II Jornada del Comité Español del Antibiograma (CoEsAnt)

Madrid, 12 de febrero de 2026

Lectura interpretada del antibiograma en Enterobacterales

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II Jornada del Comité Español del Antibiograma (CoEsAnt)

Lectura interpretada del antibiograma en Enterobacterales

Conflictos de interés

EUCAST European Committee on Antimicrobial Susceptibility Testing

Clinical data coordinator (2007 – 2012, 2016 –)
Chairman (2012 – 2016)

CLSI

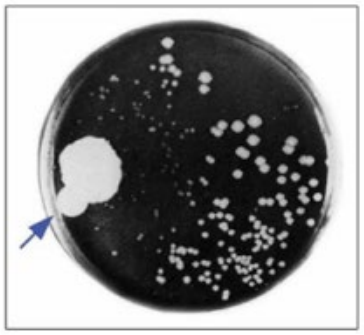
Member of the *Intrinsic Resistance Working Group* (2013 –)
Member of the Taxonomy group (2021 – 2022)
Advisor (2016 – 2017)

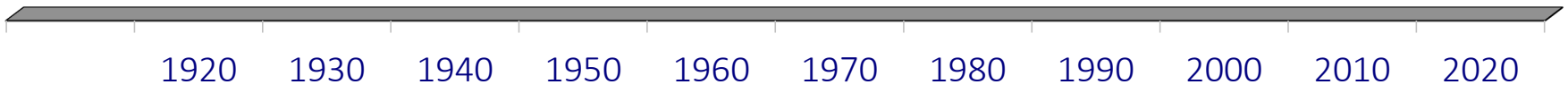
CoEsAnt

Member of *Comité Español del Antibiograma* (2014 – 2020)

Antimicrobial susceptibility testing

The antimicrobial susceptibility testing (AST) process…





Introduction of antibiotic in therapeutics

Description of resistance mechanisms and AST methods

Relation between resistance and clinical failure

Normalization of in vitro AST

Interpretive criteria (breakpoints)

Interpretive reading of the antibiogram

Automation of AST

New approaches for (*rapid*) AST

Updated from Cantón R. Enf Inf Microbiol Clin 2002; 20:176-85

FORMACIÓN MÉDICA CONTINUADA Enferm Infecc Microbiol Clin 2002;20(4):176-86

Lectura interpretada del antibiograma: ¿ejercicio intelectual o necesidad clínica?

Rafael Cantón Moreno

Servicio de Microbiología. Hospital Ramón y Cajal. Madrid. España.

Enferm Infecc Microbiol Clin. 2010;28(6):375–385

ELSEVIER DOYMA

Enfermedades Infecciosas y Microbiología Clínica

www.elsevier.es/eimc

Formación médica continuada

Lectura interpretada del antibiograma: una necesidad clínica

Rafael Cantón

Servicio de Microbiología, Hospital Ramón y Cajal, Madrid, España

Enferm Infecc Microbiol Clin. 2010;28(9):638–645

ELSEVIER DOYMA

Enfermedades Infecciosas y Microbiología Clínica

www.elsevier.es/eimc

Formación médica continuada

Lectura interpretada del antibiograma de enterobacterias ☆

Ferran Navarro [a,b,*], Elisenda Miró [a] y Beatriz Mirelis [a,b]

[a] *Servei de Microbiologia, Hospital de la Santa Creu i Sant Pau, Barcelona, España*
[b] *Universitat Autònoma de Barcelona, Barcelona, España*

Procedimientos en Microbiología Clínica

Recomendaciones de la Sociedad Española de Enfermedades Infecciosas y Microbiología Clínica

Editores: Emilia Cercenado y Rafael Cantón

38. **Detección fenotípica de mecanismos de resistencia en gramnegativos**

2 0 1 1

Coordinador: Ferran Navarro

Autores: Jorge Calvo
Rafael Cantón
Felipe Fernández Cuenca
Beatriz Mirelis
Ferran Navarro

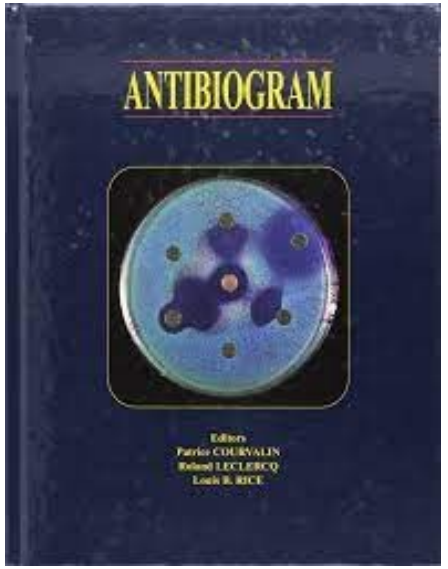
Interpretive reading of the antibiogram

1.- To determine the susceptibility and resistance phenotype

2.- To infer the potential resistance mechanism behind the phenotype

3.- To predict the phenotype previously determined from the resistance mechanism and to infer the activity of the different antimicrobials expressing the phenotype

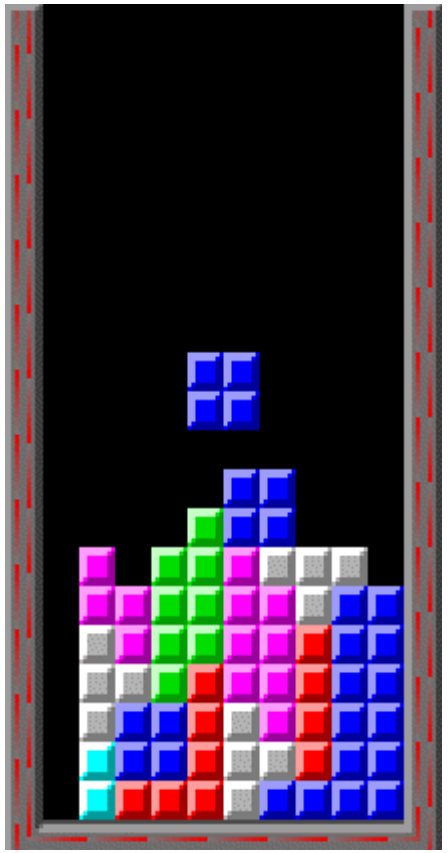
Patrice Courvalin, ASM News, 1992



Susceptibility and resistance phenotype:

Conjunction of susceptibility testing results (MICs) of a microorganisms for a group of antimicrobial agents, normally belonging to a single family

Interpretive reading of the antibiogram



Requirements

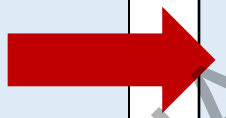
- Adequate **identification** of the microorganism
- Recognition of “intrinsic resistance” (*expected pnehotype*)
- Analysis of susceptibility/resistance phenotype
- Use of antimicrobials as **markers** of resistance mechanisms
- Analysis of antibiotic + **inhibitor** combinations
- Determine **quantitative susceptibility testing values** (MIC / mm)
- Use of high inoculum in certain situations
- To know the **local epidemiology** / trends in antimicrobial resistance
- To implement ancillary tests and reference molecular techniques

Courvalin P. ASM News 1992;58:368-75; Livermore DM et al. J Antimicrob Chemother 2001;48(Suppl 1):87-102
Cantón R. Enferm Infecc Microbiol Clin 2002; 20: 176-86; Cantón R. Enferm Infecc Microbiol Clin 2010; 28:375-85;
Leclercq R et al. Clin Microbiol infect 2013; 19:141-60; Cantón R et al. Enferm Infecc Microbiol Clin 2020;38:182-7

Interpretive reading in Enterobacterales: identification

Relevance of bacterial identification

Antimicrobial	MIC (mg/L)
Ampicillin	>64
Amox/clav	>32/16
Ticarcillin	>64
Piperacillin	32
Piper/Tazo	16/4
Cefuroxime	>64
Cefoxitin	>32
Cefotaxime	4
Ceftazidime	8
Cefepime	1
Ertapenem	4



Organisms	Potential phenoype
E. coli	AmpC hyperproduction plasmid AmpC ESBL + porin deficiency
K. pneumoniae	ESBL + porin deficiency
E. cloacae	ESBL

Cantón R. Enferm Infecc Microbiol Clin 2010; 28:375-85

Intrinsic resistance – Expected phenotypes

EUCAST abandons the term "intrinsic resistance" in favor of "expected resistant phenotype"

- No agreed definition on intrinsic resistance that might change over time
- New definitions for a practical approach for the interpretation of susceptibility testing results

  Unnecessary testing of antimicrobial for expected susceptible and expected resistance phenotypes
  A result which goes against the expected phenotype should be viewed with suspicion

- **Expected susceptible phenotype**

  A very high proportion (>99%) of the population of a microorganism exhibits MICs ≤ S PK-PD breakpoint
  The wild type populations should be considered "S" or "I"
  Resistance is virtually (or absolutely) unknown
  Detection of such resistance must prompt revision of identification or test results.

  e.g. *Streptococcus pyogenes* and benzylpenicillin

- **Expected resistant phenotype**

  The great majority (≥90%) of wild type isolates exhibit MICs for an agent or a group of agents that are so high (>R PK-PD breakpoint or similar organisms) that the agent should not be considered for therapy

  e.g. *Klebsiella pneumoniae* and ampicillin, *Haemophilus influenzae* and linezolid,

https://www.eucast.org/eucast_news/news_singleview/?tx_ttnews%5Btt_news%5D=480&cHash=e6a33871b9efef82225399f1a3ce0493 [last access 10/02/2026];
https://www.eucast.org/bacteria/important-additional-information/expected-phenotypes/ [last access 10/04/2026]
Gatermann S, Das S, Dubreuil L, Giske CG, Kahlmeter G, Lina G, Lindemann C, MacGowan A, Meletiadis J, Rossolini GM, Turnidge J, Cantón R.
Expected phenotypes and Expert Rules are Important Complements to Antimicrobial Susceptibility Testing. Clin Microbiol Infect. 2022 Mar 16:S1198-743X(22)00146-X.

Intrinsic resistance – Expected phenotypes: Enterobacterales

Rule	Organisms	Ampicillin/Amoxicillin	Amoxicilin-clavulanic acid	Ampicillin-sulbactam	Ticarcillin	Cefazolin, Cephalothin Cefalexin, Cefadroxil	Cefoxitin[2]	Cefuroxime	Tetracyclines	Tigecycline	Polymyxin B, Colistin	Fosfomycin	Nitrofurantoin
1.1	*Citrobacter koseri, Citrobacter amalonaticus*[3]	R			R	**R**		**R**					
1.2	*Citrobacter freundii*[4]	R	R	R		R	R						
1.3	*Enterobacter cloacae* complex	R	R	R		R	R						
1.4	*Escherichia hermannii*	R			R								
1.5	*Hafnia alvei*	R	R								R		
1.6	*Klebsiella aerogenes*	R	R	R		R	R						
1.7	*Klebsiella pneumoniae* complex	R			R								
1.8	*Klebsiella oxytoca*	R			R								
1.9	*Leclercia adecarboxylata*											R	
1.10	*Morganella morganii*	R	R	R		R	**R**	**R**	R	**R**	R		R
1.11	*Plesiomonas shigelloides*	R	R	R									
1.12	*Proteus mirabilis*								R	**R**	R		R
1.13	*Proteus penneri*	R				R		R	R	**R**	R		R
1.14	*Proteus vulgaris*	R				R		R	R	**R**	R		R
1.15	*Providencia rettgeri*	R	R	R		R			R	**R**	R		R

R = additional resistances considered CA-SFM*

*Comité de l'Antibiogramme de la SFM (CA-SFM) V1.1 Juillet 2025 https://www.sfm-microbiologie.org/boutique/_comite-de-lantibiogramme-de-la-sfm-ca-sfm-v1-1-juilet-2025/ [last access 10/02/2026]

https://www.eucast.org/bacteria/important-additional-information/expected-phenotypes/ [last access 10/02/2026]

Intrinsic resistance – Expected phenotypes: Enterobacterales

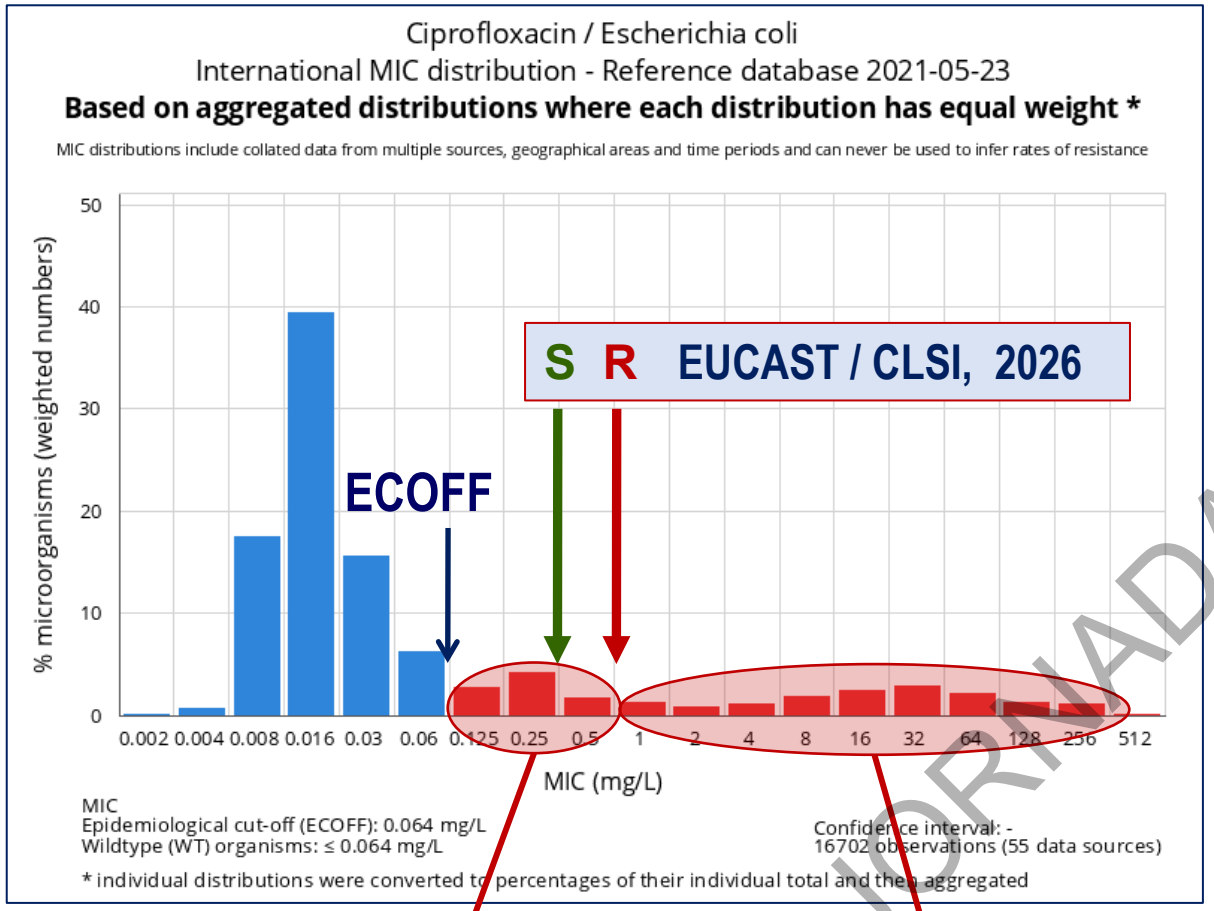
Rule	Organisms	Ampicillin/Amoxicillin	Amoxicillin-clavulanic acid	Ampicillin-sulbactam	Ticarcillin	Cefazolin, Cephalothin Cefalexin, Cefadroxil	Cefoxitin[2]	Cefuroxime	Tetracyclines	Tigecycline	Polymyxin B, Colistin	Fosfomycin	Nitrofurantoin
1.16	*Providencia stuartii*	R	R	R		R	**R**		R	**R**	R		R
1.17	*Raoultella* spp.	R			R								
1.18	*Serratia marcescens*	R	R	R		R	R	R		**R**	R		R
1.19	*Yersinia enterocolitica*	R	R	R	R	R	R						
1.20	*Yersinia pseudotuberculosis*										R		
1.21	*Aeromonas hydrophila*	R		R									
1.22	*Aeromonas veronii*	R		R	R								
1.23	*Aeromonas dhakensis*	R		R			R						
1.24	*Aeromonas caviae*	R		R									
1.25	*Aeromonas jandaei*	R		R	R								

R = additional resistances considered CA-SFM*

*Comité de l'Antibiogramme de la SFM (CA-SFM) V1.1 Juillet 2025 https://www.sfm-microbiologie.org/boutique/_comite-de-lantibiogramme-de-la-sfm-ca-sfm-v1-1-juilet-2025/ [last access 10/02/2026]

https://www.eucast.org/bacteria/important-additional-information/expected-phenotypes/ [last access 10/02/2026]

ECOFF / ECV and clinical breakpoints



Low level R mechanism
(*qnr, qyrA* single mutants)

High level R mechanism
(*qyrA, parC* double mutants)

- **The epidemiological cut-off value (ECOFF)** separates microorganisms without (**wild type**) and with **acquired resistance mechanisms** (**non-wild type**) to the agent

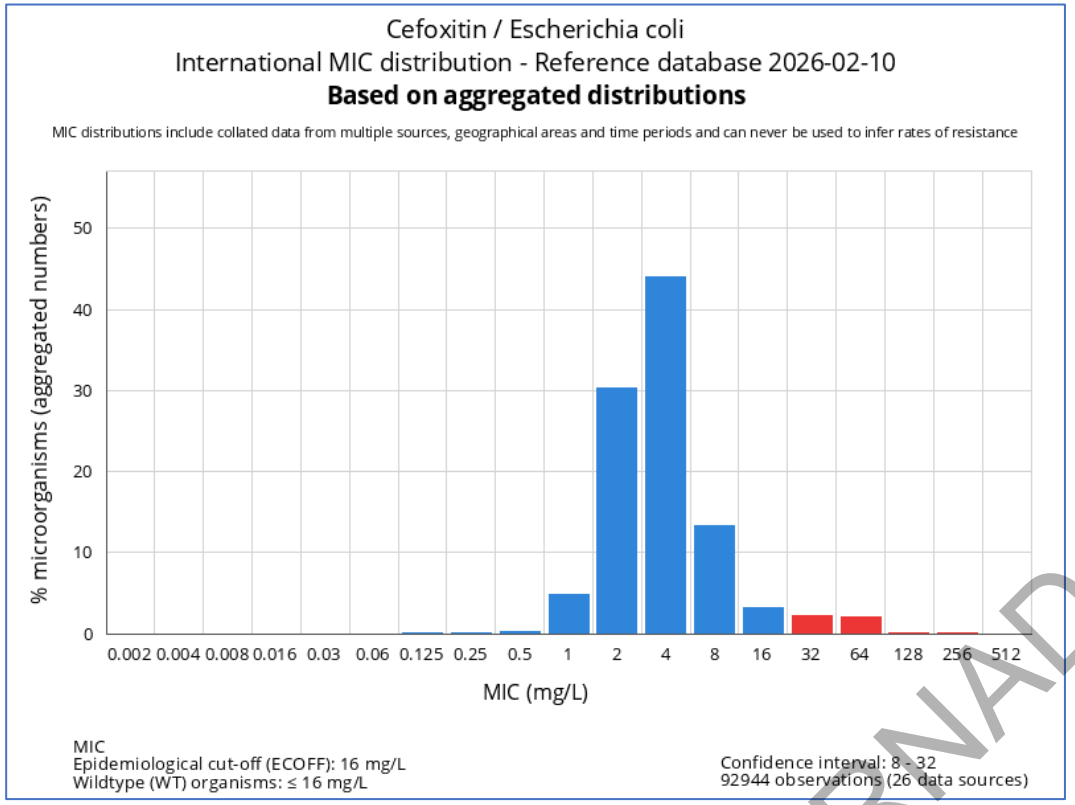
https://mic.eucast.org/search/

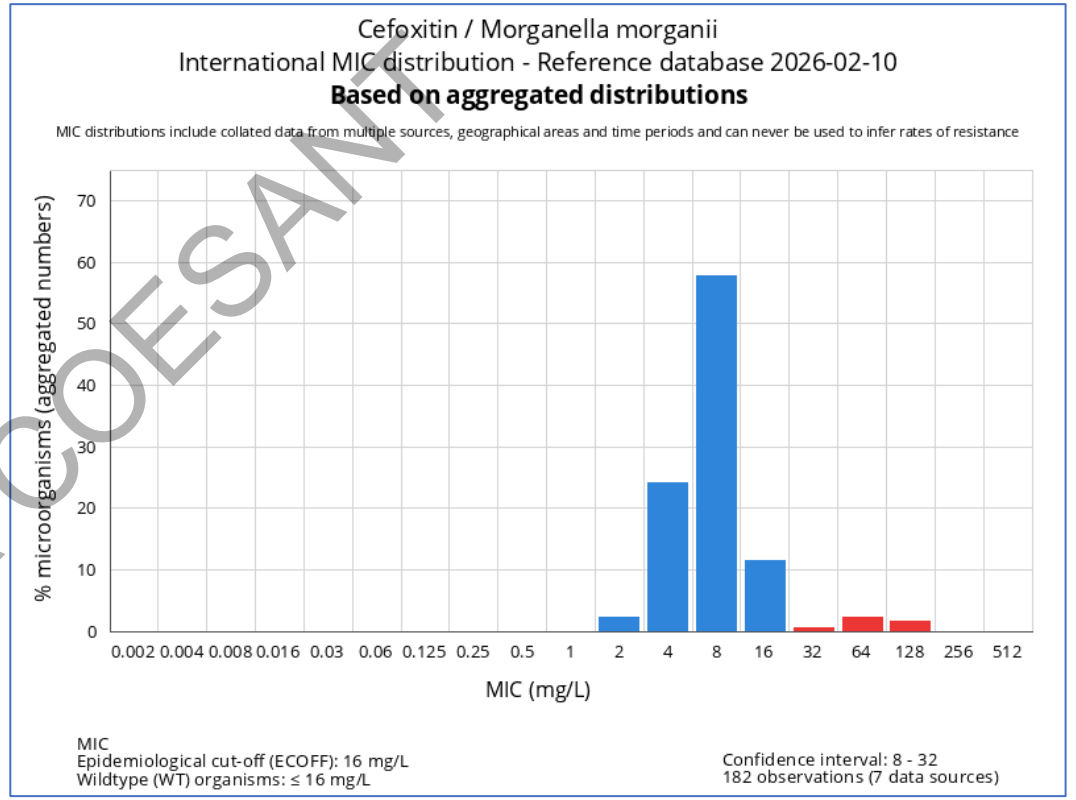
Identical ECOFF / ECV in EUCAST and CLSI

- The **clinical breakpoints** are used **to classify microorganisms** into **clinical categories** (**S/I/R**) to **predict clinical success/failure** when testing *in vitro* (antibiogram) an antimicrobial agent

Not identical breakpoints categories and criteria in CLSI and EUCAST

Intrinsic resistance – Expected phenotypes: Enterobacterales





https://mic.eucast.org/

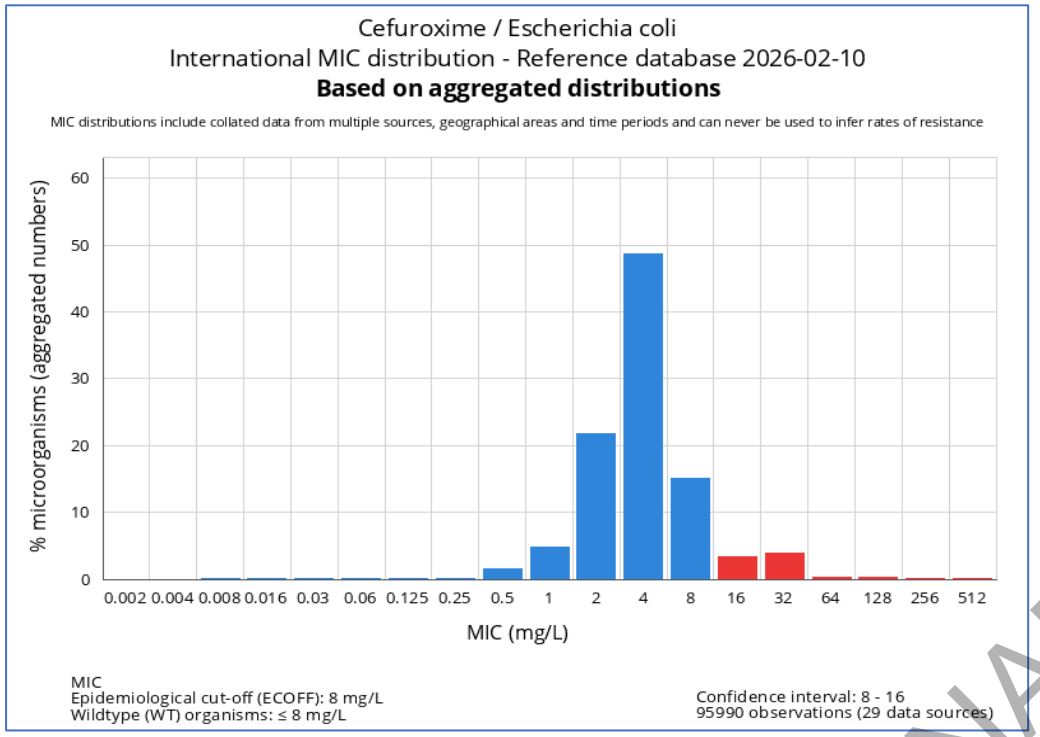
Note in breakpoint table for cefoxitin

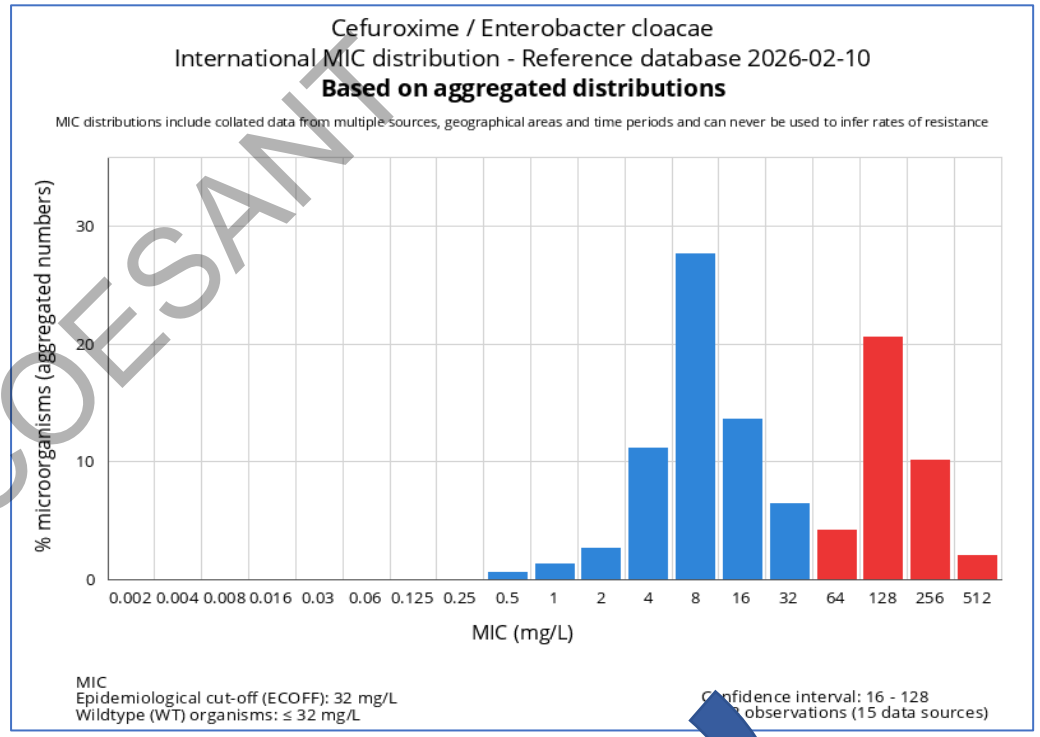
The **cefoxitin cut-off value (8 mg/L)** has a high sensitivity but poor specificity for identification of AmpC-producing Enterobacterales as this agent is also affected by permeability alterations and some carbapenemases.

Classical non-AmpC producers are wild type, whereas plasmid AmpC producers or chromosomal AmpC hyperproducers are non-wild type.

https://www.eucast.org/bacteria/clinical-breakpoints-and-interpretation/clinical-breakpoint-tables/

Intrinsic resistance – Expected phenotypes – Expert rules – Enterobacterales





Rule No.	Organisms	Indicator Agent*	Agents affected*	Rule	Remarks	Grade	References
5	*Enterobacter* spp., *K. aerogenes, Citrobacter freundii*†, *Serratia* spp., *Morganella morganii, Hafnia alvei, Providencia* spp.	cefuroxime	cefuroxime other 2nd generation cephalosporins	IF susceptible to cefuroxime, THEN report cefuroxime and/or any other 2nd generation cephalosporin as resistant	Although the breakpoint table does not list cefuroxime breakpoints for species other than *E. coli*, *P. mirabilis*, *Klebsiella* spp. (except *K. aerogenes*) and *Raoultella* spp., isolates may appear susceptible in vitro but the MICs tend to be higher than with the mentioned species and therapy with cefuroxime is not recommended. In addition, de-repressed mutants may be selected as with a third-generation cephalosporin.	C	

https://mic.eucast.org/

Expert rule

https://www.eucast.org/bacteria/important-additional-information/expert-rules/

Interpretive reading of the antibiogram: antimicrobials

Enferm Infecc Microbiol Clin. 2020;38(4):182–187

Enfermedades Infecciosas y Microbiología Clínica

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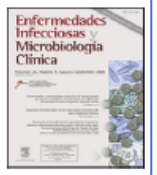


Review article

Recommendations of the Spanish Antibiogram Committee (COESANT) for selecting antimicrobial agents and concentrations for *in vitro* susceptibility studies using automated systems

Rafael Cantón[a,b,*], Antonio Oliver[b,c], Juan Ignacio Alós[d], Natividad de Benito[e], Germán Bou[b,f], José Campos[b,g], Jorge Calvo[b,h], Andrés Canut[i], Javier Castillo[j], Emilia Cercenado[k], Maria Ángeles Domínguez[b,l], Felipe Fernández-Cuenca[b,m], Jesús Guinea[k], Nieves Larrosa[b,n], Josefina Liñares[b,a], Lorena López-Cerero[b,m], Antonio López-Navas[o], Francesc Marco[b,p], Beatriz Mirelis[q], Miguel Ángel Moreno-Romo[r], María Isabel Morosini[a,b], Ferran Navarro[q], Jesús Oteo[b,g], Álvaro Pascual[b,m], Emilio Pérez-Trallero[s], María Pérez-Vázquez[b,g], Alex Soriano[t], Carmen Torres[u], Jordi Vila[b,p], Luis Martínez-Martínez[b,w]

- Antibiotics
- Range of concentrations
  - Breakpoints
  - ECOFFs

Enfermedades Infecciosas y Microbiología Clínica 41 (2023) 571–576

Enfermedades Infecciosas y Microbiología Clínica

www.elsevier.es/eimc

Review article

Recommendations of the Spanish Antibiogram Committee (COESANT) for *in vitro* susceptibility testing of antimicrobial agents by disk diffusion

Alba Rivera[a], Belén Viñado[b], Natividad Benito[c], Fernando Docobo-Pérez[d,f,g,h], Felipe Fernández-Cuenca[e,f,g], Javier Fernández-Domínguez[i,j], Jesús Guinea[j,k], Antonio López-Navas[l], Miguel Ángel Moreno[m], María Nieves Larrosa[b,g,h], Antonio Oliver[g,h,n], Ferran Navarro[a,*]

Interpretive reading in Enterobacterales: antimicrobials

Propuesta de inclusión de antimicrobianos (Procedimiento microbiológico, 2026)

Categoría A Deben estudiarse e informarse de forma rutinaria	Categoría B Deben estudiarse de manera rutinaria e informarse de forma selectiva	Categoría C Deben estudiarse e informarse de forma selectiva	Categoría D Recomendados para su estudio e informe rutinario en orina	Categoría E Deben estudiarse, pero no informar, útiles en la detección de mecanismos de resistencia
Ampicilina	Ceftazidima–avibactam	Temocilina	Cefazolina	Piperacilina
Amoxicilina-ác. clavulánico	Cefiderocol	Ceftolozano-tazobactam	Cefixima	Ticarcilina
Piperacilina-tazobactam	Aztreonam	Aztreonam-Avibactam	Norfloxacino	Temocilina
Cefuroxima	Imipenem	Imipenem-relebactam	Fosfomicina	Cefoxitina
Ceftazidima	Meropenem	Meropenem-vaborbactam	Nitrofurantoina	Pefloxacino
Cefotaxima	Minociclina	Delafloxacino		
Cefepime		Azitromicina		
Ertapenem		Eravaciclina		
Ciprofloxacino		Tigeciclina		
Gentamicina		Cloramfenicol		
Tobramcina		Colistina		
Amikacina				
Trimetoprim–sulfametoxazol				

Arca-Suárez J, Cantón R, Larrosa Escartín N, López-Calleja AI, Rivera A. Lectura interpretada del antibiograma de bacilos Gram-negativos Enterobacterales (*in press*)

Interpretive reading of the antibiogram: *K. pneumoniae*

Antibiotic	MIC (mg/L)	Interpre-tation
Amoxicillin	>16	R
Amoxi-clav	≤4/2	S
Piper-tazo	≤8/4	S
Cefuroxime	≤0.5	S
Cefotaxime	≤0.06	S
Ceftazidime	≤0.06	S
Cefepime	≤0.06	S
Aztreonam	≤0.06	S
Ceftol-Tazo	≤0.5/4	S
Cefta-avib	≤0.5/4	S
Ertapenem	≤0.5	S
Imipenem	≤0.5	S
Meropenem	≤0.5	S

Wild type

Antibiotic	MIC (mg/L)	Interpre-tation
Amoxicillin	>16	R
Amoxi-clav	≤4/2	S
Piper-tazo	≤8/4	S
Cefuroxime	>16	R
Cefotaxime	>16	R
Ceftazidime	2	I
Cefepime	0.5	S
Aztreonam	0.5	S
Ceftol-Tazo	1/4	S
Cefta-avib	1/4	S
Ertapenem	2	R
Imipenem	≤0.5	S
Meropenem	≤0.5	S

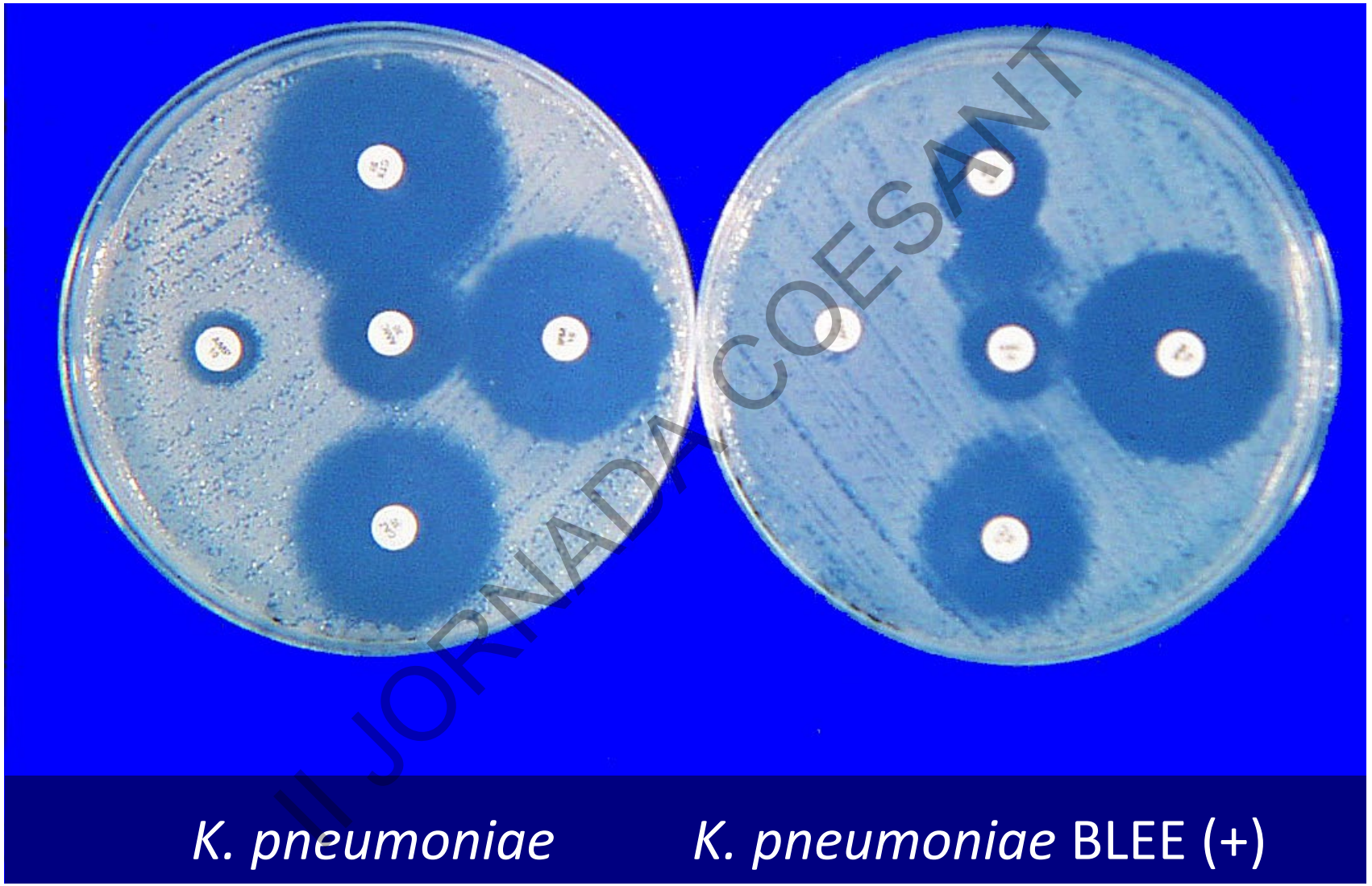
ESBL

Antibiotic	MIC (mg/L)	Interpre-tation
Amoxicillin	>16	R
Amoxi-clav	>16/8	R
Piper-tazo	>64/4	R
Cefuroxime	>16	R
Cefotaxime	>16	R
Ceftazidime	>16	R
Cefepime	>16	R
Aztreonam	>4	R
Ceftol-Tazo	>8/4	S
Cefta-avib	4/4	S
Ertapenem	>8	R
Imipenem	<8	R
Meropenem	8	I

Carbapenemase

EUCAST, 2020 interpretive criteria (www.eucast.org)

Interpretive reading of the antibiogram: *K. pneumoniae*



K. pneumoniae *K. pneumoniae* BLEE (+)

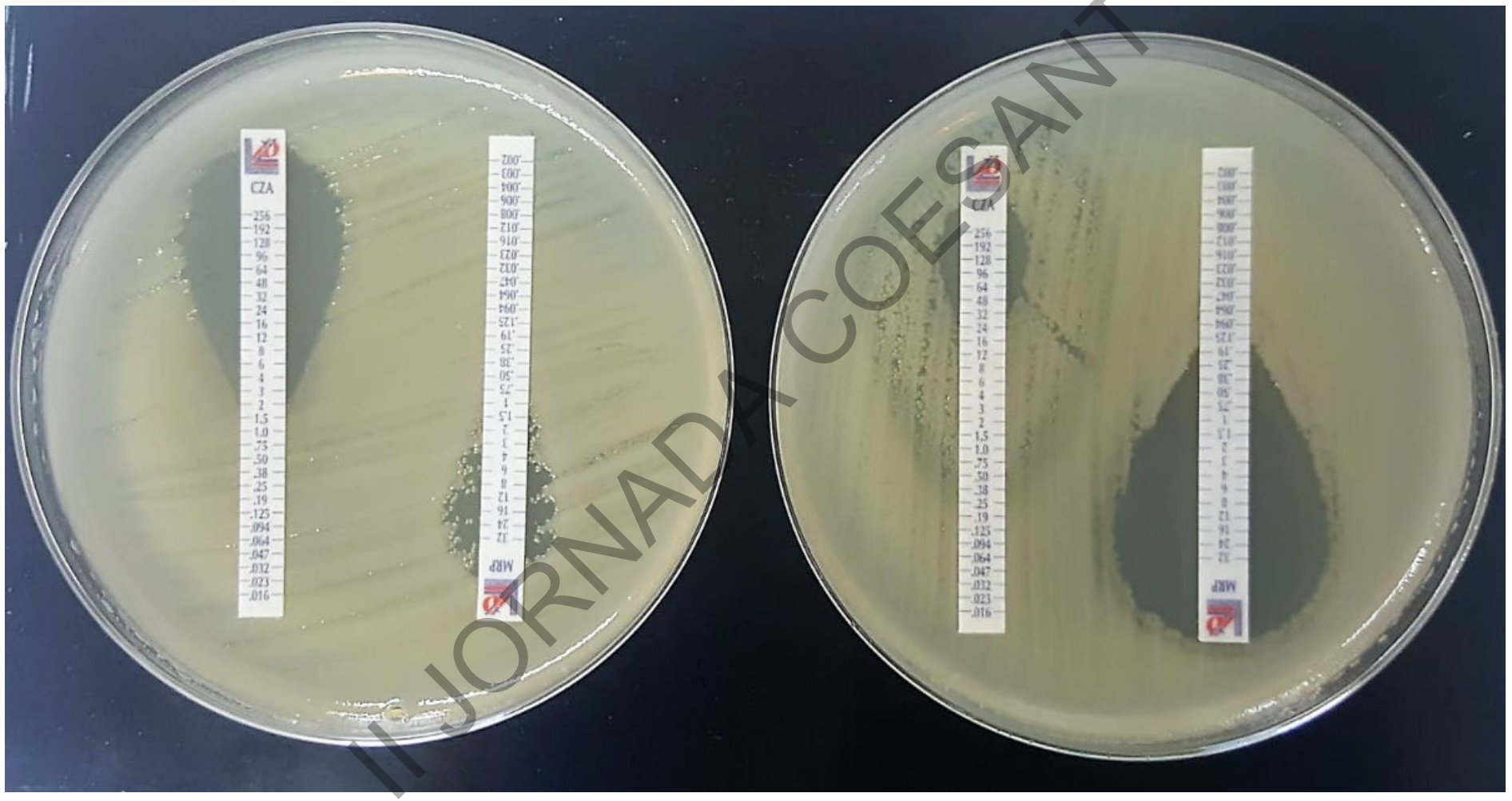
Interpretive reading of the antibiogram: *K. pneumoniae*

Antibiotic	MIC in mg/L (clinical interpretation)						
	Wild type	VIM-1	VIM-1 + CTX-M-15	KPC-2/3	KPC-2/3-mutants	OXA-48	OXA-48 + CTX-M-15
Amoxicillin	>16 (R)	>16 (R)	>16 (R)	>16 (R)	>16 (R)	>16 (R)	>16 (R)
Amox./clav.	≤4/2 (S)	>16/2(R)	>16/2(R)	>16/2 (R)	>16/2 (R)	>16/2 (R)	>16/2 (R)
Pip./taz.	≤16/4 (S)	>64/4 (R)	>64/4 (R)	>64/4 (R)	>64/4 (R)	>64/4 (R)	>64/4 (R)
Cefuroxime	8 (S)	>16 (R)	>16 (R)	>16 (R)	>16 (R)	8 (S)	>16 (R)
Cefoxitin	≤8(S)	>32 (R)	>32 (R)	16 (R)	16 (R)	≤8 (S)	16 (R)
Cefotaxime	≤1(S)	>16 (R)	>16 (R)	>16 (R)	>16 (R)	≤1 (S)	>16 (R)
Ceftazidime	≤1(S)	>8 (R)	>8 (R)	>8 (R)	>8 (R)	≤1 (S)	>8 (R)
Ceftazidime-avibactam	≤1/4 (S)	>8/4 (R)	>8/4 (R)	≤1/4 (S)	>8/4 (R)	≤1/4 (S)	≤1 /4 (S)
Cefepime	≤1(S)	8 (R)	8 (R)	8 (R)	8 (R)	≤1 (S)	8 (R)
Aztreonam	≤1(S)	1 (S)	>8 (R)	>16 (R)	>16 (R)	≤1 (S)	>16 (R)
Aztreonam-avibactam	≤1/4(S)	1/4 (S)	2/4 (S)	≤1/4 (S)	>16/4 (R)	2/4 (S)	2/4 (2)
Imipenem	≤0.5 (S)	>8 (R)	>8 (R)	>4 (R)	≤2 (S)	8 (R)	8 (R)
Imipenem-relebactam	≤0.5/4 (S)	>8/4 (R)	>8/4 (R)	≤2/4 (S)	≤2/4 (S)	8/4 (R)	8/4 (R)
Meropenem	≤0.5 (S)	>8 (R)	>8 (R)	>8 (R)	≤2 (S)	8 (I)	8 (I)
Meropenem-vaborbactam	≤0.5/8 (S)	>8/8 (R)	>8/8 (R)	≤2/8 (S)	≤2/8 (S)	8/8 (S)	8/8 (S)
Ertapenem	≤0.5 (S)	4 (R)	4 (R)	>0.5 (R)	>0.5 (R)	> 0.5 (R)	>0.5 (R)
Cefiderocol	≤0.25 (S)	0.5 (S)	0.5 (S)	2 (S)	1 (S)	0.5 (S)	0.5 (S)

Following EUCAST, 2024 interpretive criteria (www.eucast.org)

Emergence of KPC-variants ceftazidime/avibactam resistant

Klebsiella pneumoniae ST307

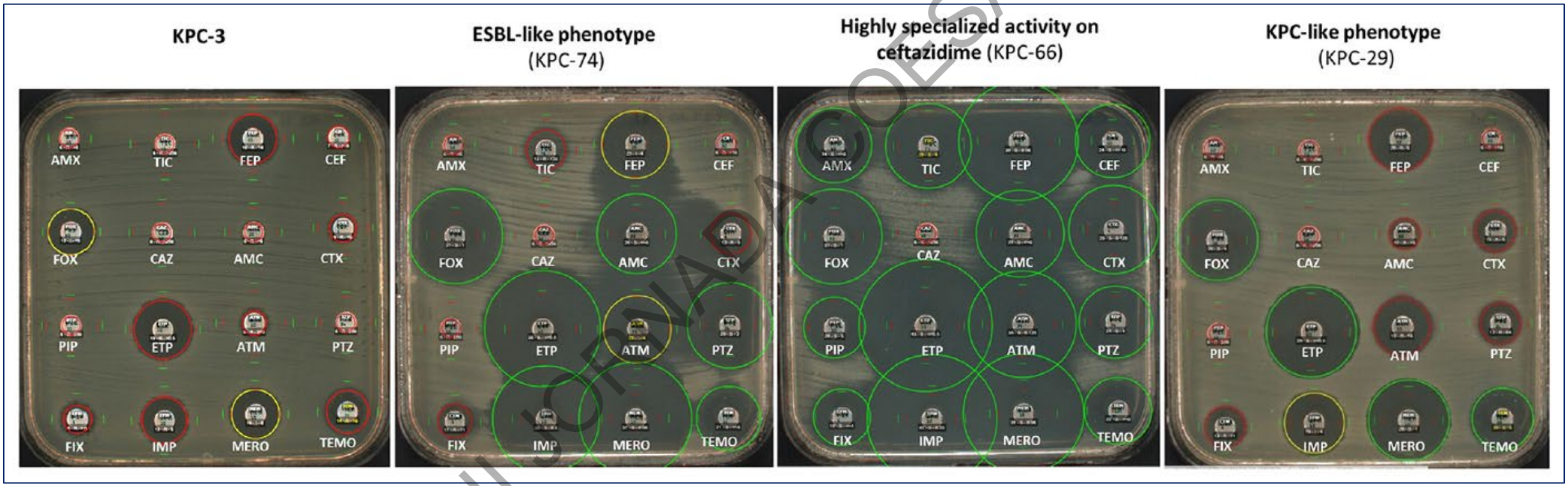


KPC-3 KPC-46

Hernández-García M et al. J Clin Microbiol. 2022 Mar 16;60(3):e0224521

Emergencia de variantes KPC con resistencia a ceftazidima-avibactam

Fenotipos debidos a mutaciones KPC implicadas en la resistencia a la ceftazidima-avibactam (expresadas en *Escherichia coli*)



Hobson CA et al. Antimicrob Agents Chemother. 2022 Sep 20;66(9):e0044722

New beta-lactamases conferring resistance to ceftazidime-avibactam

Journal of Global Antimicrobial Resistance 46 (2026) 46–48

Contents lists available at ScienceDirect

Journal of Global Antimicrobial Resistance

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

Letter to the Editor

A novel plasmid-mediated PAC ß-lactamase (PAC-2) variant confers resistance to ceftazidime-avibactam in *Klebsiella quasipneumoniae* ST526 in Colombia

Editor: Ana Gales

Sandra Yamile Saavedra*, Efrain Montilla-Escudero, María Victoria Ovalle, Jeisson Alejandro Triana, Yeison Stid Torres, Nathalia Vargas-Flórez, María Alejandra Gutiérrez, Andrés Felipe Barrera
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Carolina Duarte
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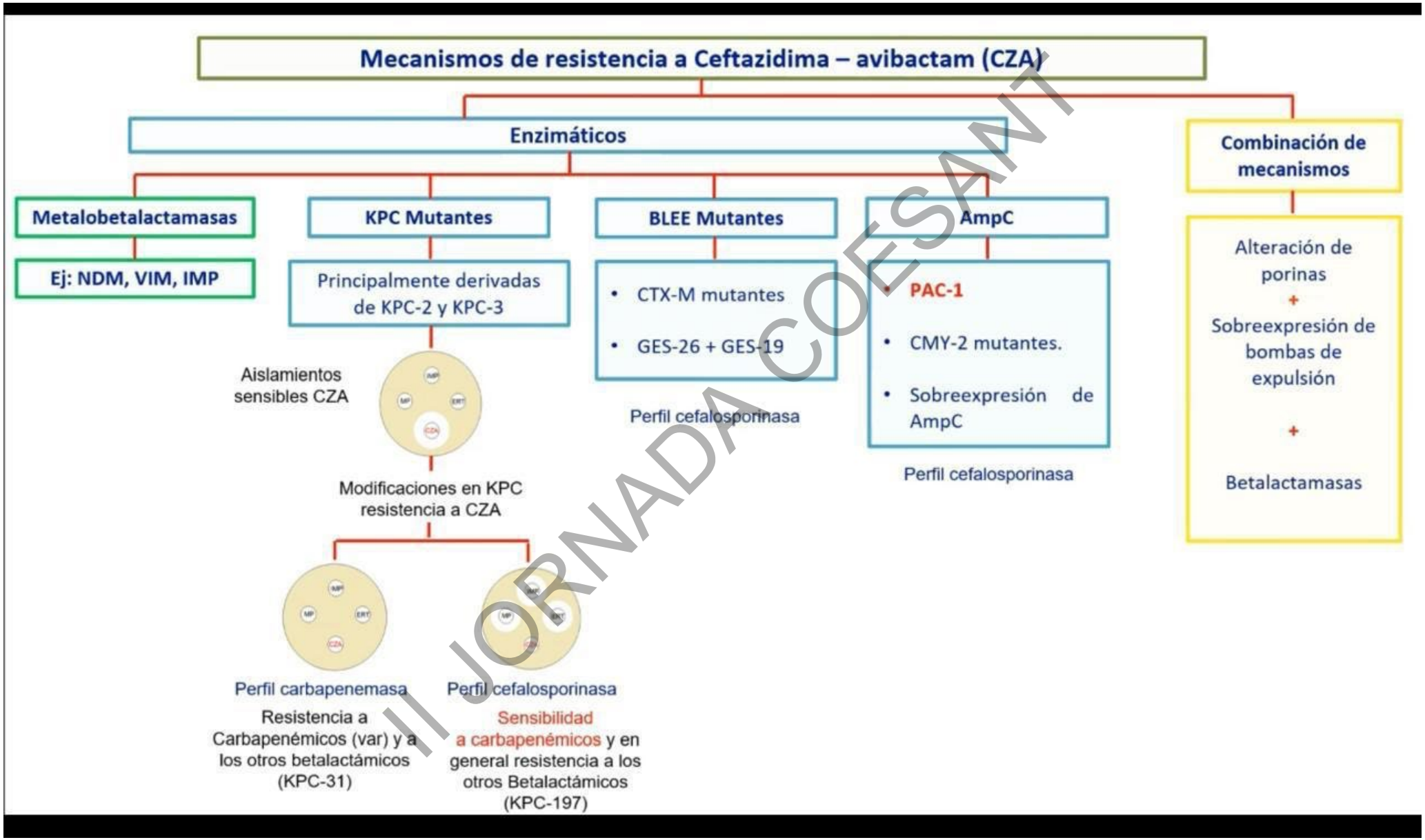
Antibiotic	Interpretation
Piperacillin/tazobactam	R
Cefoxitina	S
Cefotaxime	R
Ceftazidime	R
Cefepime	R
Aztreonam	S
Ceftolozane/tazobactam	R
Ceftazidime/avibactam	(>256 mg/l) R
Imipenem	S
Meropenem	S
Ertapenem	S

- **PAC-2** shares 99% identity with **PAC-1** and differs by three substitutions in its amino acids (K44Q, E309A, and N339K)
- **PAC-1:** 65% sequence identity with the AmpC from *Cronobacter turicensis* (formerly *Enterobacter sakazakii*) and 47% with the AmpC enzyme from *Pseudomanas aeruginosa* PAO1 (PDC-1)*

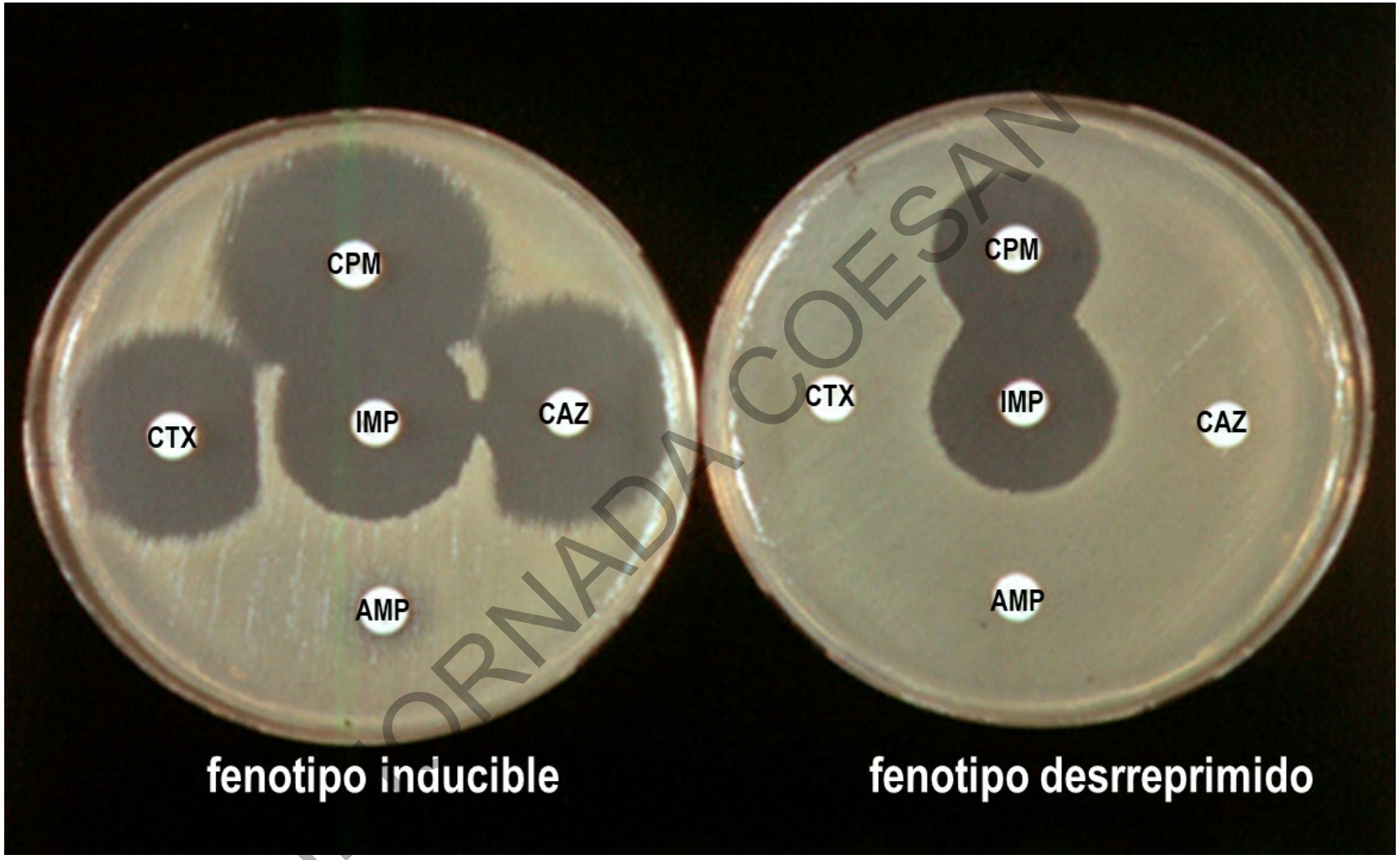
*Bour M, et al. Acquisition of class C β-lactamase PAC-1 by ST664 strains of *Pseudomonas aeruginosa*. Antimicrob Agents Chemother. 2019 Sep 9;63(12):e01375-19.

Emergencia de variantes KPC con resistencia a ceftazidima-avibactam



Cortesia de Germán Esparza (Colombia)

AmpC – *Enterobacter cloacae*



Interpretive reading in Enterobacterales: Beta-lactams

Enterobacterales grupo I (productores de AmpC inducibles): *Enterobacter cloacae* complex, *Klebsiella aerogenes*, *Citrobacter freundii*, *Serratia marcescens*, *Morganella morganii*, *Providencia* spp., *Hafnia alvei* y *Yersinia enterocolitica*

AMP AMX-CLAV	PIP/TAZ	CEF	FOX	CXM	CTX CAZ	FEP	ATM	IMI MEM	CAZ/AVI	MEV	IMR	AZA	FDC	Interpretation
S	S	R	S	r	S	S	S	S	S	S	S	S	S	WT (AmpC basal)
R	S	R	r/R	r/R	S	S	S	S	S	S	S	S	S	WT (AmpC inducible)
R	r/R	R	r/R	R	r/R	S	R	S	S	S	S	S	S	AmpC desreprimida
R	S/r	R	r/R	R	r/R	S/r/R	R	S	S	S	S	S	S	BLEE + AmpC inducible
R	R	R	r/R	R	R	S/r/R	R	S	S	S	S	S	S	BLEE+ AmpC desreprimida
R	R	R	R	R	R	R	R	R	S	S	S	S	S	Carbapenemasa Clase A (KPC) + AmpC inducible
R	R	R	R	R	R	R	S	r/R	R	R	R	S	S/r	Carbapenemasa Clase B (NDM, VIM) + AmpC inducible
R	R	R	R	R	S/r/R	S/r/R	r/R	r/R	S	r/R	r/R	S	S	Carbapenemasa Clase D (OXA-48) + AmpC inducible
R	R	R	R	R	R	r/R	S/r/R	r/R	S/r/R	r/R	r/R	S	S/r	Carbapenemasa + AmpC desreprimida
R	R	R	R	R	R	R	R	R	R	R	R	S/r	S/r	Carbapenemasa Clase B + Clase D + AmpC inducible/desreprimida AmpC

BLEE: betalactamasa de espectro-extendido;
AMP, ampicilina; AMX/CLAV, amoxicilina/clavulanico; PIP/TAZ, piperacilina/tazobactam; CEF, cefalotina; FOX, cefoxitina; CMX, cefuroxima; CTX, cefotaxima; CAZ, ceftazidima; FEP, cefepima; ATM, aztreonam; IMI, imipenem; MEM, meropenem; CAZ/AVI, ceftazidima/avibactam; MEV, meropenem/vaborbactam; IMR, imipenem/relebactam; AZA, aztreonam/avibactam; FCD, cefiderocol;
R, resistente; r, CMI elevada o reducido halo de inhibición; S, sensible; WT, fenotipo salvaje

Arca-Suárez J, Cantón R, Larrosa Escartín N, López-Calleja AI, Rivera A. Lectura interpretada del antibiograma de bacilos Gram-negativos Enterobacterales (*in press*)

Cooperative pathways of resistance mechanisms

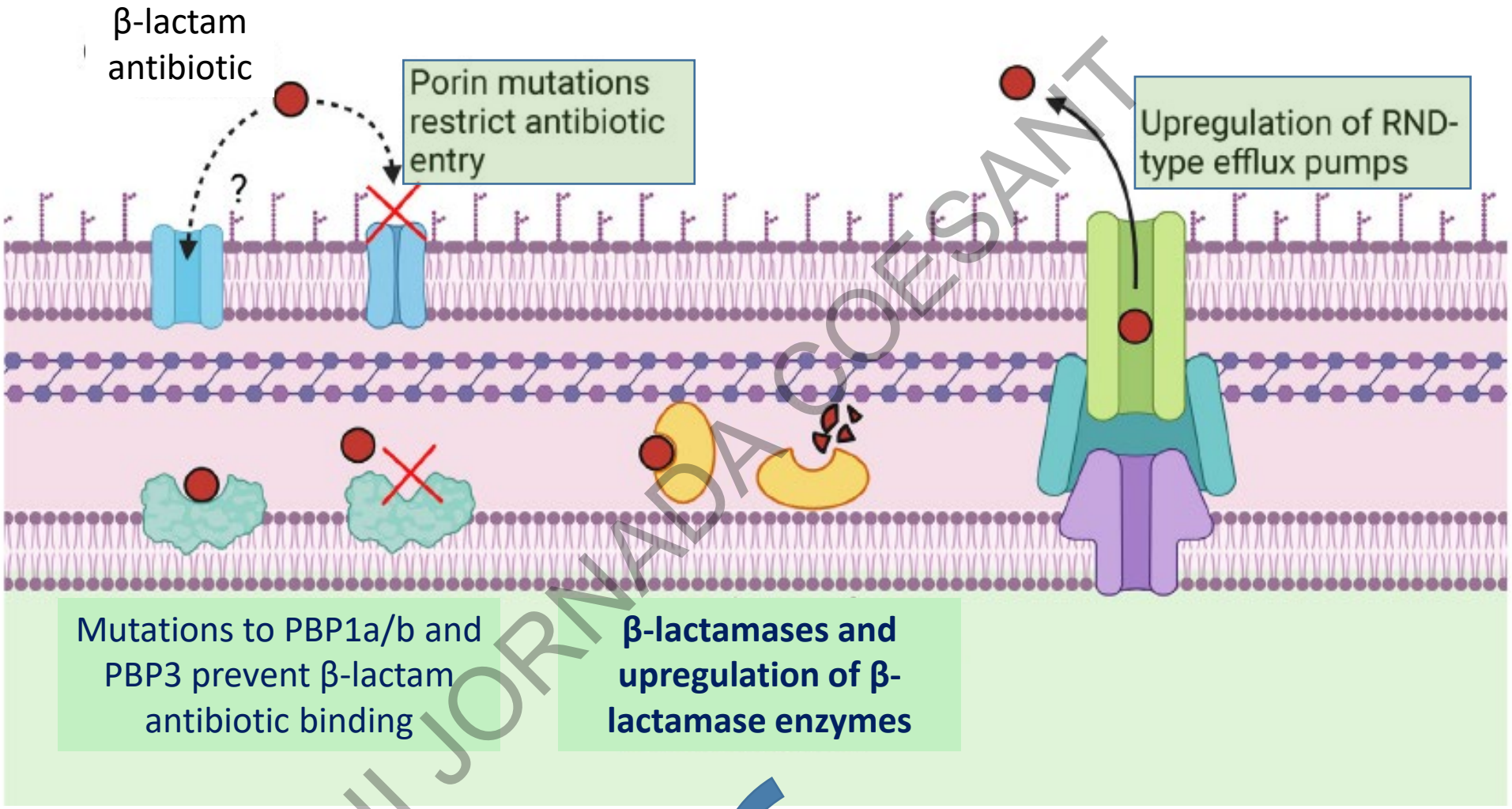


Imagen extraída de Hardie Boys MT, et al. Int J Antimicrob Agents. 2025

Normally higher level of expression

Hardie Boys MT, Pletzer D. A review of recently discovered mechanisms of cephalosporin resistance in *Pseudomonas aeruginosa*. Int J Antimicrob Agents. 2025;66(2):107527.

Interpretive reading in Enterobacterales: Beta-lactams

Mechanisms of resistance to new β-lactams and combinations of β-lactams/β-lactamase inhibitors

Antimicrobial	Mutations in β-lactamases	Increase in the number of *bla*CARBAPENEMASE/ESBL copies	Association of *bla*CARBAPENEMASE and *bla*ESBL/pAmpC	Mutations in porins (OmpC/F or OmpK35/36)	Overexpression of expulsion pumps	PBP2 modifications	PBP3 modifications	Siderophore mutation
DBO (Diazabicyclooctanes)								
Ceftazidime/avibactam	R	Y	Y	Y	Y	G	Y	G
Aztreonam/avibactam	G	Y	Y	Y	Y	G	R	G
Imipenem/relebactam	Y	Y	Y	R	Y	G	G	G
Meropenem/nacubactam	W	Y	Y	Y	Y	W	G	G
Aztreonam/nacubactam	W	Y	Y	R	Y	W	G	G
Cefepime/zidebactam	Y	Y	Y	Y	Y	R	G	G
Cyclic boronate								
Meropenem/vaborbactam	R	Y	Y	Y	Y	G	G	G
Cefepime/taniborbactam	R	Y	Y	Y	Y	G	Y	G
Meropenem/xeruborbactam	R	W	W	Y	W	W	W	G
Ceftibuten/ledaborbactam	R	W	R	Y	W	W	W	G
Penicillanic acid sulfone								
Cefepime/enmetazobactam	G	Y	Y	Y	Y	G	Y	G
Siderophore cephalosporin								
Cefiderocol	R	Y	Y	Y	W	G	Y	R

- Mechanism does not affect
- Mechanism conferring resistance in combinations with others
- Mechanism conferring resistance
- No available data (there is no clinical trial or use)

Delgado-Valverde M, et al. Mechanisms of resistance to newer drugs against Gram negative bacteria in Enterobacterales. Clin Microbiol Infect. 2026. Jan 7:S1198-743X(25)00653-6.

Emergence of Enterobacterales with PBP3 modifications

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Detection of cefiderocol and aztreonam/avibactam resistance in epidemic *Escherichia coli* ST-361 carrying bla_{NDM-5} and bla_{KPC-3} from foreign fighters evacuated from Ukraine

Melissa J. Martin,[1] Ting L. Luo,[1] Valentyn Kovalchuk,[2] Viacheslav Kondratiuk,[3] Henry D. Dao,[1,4] Iryna Kovalenko,[2] Brandon J. Plaza,[4] Joanna M. Kettlewell,[4] Cole P. Anderson,[4] Jason R. Smedberg,[4] Ana C. Ong,[1] Yoon I. Kwak,[1] Joshua S. Hawley-Molloy,[5] Jason W. Bennett,[1] Patrick T. McGann,[1] Francois Lebreton[1]

E. coli ST361

bla_{NDM-5}, bla_{KPC-3}, $bla_{CTX-M-15}$, *rmtB1*

$bla_{CMY-145}$ AmpC + PBP3 (YRIN insertion)

FDC (4-≥16 mg/L) + ATM-AVI (4/4-≥16/4 mg/L)

Martin MJ et al. Detection of cefiderocol and aztreonam/avibactam resistance in epidemic *Escherichia coli* ST-361 carrying bla_{NDM-5} and bla_{KPC-3} from foreign fighters evacuated from Ukraine. Antimicrob Agents Chemother 2024 Nov 6;68(11):e0109024.

JAC Antimicrob Resist
https://doi.org/10.1093/jacamr/dlae141

JAC-Antimicrobial Resistance

Emergence of high-level aztreonam–avibactam and cefiderocol resistance following treatment of an NDM-producing *Escherichia coli* bloodstream isolate exhibiting reduced susceptibility to both agents at baseline

Ghady Haidar[1,2], Ellen G. Kline[1], Georgios D. Kitsios[3,4], Xiaohong Wang[3,4], Eun Jeong Kwak[1], Anthony Newbrough[1], Kelly Friday[1], Kailey Hughes Kramer[1] and Ryan K. Shields[1,2,5*]

E. coli ST361

bla_{NDM-5}, $bla_{CMY-145}$, PBP3 (YRIN insertion)

FDC (8 mg/L) + ATM-AVI (16/4 mg/L)

bla_{NDM-5}, $bla_{CMY-145(L139R, N366Y),}$ PBP3 (YRIN insertion, A417V)

FDC (32 mg/L) + ATM-AVI (> 128/4 mg/L)

Haidar G et al. Emergence of high-level aztreonam-avibactam and cefiderocol resistance following treatment of an NDM-producing *E. coli* bloodstream isolate exhibiting reduced susceptibility to both agents at baseline. JAC Antimicrob Resist. 2024 Sep 5;6(5):dlae141.

Interpretive reading in Enterobacterales: aminoglycosides

Acquired resistance mechanisms

Klebsiella pneumoniae

Antimicrobial agent	MIC (mg/L)	Interpretation
Gentamicin	≤2	S
Tobramycin	>8	R
Amikacin	8	S

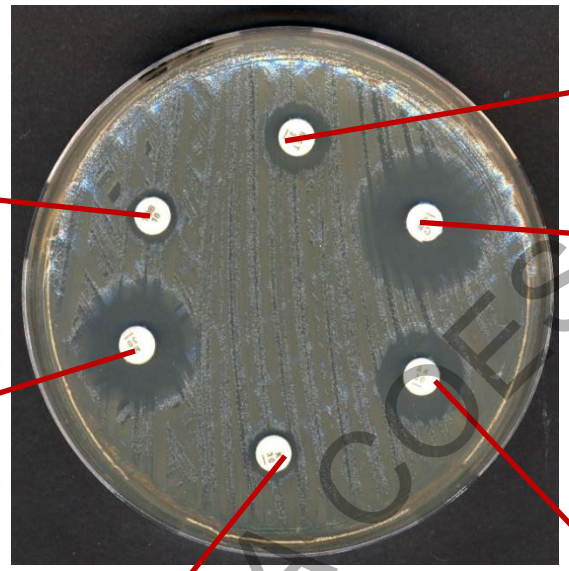
Fenotipo	Enzima/mecanismo	S	Sp	K	A	G	Nt	T	Nm
St	APH(3'')	R	S	S	S	S	S	S	S
St Sp	ANT(3'')(9)	R	R	S	S	S	S	S	S
G	AAC(3)-I	S	S	S	S	R	s/r	s/r	S
K	APH(3')-I	S	S	R	S	S	S	S	R
K A	APH(3')-VI	S	S	R	R	S	S	S	R
G T	AAC(3)-VI*	S	S	S	S	R	s/r	R	S
T K A	ANT(4')-II	S	S	R	R	S	S	R	S
G T Nt	AAC(2')-I AAC(3)-IV	S	S	S	S	R	R	R	R
K G T	ANT(2'')-I	S	S	R	S	R	S	r	S
K T A Nt	AAC(6')-I	S	S	R	r	S	R	R	S
K T G Nt	AAC(3)-II	S	S	R	S	R	R	R	S
K T G A Nt	Impermeability ± different enzymes	R	R	R	R	R	R	R	R
K T G A Nt	Metilasas (ArmA, …)	S	R	R	R	R	R	R	s

*= AAC(3)-IIa

Bush K, Miller GH. Bacterial enzymatic resistance: beta-lactamases and aminoglycoside-modifying enzymes. Curr Opin Microbiol. 1998; 1:509-15; Wright GD. Aminoglycoside-modifying enzymes. Curr Opin Microbiol. 1999; 2:499-503; Azucena E, Mobashery S. Aminoglycoside-modifying enzymes: mechanisms of catalytic processes and inhibition. Drug Resist Updat. 2001; 4:106-17; Navarro F, et al. Lectura interpretada del antibiograma de enterobacterias [Interpretive reading of enterobacteria antibiograms]. Enferm Infecc Microbiol Clin. 2010; 28:638-45. Ramirez MS, Tolmasky ME. Aminoglycoside modifying enzymes. Drug Resist Updat. 2010; 13:151-71. Zhang Y, et al. The prevalence and distribution of aminoglycoside resistance genes. Biosaf Health. 2023; 5:14-20.

Interpretive reading in Enterobacterales: aminoglycosides

Acquired resistance mechanisms



Netilmicin (R)

Tobramycin (R)

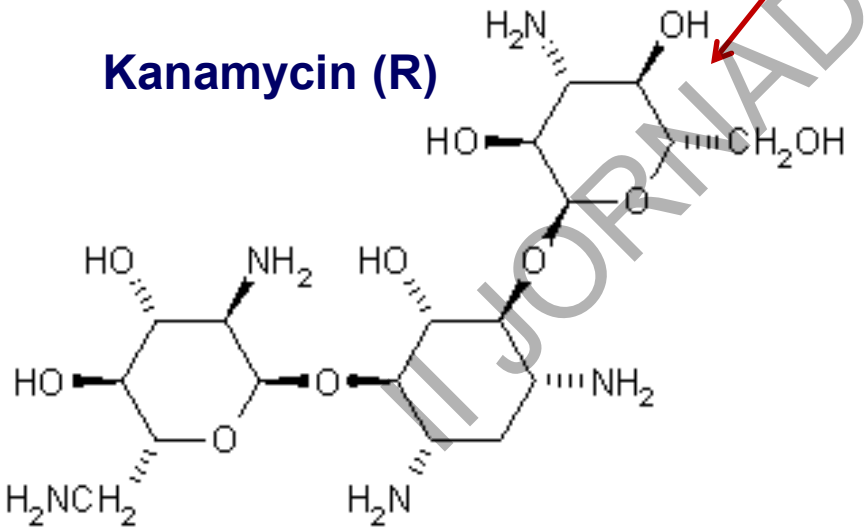
Gentamicin (S)

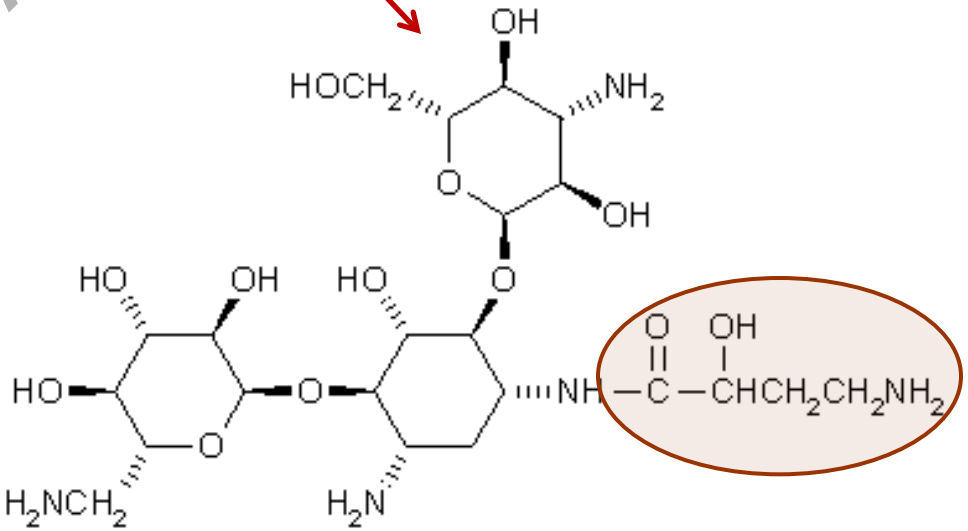
Neomycin (S)

AAC(6')-I

Amikacin (S)

Kanamycin (R)





Interpretive reading in Enterobacterales: aminoglycosides

Acquired resistance mechanisms

ANT(2”)-I

Escherichia coli

Antimicrobial agent	MIC (mg/L)	Interpretation
Gentamicin	>8	R
Tobramycin	4	I
Amikacin	8	S

Fenotipo	Enzima/mecanismo	S	Sp	K	A	G	Nt	T	Nm
St	APH(3”)	R	S	S	S	S	S	S	S
St Sp	ANT(3”)(9)	R	R	S	S	S	S	S	S
G	AAC(3)-I	S	S	S	S	R	s/r	s/r	S
K	APH(3’)-I	S	S	R	S	S	S	S	R
K A	APH(3’)-VI	S	S	R	R	S	S	S	R
G T	AAC(3)-VI*	S	S	S	S	R	s/r	R	S
T K A	ANT(4’)-II	S	S	R	R	S	S	R	S
G T Nt	AAC(2’)-I AAC(3)-IV	S	S	S	S	R	R	R	R
K G T	ANT(2”)-I	S	S	R	S	R	S	r	S
K T A Nt	AAC(6’)-I	S	S	R	r	S	R	R	S
K T G Nt	AAC(3)-II	S	S	R	S	R	R	R	S
K T G A Nt	Impermeability ± different enzymes	R	R	R	R	R	R	R	R
K T G A Nt	Metilasas (ArmA, …)	S	R	R	R	R	R	R	s

*= AAC(3)-IIa

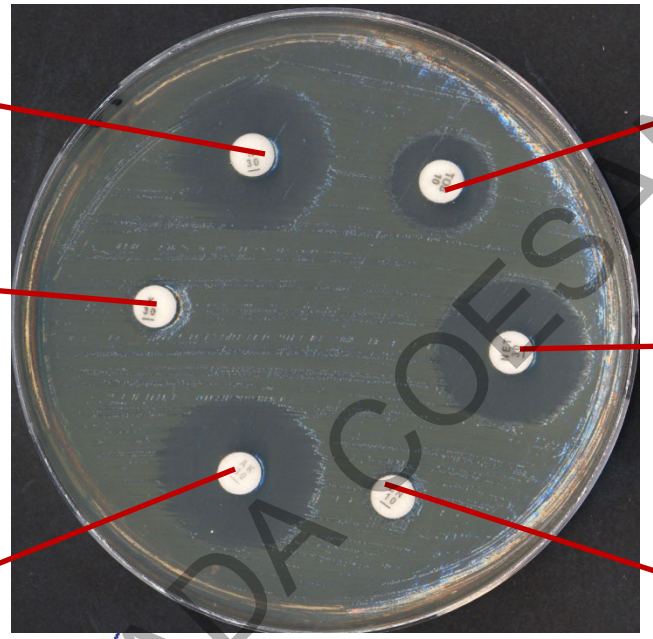
Bush K, Miller GH. Bacterial enzymatic resistance: beta-lactamases and aminoglycoside-modifying enzymes. Curr Opin Microbiol. 1998; 1:509-15; Wright GD. Aminoglycoside-modifying enzymes. Curr Opin Microbiol. 1999; 2:499-503; Azucena E, Mobashery S. Aminoglycoside-modifying enzymes: mechanisms of catalytic processes and inhibition. Drug Resist Updat. 2001; 4:106-17; Navarro F, et al. Lectura interpretada del antibiograma de enterobacterias [Interpretive reading of enterobacteria antibiograms]. Enferm Infecc Microbiol Clin. 2010; 28:638-45. Ramirez MS, Tolmasky ME. Aminoglycoside modifying enzymes. Drug Resist Updat. 2010; 13:151-71. Zhang Y, et al. The prevalence and distribution of aminoglycoside resistance genes. Biosaf Health. 2023; 5:14-20.

Interpretive reading in Enterobacterales: aminoglycosides

Acquired resistance mechanisms

Neomycin (S)

Kanamycin (R)



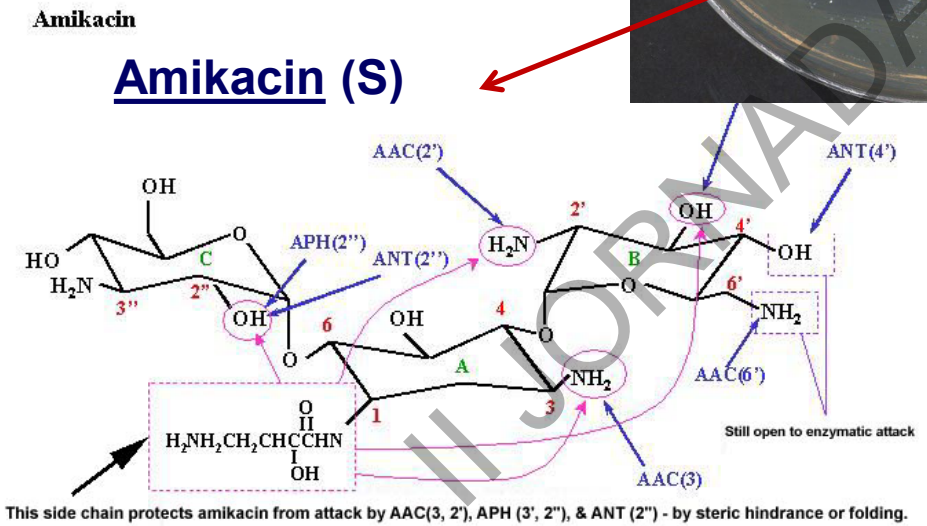
Tobramycin (I/r→ R)

Netilmicin (S)

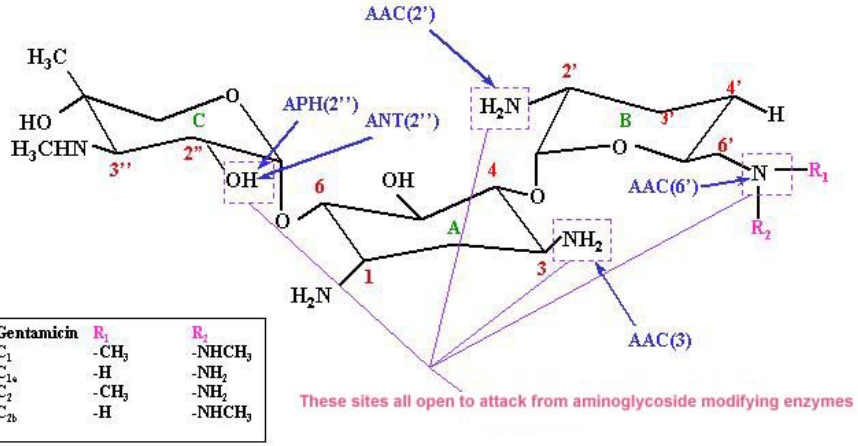
ANT(2”)-I

Amikacin (S)

Gentamicin (R)



Modified from Antimicrob Agents Chemother 1999;43:727-37

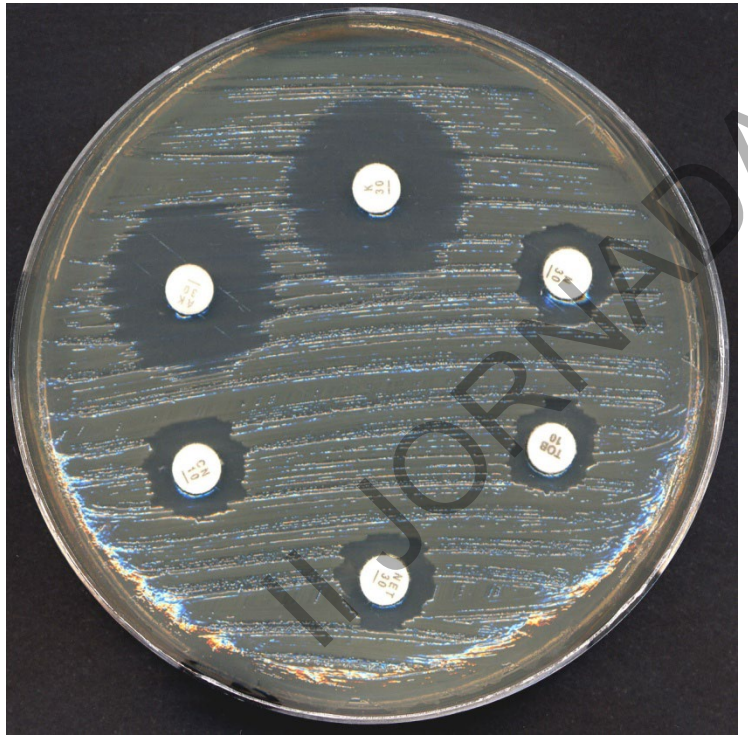


Gentamicin	R_1	R_2
C_1	$-CH_3$	$-NHCH_3$
C_{1a}	-H	$-NH_2$
C_2	$-CH_3$	$-NH_2$
C_{2b}	-H	$-NHCH_3$

Modified from Antimicrob Agents Chemother 1999;43:727-37

Interpretive reading in Enterobacterales: aminoglycosides

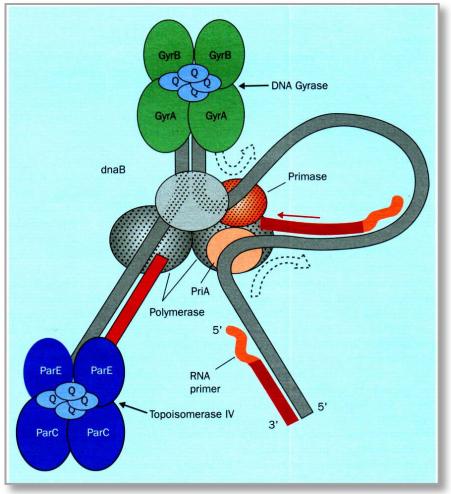
- ***Providencia* stuartiispp.** constitutively expressed the chromosomal aminoglycoside enzyme AAC(2')-Ia
  - this enzyme can be variably expressed
  - mutations can result in over-production of the enzyme
  - do not confer resistance to amikacin (and kanamycin)



Aminoglyc.	MIC (mg/L)	
	Low-level	High-level
GEN	4-8	>8
TOB	4-8	>8
AMK	≤4	≤4

Macinga DR, Rather PN. The chromosomal 2'-N-acetyltransferase of *Providencia stuartii:* physiological functions and genetic regulation. Front Biosci. 1999 Feb 1;4:D132-40.

Interpretive reading in Enterobacterales: fluoroquinolones



	Gene	Relevance/incidence Gram (+)	Relevance/incidence Gram (–)	Expression
Topoisomerase modifications				
- *gyr*A mutations	Cr	+	++++	low / high
- *par*C mutations	Cr	+++/++	+	
- mosaic *gyrA*, *parC* genes	Cr	+	–	
Reduction to target access				
- porin modification	Cr	–	+	low
- efflux system: AcrAB, ...	Cr	++	++	
QepA	Pl	–	+	
Target protection				
- Qnr proteins (QnrA, QnrB, QnrS)	Pl	–	+/–	low
Quinolone modification				
- AAC(6')-Ib-cr	Pl	–	+/–	low

Cattoir V, Nordmann P. Plasmid-mediated quinolone resistance in gram-negative bacterial species: an update. Curr Med Chem. 2009; 16:1028-46; Hooper DC, Jacoby GA. Mechanisms of drug resistance: quinolone resistance. Ann N Y Acad Sci. 2015; 1354:12-31. Hooper DC, Jacoby GA. Topoisomerase Inhibitors: Fluoroquinolone Mechanisms of Action and Resistance. Cold Spring Harb Perspect Med. 2016 Sep 1;6(9):a025320.

Interpretive reading in Enterobacterales: fluoroquinolones

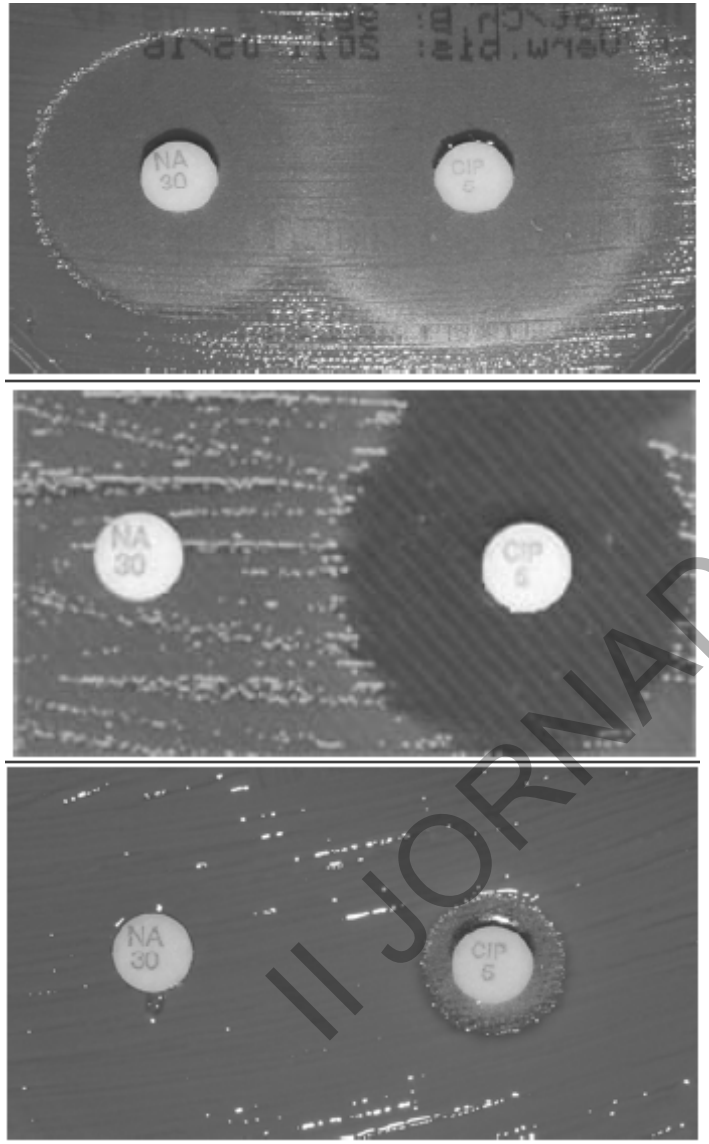
Expression of fluroquinolone resistance mechanisms in *E. coli*

Mutation in:		Efflux	MIC (µg/ml)			
gyrA	*parC*		NAL	CIP	LEV	MOX
-	-	-	2	0.01	0.06	0.06
+	-	-	32-256	0.5	0.5	1
-	+	-	64	0.01	0.03	0.2
+ +	-	-	>1024	1	2	2
+	-	+	32->1024	2	4	4
+ +	+	-	>1024	64	32	32
+ +	+	+	>1024	256	64	128

CIP: ciprofloxacin; LEV: levofloxacin; MOX: moxifloxacin

Modified from Schedletzky et al. J Antimicrob Chemother, 1999 34 (Suppl B):31-7
Saenz et al. J Antimicrob Chemother 2004; 51:1001-5

Interpretive reading in Enterobacterales: fluoroquinolones



NAL^S and CIP^S

↳ Wild type *E. coli*

NAL^R and CIP^S

↳ *E. coli* with a *gyrA* mutation

NAL^R and CIP^R

↳ *E. coli* with a *gyrA* mutation and a *parC* mutation

Procedimientos en Microbiología Clínica nº 38. SEIMC, 2011

Interpretive reading in Enterobacterales: fluoroquinolones

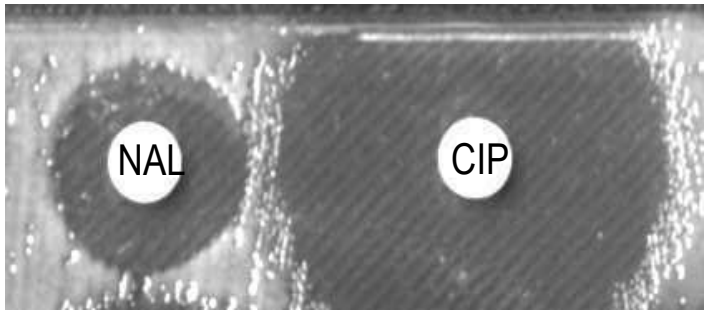
Escherichia coli phenotypes

Low level fluoroquinolone resistance (NAL$^{S/I}$ and CIP$^{S/I}$)

Resistance mechanisms	MIC (mg/L)			
	NAL	CIP	LEV	MOX
Wild type	2-4	0.008-0.02	0.08-1	0.03
QnrA	8-32	0.12-2	0.25-0.5	0.5-1
QnrB	16	0.25-1	0.5	1-2
QnrS	8-32	0.12-0.5	--	0.25
AAC(6')-Ib-cr	--	0.08	0.08	--
QepA	1-2	0.25	0.03-0.06	0.06-0.09

NAL: nalidixic acid; CIP: ciprofloxacin; LEV: levofloxacin; MOX: moxifloxacin

- MICs not always higher than ECOFF (16 mg/L) for nalidixic acid
- MICs for ciprofloxacin higher than ECOFF (0.032 mg/L) but lower than S breakpoint (0.5 mg/L)



www.seimc.org

Robisek et al. Nat Med 2006; 12:83-88
Robicsek et al. Lancet Infect Dis 2006; 6:629-40
Yamane et al. Antimicrob Agents Chemother 2007; 51:3354-60

Interpretive reading in Enterobacterales: fluoroquinolones

EUCAST European Committee on Antimicrobial Susceptibility Testing

About EUCAST | Bacteria | Mycobacteria (AMST) | Fungi (AFST) | VetCAST | Industry | Education

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Pefloxacin screening for fluoroquinolone resistance in Enterobacterales

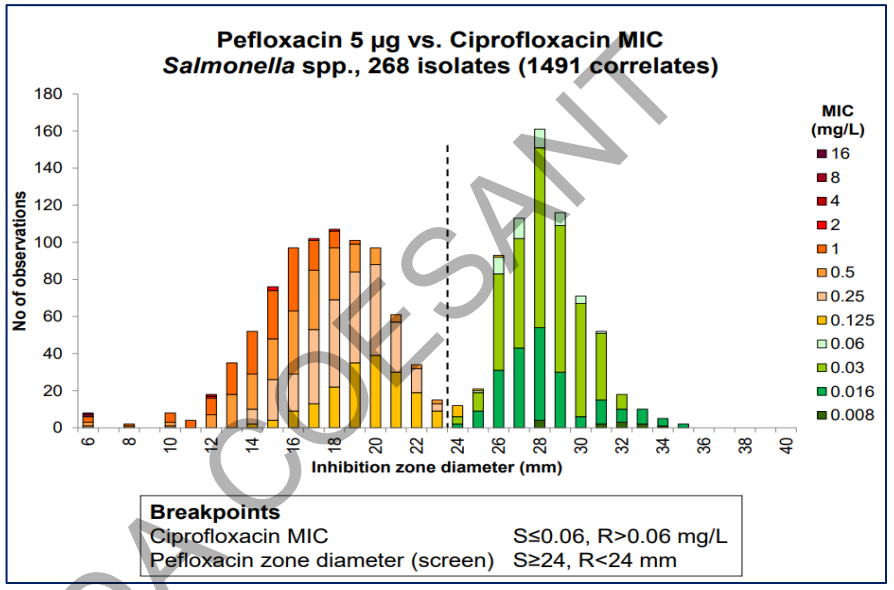
07 October 2025 | Bacteria

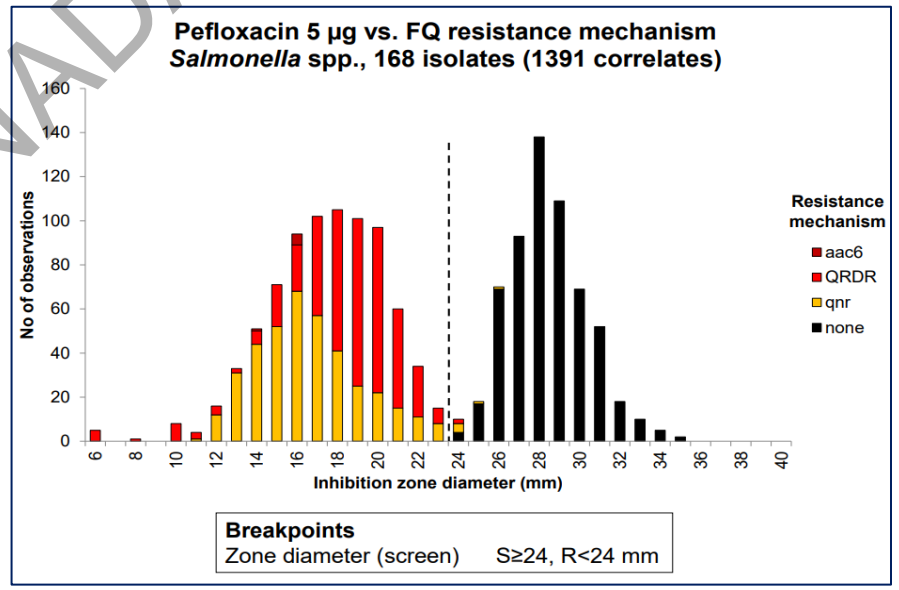
Fluoroquinolone breakpoints are under review. Shortly there will be a public consultation.

Since industry and users sometimes complain that EUCAST fails to warn of upcoming changes we now emphasize that (a) a change is coming, (b) breakpoints will be reduced further and that (c) screening for fluoroquinolone resistance using pefloxacin will be an integral part of proposed changes. We urge laboratories and manufacturers to familiarise themselves with the pefloxacin screen test (already described in the EUCAST breakpoint tables for *Enterobacterales*, *Salmonella enterica* and *Vibrio* spp). Also contact your suppliers of material to ensure that they are ready to meet your requirements.

EUCAST has checked with several major suppliers, and pefloxacin availability is secured for the foreseeable future.

https://www.eucast.org/news-detail/pefloxacin-screening-for-fluoroquinolone-resistance-in-enterobacterales/





https://www.eucast.org/bacteria/development-of-clinical-breakpoints-and-ecoffs/mic-zone-diameter-correlations/

Other Enterobacterales (*coming soon*)

Interpretive reading in Enterobacterales: fluoroquinolones

Mecanismo de resistencia	Sustituciones frecuentes	Tipo de mutación	Efecto molecular	Impacto esperado CMI respecto *E. coli* WT	Patrón característico
Cambio simple en región QRDR	GyrA: Ser83Leu ParC: Ser80Arg	Ganancia de función	Disminuye afinidad de quinolonas por ADN-girasa o ADN-topoisomerasa	Ác. nalidíxico: 4 mg/L → ≥256 mg/L Ciprofloxacino: 0,008 mg/L → 0,25 mg/L	Resistencia a ác. nalidíxico. Elevación CMI de ciprofloxacino y levofloxacino puede ser "I"
Acumulación de cambios en QRDR	Combinación de cambios. ej.: GyrA Ser83Leu + GyrA Asp87Asn + ParC Ser80Arg	Ganancia de función	Reducción de unión a varias dianas: ADN girasa y ADN toposiomerasa	Ác. nalidíxico ≥256 mg/L Ciprofloxacino 0,008 mg/L → 2 mg/L	Resistencia alto nivel a quinolonas
Hiperproducción de AcrAB-TolC	Mutaciones inactivantes en genes reguladores negativos de AcrAB-TolC (*acrR*, *marR*)	Pérdida de función	Expulsión activa de quinolonas del interior celular	Ciprofloxacino 0,008 mg/L → 0,0032 mg/L	Resistencia bajo nivel Resistencia alto nivel al combinar con otros
Inactivación/ disminución expresión porinas	Pérdida de OmpF/OmpC	Pérdida de función	Disminución entrada quinolonas al interior celular	-	Bajo nivel resistencia Resistencia alto nivel al combinar con otros

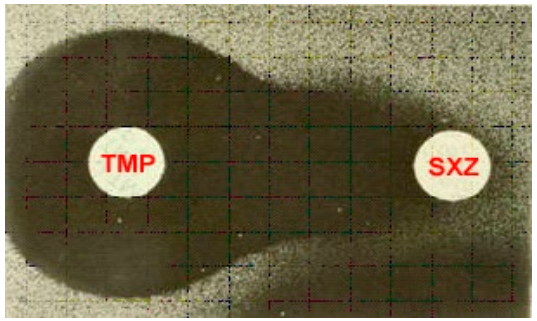
Arca-Suárez J, Cantón R, Larrosa Escartín N, López-Calleja AI, Rivera A. Lectura interpretada del antibiograma de bacilos Gram-negativos Enterobacterales (*in press*)

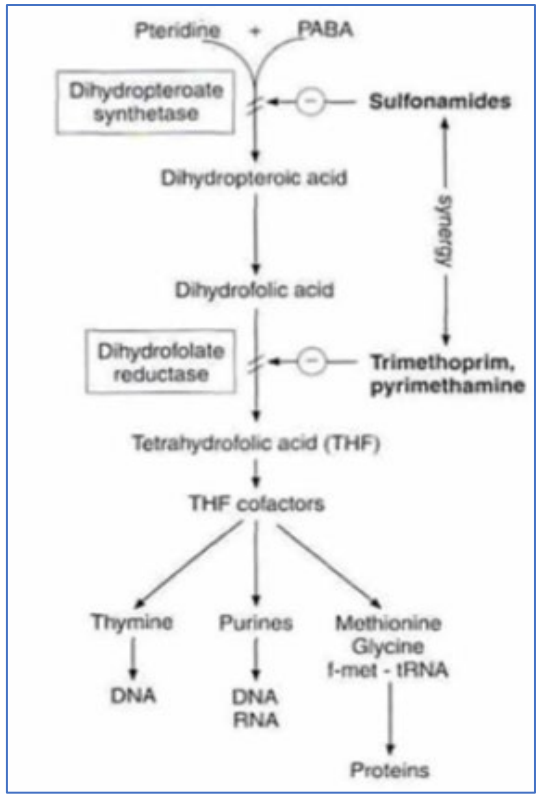
Interpretive reading in Enterobacterales: fluoroquinolones

Mecanismo de resistencia	Sustituciones frecuentes	Tipo de mutación	Efecto molecular	Impacto esperado CMI respecto *E. coli* WT	Patrón característico
Qnr	*qnrA, qnrB, qnrS*	-	Protección de girasa/topoisomerasa	Ác. nalidíxico: 4 mg/L ⟶ 16 mg/L Ciprofloxacino: 0,008 mg/L ⟶ 0,25 mg/L	Resistencia a fluoroquinolonas. Afecta menos a ác. nalidíxico que a fluoroquinolonas. Contribuye a resistencia de alto nivel al combinar con otros mecanismos.
Aac(6')-Ib-cr	*aac(6')-Ib-cr*	-	Acetilación de fluoroquinolas	Ciprofloxacino: 0,008 --> 0,032 mg/L	Resistencia bajo nivel fluoroquinolonas. Contribuye a alto nivel al combinar con otros mecanismos
QepA	*qepA*	-	Expulsión activa de quinolonas del interior celular	Ciprofloxacino: 0,008-⟶0,0032 mg/L	Resistencia bajo nivel fluoroquinolonas. Contribuye a alto nivel al combinar con otros mecanismos
OqxAB	*oqxA*, *oqxB*	-	Expulsión activa de quinolonas del interior celular	-	Resistencia bajo nivel fluoroquinolonas. Contribuye a alto nivel al combina con otros mecanismos
Combinación de PMQR + QRDR	*qnr / aac(6')-Ib-cr* + *gyrA/parC*	-	Sinergia que aumenta resistencia	Ciprofloxacino > 4 mg/L	Resistencia alto nivel quinolonas.

Arca-Suárez J, Cantón R, Larrosa Escartín N, López-Calleja AI, Rivera A. Lectura interpretada del antibiograma de bacilos Gram-negativos Enterobacterales (*in press*)

Interpretive reading in Enterobacterales: trimethoprim-sulfamethoxazole



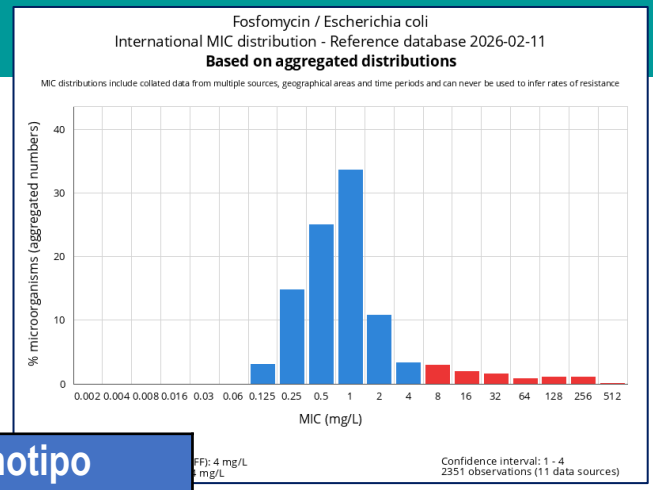


Mecanismo de resistencia	Genes implicados	Efecto molecular	CMI (mg/L)* SMX	TMP	SMX+TMP
—	—	Inhibición de DHPS y DHFR	32–128 (S)	0,25–1 (S)	≤ 2/38 (S)
SMX	Mutaciones *folP* (cromosómico)	DHPS modificada	512–1024 (R)	0,25–1 (S)	2/38–4/76 (R)
	sul1, sul2, sul3 (plasmídico)	DHPS alternativa	≥1024 (R)	0,25–1 (S)	2/38–4/76 (R)
	Hiperproducción de PABA	Competencia con SMX	≥ 512 (R)	0,25–1 (S)	≤ 0,5/9,5–4/76 (S–R)
TMP	Mutaciones *folA* (cromosómico)	DHFR modificada	32–128 (S)	4–8 (R)	≤ 0,5/9,5–4/76 (S–R)
	dfrA y variantes (plasmídico)	DHFR alternativa	32–128 (S)	32–128 (R)	2/38–4/76 (R)
SMX+TMP	*sul* + *dfrA*	Síntesis normal del folato	≥ 1024 (R)	≥ 64 (R)	≥ 8/152 (R)

SMX: sulfametoxazol, TMP: trimetoprim; SMX+TMP: cotrimoxazol;
***Puntos de corte de EUCAST**.
TMP (solo en infección urinaria no complicada para *E. coli* y *Klebsiella* spp., excepto *K. aerogenes*): Sensible ≤ 2mg/L, Resistente >2 mg/L;
SMT+TMP (excepto *Serratia* spp.): ≤0.5 mg/L, sensible >0.5 mg/L. Para *S. marcescens*: ≤0.001 mg/L, sensible >0.5 mg/L.
No existen punto de corte a SMX (ECOFF ≤64 mg/L)

Huovinen P. Increases in rates of resistance to trimethoprim. Clin Infect Dis. 1997 Jan;24 Suppl 1:S63-6. doi: 10.1093/clinids/24.supplement_1.s63.
Then RL. Mechanisms of resistance to trimethoprim, the sulfonamides, and trimethoprim-sulfamethoxazole. Rev Infect Dis. 1982 Mar-Apr;4(2):261-9. doi: 10.1093/clinids/4.2.261.

Interpretive reading in Enterobacterales: fosfomycin



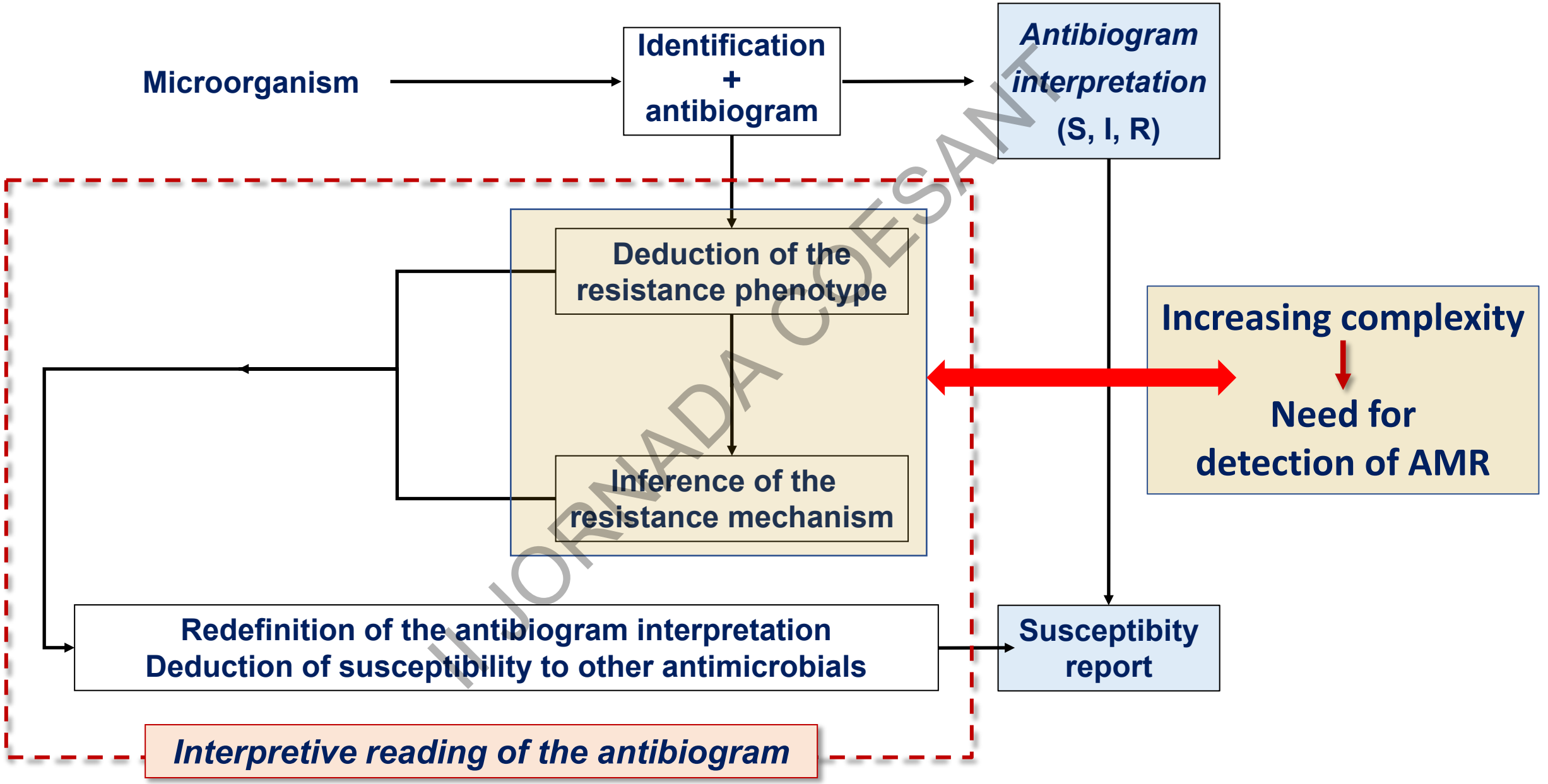
Mecanismos de resistencia adquiridos a fosfomicina y expresión fenotípica

Proceso afectado	Mecanismo de resistencia	Microorganismo	Localización	Fenotipo (CMI fosfomicina)
Wild type	-	*E. coli*	-	0.125 – 4 mg/L
Transporte reducido	Mutaciones en genes *glpT* y/o *uhpT* Mutaciones en genes reguladores de *glpT* y/o *uhpT* Mutaciones en genes *cyaA* y *ptsI* (regulan cAMP necesario para la expresión de *glpT*)	*E. coli*	Crom	64-256 mg/L
Cambios en la diana o en su expresión	Mutaciones en *murA* Incremento de la expresión de *murA*	*E. coli*	Crom	64–512 mg/L
Inactivación	Metaloenzimas (FosA, FosA2-A6, etc): incorporan glutation Fosforil-transferasas (FosC2): incorporan monosfato	Enterobacterales *E. coli*	Pl/Crom Pl/Crom	256–1024 mg/L

[1]Algunas Enterobacterales (*Serratia marcescens, Klebsiella* spp., *Enterobacter* spp, *Kluyvera* spp, etc.) tienen genes cromosómicos homólogos de *fosA* cuya expresión reduce la sensibilidad de fosfomicina (0,5-256 mg/L)

Díez-Aguilar M, Cantón R. New microbiological aspects of fosfomycin. Rev Esp Quimioter. 2019 May;32 Suppl 1(Suppl 1):8-18; Mattioni Marchetti V, Hrabak J, Bitar I. Fosfomycin resistance mechanisms in Enterobacterales: an increasing threat. Front Cell Infect Microbiol. 2023 Jul 4; 13:1178547.

Antibiogram interpretation and interpretive reading



Modified from Cantón R. Enferm Infecc Microbiol Clin 2010; 28:375-85

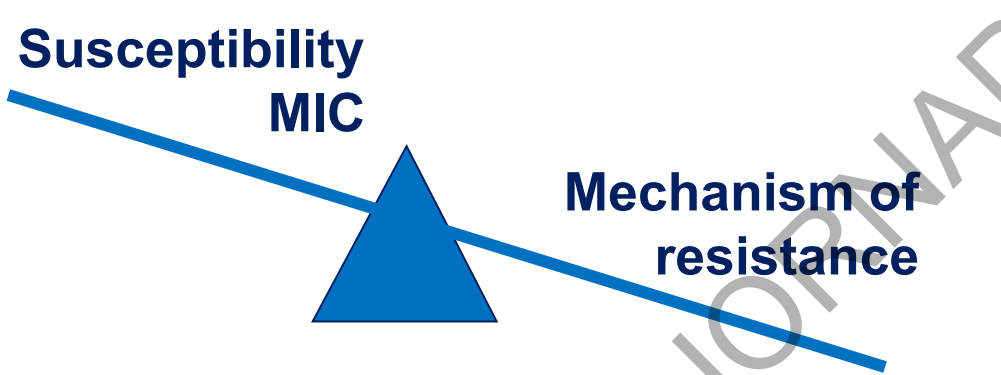
“Antimicrobial Susceptibility Testing” *vs* “Antimicrobial Resistant Testing”

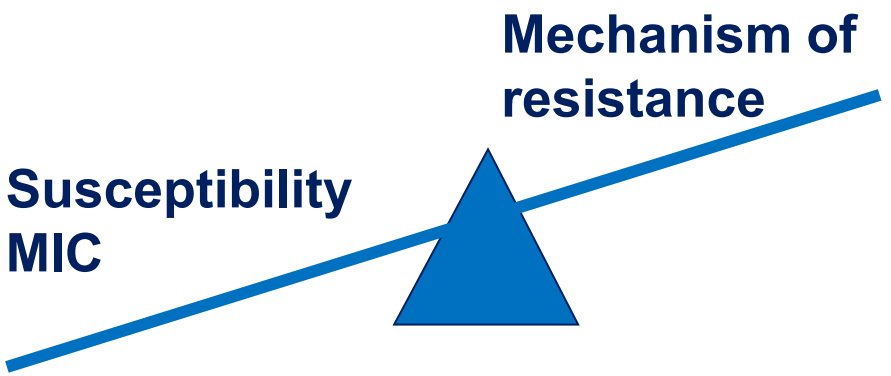
Antimicrobial susceptibility testing

Phenotypic response of a microorganism to the killing or inhibitory effect of an antimicrobial agents (*antibiogram*) to **predict clinical outcome/failure**

Antimicrobial resistance testing

Detection of **antimicrobial resistance mechanism** in a microorganism or directly in a biological sample with a **phenotypic** or a **genotypic** (molecular) **method**





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EUCAST EUROPEAN COMMITTEE ON ANTIMICROBIAL SUSCEPTIBILITY TESTING
European Society of Clinical Microbiology and Infectious Diseases

Artificial intelligence and phenotypes

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0893-8512/11/$12.00 doi:10.1128/CMR.00061-10

Expert Systems in Clinical Microbiology

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Journal of Antimicrobial Chemotherapy (2002) **49**, 289–300

JAC

Multicentre evaluation of the VITEK 2 Advanced Expert System for interpretive reading of antimicrobial resistance tests

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ARTICLE
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AI-based mobile application to fight antibiotic resistance

Marco Pascucci[1,2,3,12], Guilhem Royer[4,5,6,12], Jakub Adamek[7], Mai Al Asmar[8], David Aristizabal[7], Laetitia Blanche[1], Amine Bezzarga[1,9], Guillaume Boniface-Chang[7], Alex Brunner[7], Christian Curel[10], Gabriel Dulac-Arnold[11], Rasheed M. Fakhri[8], Nada Malou[1✉], Clara Nordon[1], Vincent Runge[2], Franck Samson[2], Ellen Sebastian[7], Dena Soukieh[7], Jean-Philippe Vert[11], Christophe Ambroise[2,13✉] & Mohammed-Amin Madoui[5,13✉]

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Original article

Antilogic, a new supervised machine learning software for the automatic interpretation of antibiotic susceptibility testing in clinical microbiology: proof-of-concept on three frequently isolated bacterial species

Andriamiharimamy Rajaonison [1, 2], Stéphanie Le Page [1, 3], Thomas Maurin [1, 3], Hervé Chaudet [1, 3], Didier Raoult [1, 3], Sophie Alexandra Baron [1, 3, *], Jean-Marc Rolain [1, 3]

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

Artificial intelligence in bacterial diagnostics and antimicrobial susceptibility testing: Current advances and future prospects

Seungmin Lee [a,b,1], Jeong Soo Park [a,c,1], Ji Hye Hong [a,b], Hyowon Woo [a], Chang-hyun Lee [d], Ju Hwan Yoon [a,d], Ki-Baek Lee [d], Seok Chung [c,2,***], Dae Sung Yoon [b,e,f,2,**], Jeong Hoon Lee [a,g,2,*]

AMERICAN SOCIETY FOR MICROBIOLOGY | Antimicrobial Agents and Chemotherapy
October 2024 Volume 68 Issue 10
| Antimicrobial Chemotherapy | Full-Length Text

Retrospective validation study of a machine learning-based software for empirical and organism-targeted antibiotic therapy selection

Maria Isabel Tejeda,[1] Javier Fernández,[2,3,4,5] Pablo Valledor,[2] Cristina Almirall,[6] José Barberán,[1,7] Santiago Romero-Brufau[2,8,9]

AMERICAN SOCIETY FOR MICROBIOLOGY | mBio
February 2026 Volume 17 Issue 2
| Computational Biology | Research Article

Confidence-based prediction of antibiotic resistance at the patient level

Juan S. Inda-Díaz,[1,2,3] Anna Johnning,[1,2,4] Magnus Hessel,[2,5] Anders Sjöberg,[4,6] Anna Lokrantz,[4] Lisa Helldal,[5] Mats Jirstrand,[4,6] Lennart Svensson,[6] Erik Kristiansson[1,2]

Lectura interpretada del antibiograma de bacilos Gram-negativos Enterobacterales

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II Jornada del Comité Español del Antibiograma (CoEsAnt)

Madrid, 12 de febrero de 2026