.5 (S)	>8 (R)	>8 (R)
Meropenem	2	8	0.5 (S)	0.5 (S)	2 (S)	8 (R)	>8 (R)	>8 (R)
Meropenem-vaborbactam	8 ¹	8 ¹	0.5(S)	0.5 (S)	2 (S)	8 (R)	>8 (R)	>8 (R)

For susceptibility testing purposes, the concentration of the inhibitor is fixed at ¹⁴ mg/L

I = Susceptible, increased exposure to the agent provided higher exposure of the microorganism can be achieved (dose, frequency, mode of administration).

Multi-drug resistant *Pseudomonas aeruginosa* in Spain



Antimicrobial Agents
and Chemotherapy®



March 2022 Volume 66 Issue 3 e02161-21

In Vitro Activity of Cefepime-Taniborbactam against Carbapenemase-Producing *Enterobacteriales* and *Pseudomonas aeruginosa* Isolates Recovered in Spain

© Marta Hernández-García,^{a,b} María García-Castillo,^{a,b} Patricia Ruiz-Garbajosa,^{a,b} Germán Bou,^{b,c} María Siller-Ruiz,^d Cristina Pitart,^e Irene Gracia-Ahufinger,^f Xavier Mulet,^{b,g} Álvaro Pascual,^{b,h,i,j} Nuria Tormo,^k Rafael Cantón^{a,b}

Cefepime-taniborbactam MICs and carbapenemases

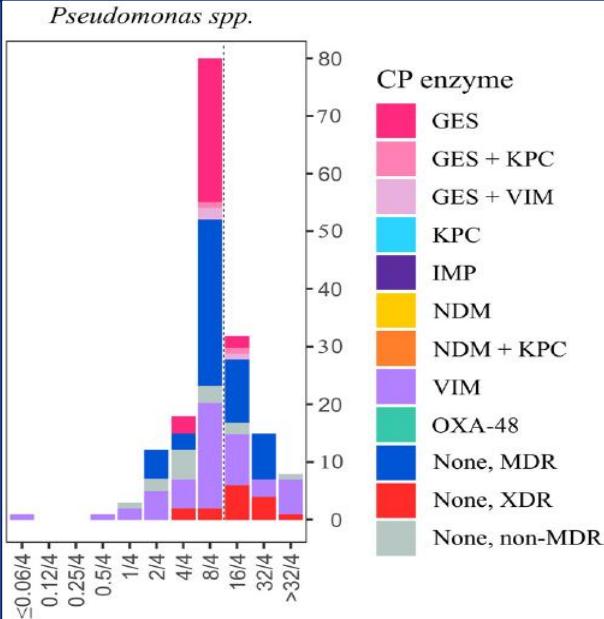


TABLE 2 Activities of cefepime-taniborbactam and comparators in meropenem-resistant isolates according to EUCAST breakpoints by the carbapenemase group detected^a

Carbapenemase group	FEP		FTB		CZA		CT		IMR		MEV		
	MIC ₅₀	MIC ₉₀	% S	MIC ₅₀	MIC ₉₀	% S	MIC ₅₀	MIC ₉₀	% S	MIC ₅₀	MIC ₉₀	% S	
<i>Pseudomonas</i> spp. (n = 170)	32	>32	20.0	8/4	32/4	67.6	8/4	>32/4	61.2	8/4	>32/4	34.7	16/4
MER-R (71.8% [122/170])	32	>32	10.7	8/4	32/4	63.9	8/4	>32/4	51.6	8/4	>32/4	17.2	32/4
GES (30/122) ^b	>32	>32	0	8/4	8/4	93.3	4/4	8/4	96.7	8/4	8/4	0	32/4
VIM (49/122) ^c	>32	>32	13.0	8/4	>32/4	61.2	>32/4	>32/4	14.3	>32/4	>32/4	0	>32/4
Non-carbapenemase (43/122)	32	>32	16.3	16/4	32/4	46.5	8/4	>32/4	62.8	8/4	>32/4	48.8	4/4

^aMER, meropenem (S, ≤2 mg/L; R, >8 mg/L); FTB, cefepime-taniborbactam (provisional breakpoint: S, ≤8/4 mg/L; R, >8/4 mg/L); CZA, ceftazidime-avibactam (S, ≤8/4 mg/L; R, >8/4 mg/L); CT, ceftolozane-tazobactam (*Enterobacteriales* spp., S, ≤2/4 mg/L, and R, >2/4 mg/L; *Pseudomonas* spp., S, ≤4/4 mg/L, and R, >4/4 mg/L); IMR, imipenem-relebactam (S, ≤2/4 mg/L; R, >2/4 mg/L); and MEV, meropenem-vaborbactam (S, ≤8/8 mg/L; R, >8/8 mg/L).

^bThe GES group includes 29 *bla*_{GES} isolates and 1 *bla*_{GES}+*bla*_{KPC} isolate.

^cThe VIM group includes 46 *bla*_{VIM} and 3 *bla*_{VIM}+*bla*_{GES} isolates.

Resistance mechanism to new compounds: beta-lactamases

Impact of different beta-lactamases in the susceptibility of new beta-lactams

Microorganisms	Enzyme	C/T	CAZ-AVI	IMP-REL	MER-VAB	FCD
<i>P. aeruginosa PAO1</i>	-	0.25	1	0.25	0.25	0.5
	GES-1	16	1	0.25	0.25	0.5
	GES-6	64	2	1	2	2
	BEL-2	32	4	0.25	0.25	4
	KPC-2	32	2	2	8	1
	PER-1	>256	32	0.25	0.5	16
	NDM-1	>256	256	32	>32	4
	SPM-1	>256	128	4	32	8
	OXA-427	>256	128	2	4	4

*MIC, mg/L



Resistance mechanism to new compounds: beta-lactamases

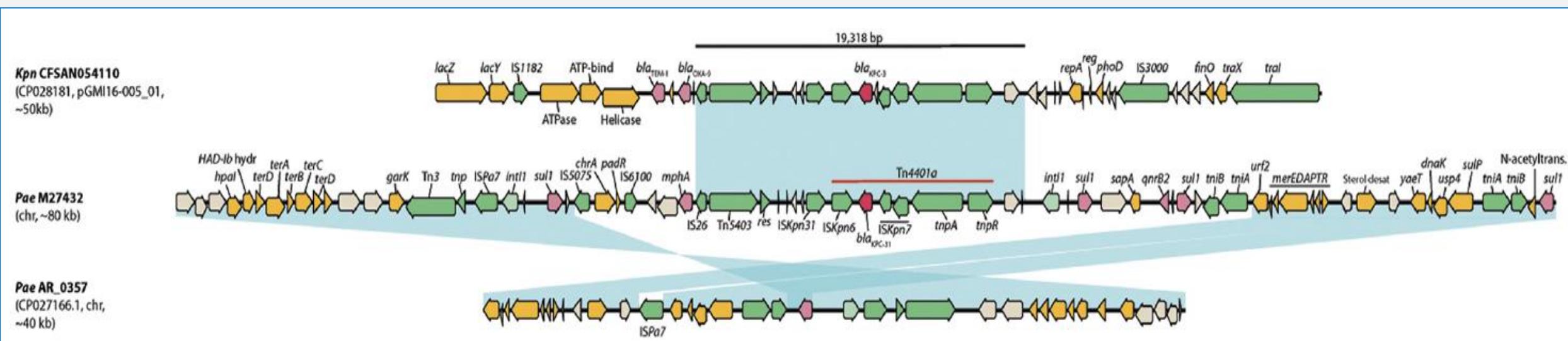


November 2022 Volume 66 Issue 11

Emergence of KPC-31, a KPC-3 Variant Associated with Ceftazidime-Avibactam Resistance, in an Extensively Drug-Resistant ST235 *Pseudomonas aeruginosa* Clinical Isolate

Diego Faccone,^{a,b} Juan M. de Mendieta,^a Ezequiel Albornoz,^a Magali Chavez,^a Fabiana Genero,^c Mariano Echegorry,^a Paola Ceriana,^a Andrea Mora,^d Christine Seah,^e Alejandra Corso,^a Roberto G. Melano,^{e,f} Fernando Pasteran^a

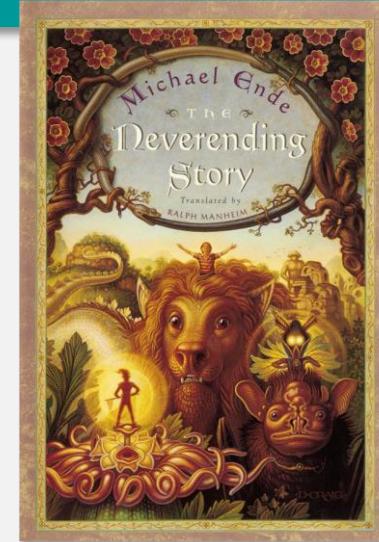
Chronic osteomyelitis patient treated with ceftazidime-avibactam in combination with other agents for 130 days (!)



Comparison of sequence with plasmid pGM16-005_01 from *K. pneumoniae* CFSAN054110 and the chromosome of *P. aeruginosa* AR_0357 suggesting a plasmidic origin of an ≈19-kb fragment containing *bla_{KPC-31}*

Evolución de las resistencias

- Resistance is a growing global problem that complicates its control
- High-risk clones play an important role in the maintenance and spread of resistance
- The COVID-19 pandemic has exacerbate the problem of resistance, particularly in carbapenemase-producing Enterobacterales and multidrug-resistant *P. aeruginosa*
- In Spain, an epidemiological change in carbapenemase-producing Enterobacterales, particularly in *K. pneumoniae* has been produced during the COVID-19 pandemics
 - increase of KPC carbapenemases and emergence of new KPC variants determining resistance to some of the beta-lactam/beta-lactamase inhibitors combinations
 - maintenance of OXA-48
 - emergence of metallo-beta lactamase (NDM), also in socio-sanitary institutions
 - emergence of cefiderocol-resistant isolates
- In Spain, increased complexity of resistance mechanisms in multidrug-resistant *P. aeruginosa*
 - consolidation of GES carbapenemases affecting ceftolozane-tazobactam, meropenem-vaborbactam and imipenem-relebactam but not ceftazidime-avibactam
- There is a need for a continuous follow-up of antimicrobial resistance at local and international level with phenotypic and molecular techniques, including whole genome sequencing





ReFORMÚLA**T**E

En busca del tesoro

“La evolución de las resistencias”



Dr. Rafael Cantón
Hospital Universitario Ramón y Cajal
SERVICIO DE MICROBIOLOGÍA Y PARASITOLOGÍA



@RafaMCanton



@microRyC



Departamento de
Microbiología y
Parasitología
Universidad
Complutense. Madrid

