



Better Training for Safer Food *Initiative*

Antimicrobial Resistance One Health approach

**BREAKPOINT-CUT OFF VALUES:
DECISIONS TAKEN UPON THE
RESULTS**

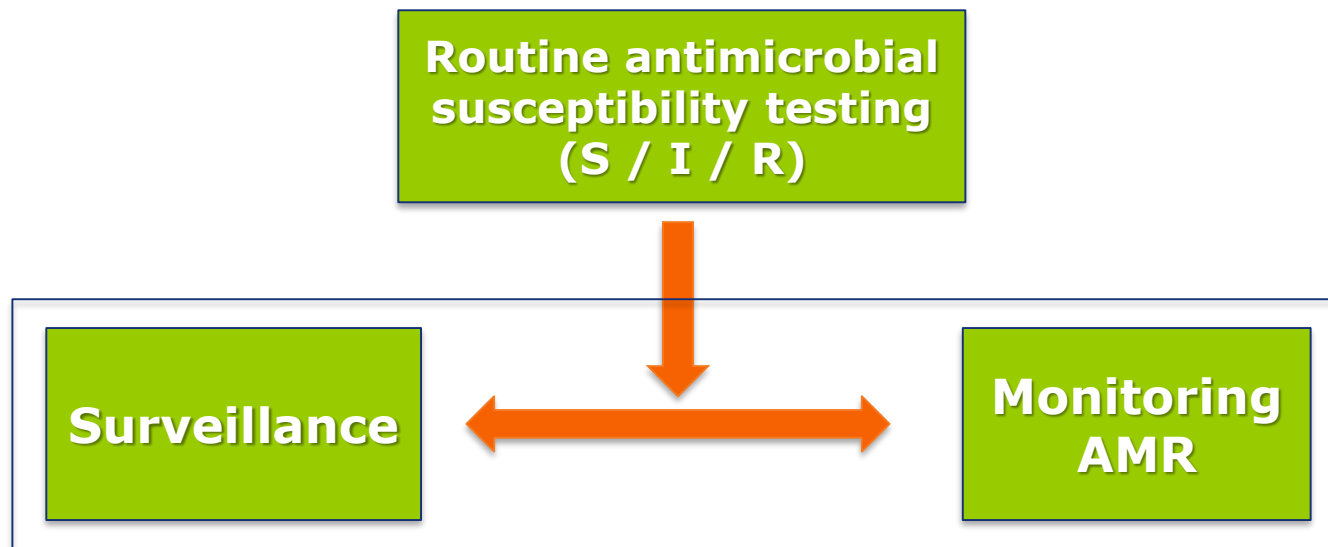
BTSEF

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Food safety

Malaga, Spain – 25-28 November 2019



Do we need MIC values in surveillance programs for Public Health?

**THE ROLE OF THE MIC VALUE:
Not just a number!**

INTERNATIONAL
STANDARD

ISO
20776-1

First edition
2006-11-15

Clinical laboratory testing and *in vitro*
diagnostic test systems — Susceptibility
testing of infectious agents and
evaluation of performance of
antimicrobial susceptibility test
devices —

Part 1:
Reference method for testing the *in vitro*
activity of antimicrobial agents against
rapidly growing aerobic bacteria involved
in infectious diseases

MIC

- Microbiological data based in **MIC** values
- PK/PD analysis using **MIC** values as PD
- Clinical outcome correlation with **MIC** values

Clinical categories and ECOFFs

Setting MIC clinical breakpoints and ECOFFs

MIC distribution data

- **Methodology**. different processes using a variety of methods
- **Source**. Databases fed by a wide variety of sources
 - Breakpoint committees
 - Individual researchers, human (mainly) and veterinary medicine
 - Surveillance AMR programs programmes in humans and animals
 - EUCAST development projects
 - Food safety projects (EFSA)
 - Environmental studies

ECOFF: the highest MIC for organisms devoid of phenotypically detectable acquired resistance mechanisms.

It defines the upper end of the wild-type MIC distribution for a given microbial species and antimicrobial agent.

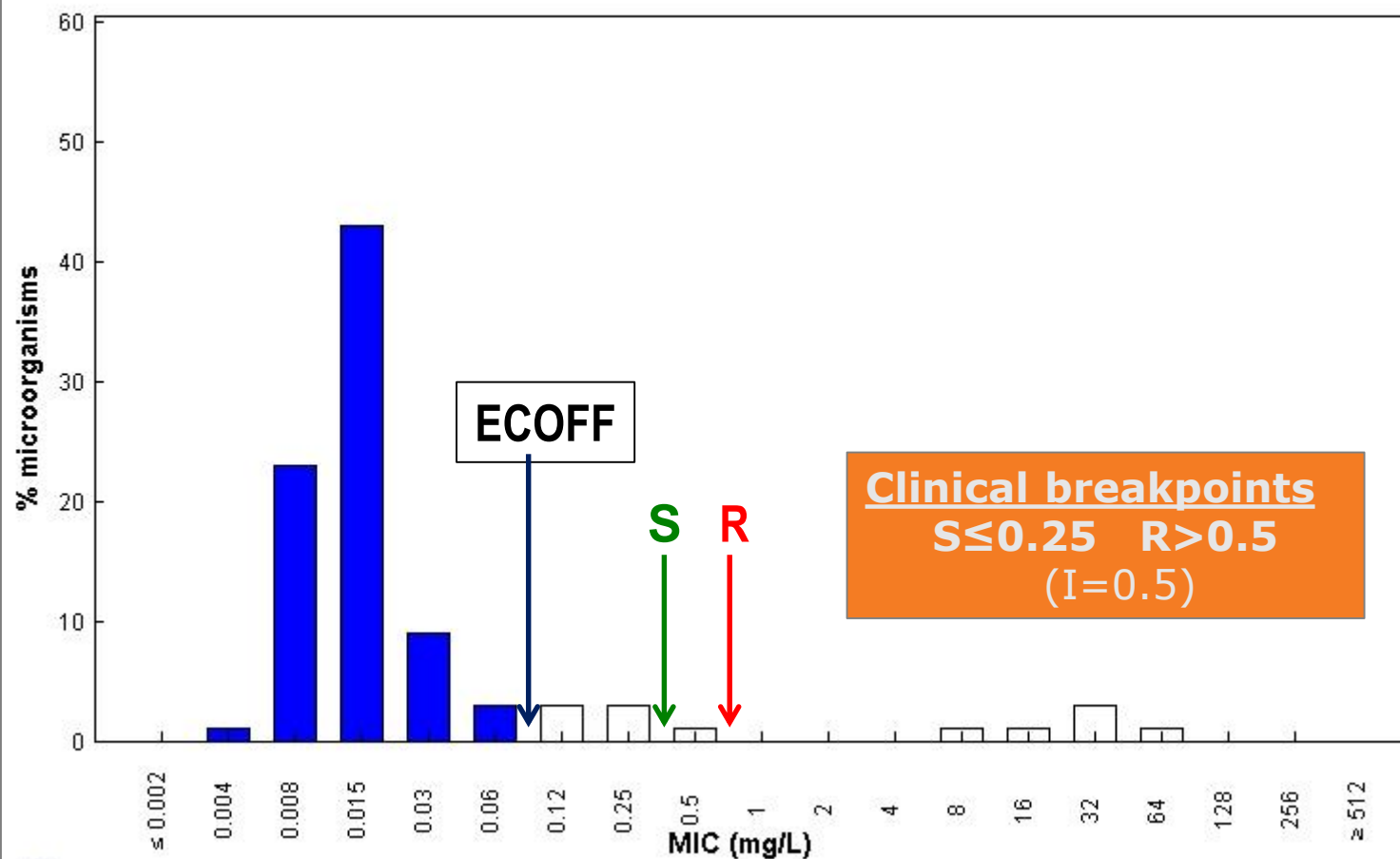
It allows comparing rates of acquired resistance when clinical breakpoints differ (e.g. between organisations, between humans and animals), change over time or have not been set



Ciprofloxacin / Escherichia coli

International MIC Distribution - Reference Database 2018-02-17

MIC distributions include collated data from multiple sources, geographical areas and time periods and can never be used to infer rates of resistance



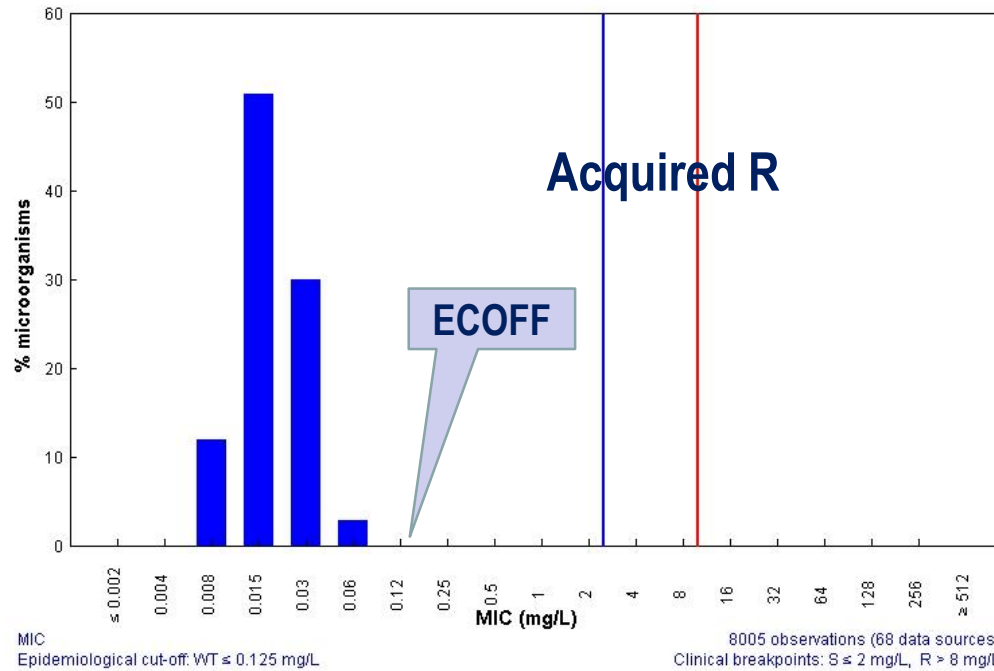
MIC
Epidemiological cut-off (ECOFF): 0.064 mg/L
Wildtype (WT) organisms: ≤ 0.064 mg/L

16702 observations (55 data sources)

EUCAST, ECOFFs and intrinsic resistance

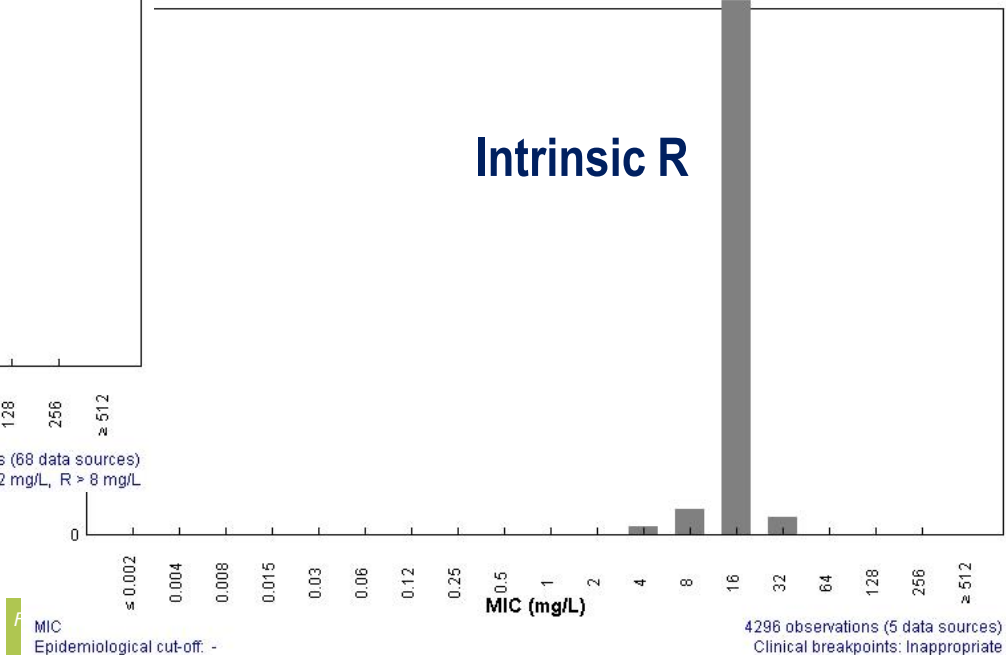
Meropenem / *Escherichia coli*
EUCAST MIC Distribution - Reference Database 2013-03-17

MIC distributions include collated data from multiple sources, geographical areas and time periods and can never be used to infer rates of resistance



Meropenem / *Stenotrophomonas maltophilia*
EUCAST MIC Distribution - Reference Database 2013-03-17

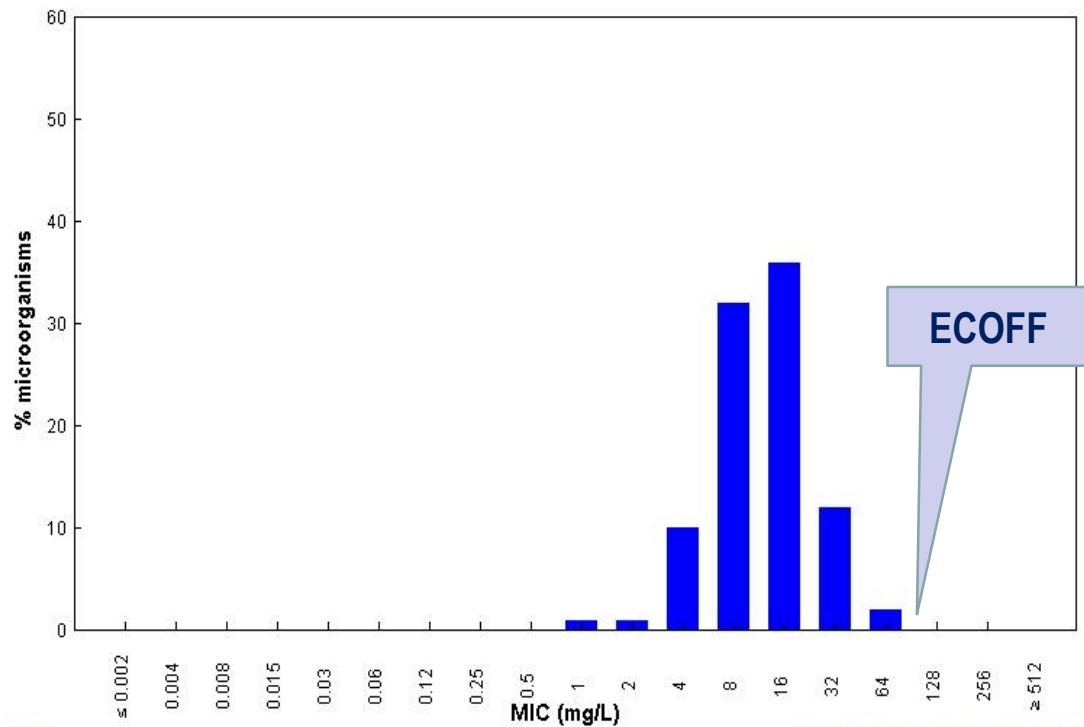
include collated data from multiple sources, geographical areas and time periods and can never be used to infer rates of resistance



EUCAST, ECOFFs and intrinsic resistance

Tigecycline / *Pseudomonas aeruginosa*
EUCAST MIC Distribution - Reference Database 2012-03-03

MIC distributions include collated data from multiple sources, geographical areas and time periods and can never be used to infer rates of resistance



MIC
Epidemiological cut-off: WT ≤ 64 mg/L

1120 observations (8 data sources)
Clinical breakpoints: Inappropriate

Food safety

MIC distributions

Organization

EUCAST News

Clinical breakpoints

Expert rules

Resistance mechanisms

MIC distributions ECOFFs

Zone distributions ECOFFs

AST of bacteria

AST of fungi

AST of veterinary pathogens

Frequently Asked Questions (FAQ)

Meetings

EUCAST Presentations

Documents

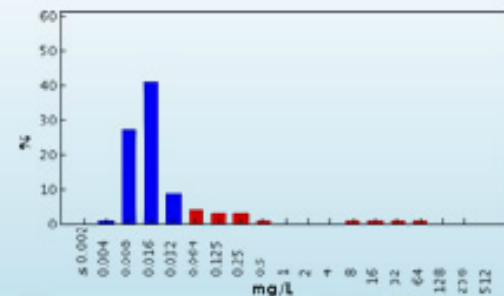
Translations

Information for industry

Links

Contacts

Ciprofloxacin/*Escherichia coli*
Antimicrobial wild type distributions
of microorganisms – references
database EUCAST



MIC distributions and ECOFFs

🔗 [Link to the website with MIC distributions and ECOFFs](#)

The website gives MIC distributions (and since 2010 inhibition zone diameter distributions generated with the new EUCAST disk diffusion method) for a wide range of organisms and antimicrobial agents, including antifungals.

The distributions are based on collated data from a total of more than 24000 MIC distributions from worldwide sources. The distributions include MICs from national and international studies such as resistance surveillance programs (Alexander, BSAC, ECO-SENS, MYSTIC, NORM and SENTRY), as well as MIC distributions from published articles, the pharmaceutical industry, veterinary programmes and individual laboratories. Histograms display wild type organisms, together with EUCAST clinical breakpoints and epidemiological cut-off values (ECOFFs). The distributions should **never be referred to in any epidemiological context** since data from many time periods and many countries have been aggregated.

Contributions of MIC and/or Zone diameter distributions can be made using the following Excel file templates:

- MIC distributions organised by agent or species
- Zone diameter distributions organised by agent or species

Please send the completed file to Erika.Matuschek@ltkronoberg.se



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MIC distributions and ECOFFs



Optimized for Explorer 8 or higher
You're using Explorer 7

Number of visitors since May 1
EUCAST

Antimicrobial wild type distributions of microorganisms

- [Search database](#)

MIC- and Inhibition zone diameter distributions of microorganisms without and with resistance mechanisms

MIC distributions

The website gives MIC distributions for individual organisms and antimicrobial agents in tables and histograms. The distributions are based on collated data from an increasing total of more than 20000 MIC distributions from worldwide sources. Unless otherwise specifically stated, the data are representative of results obtained with a variety of MIC methods. Different methods do not give exactly the same results but the results rarely vary by more than one doubling dilution step. In this way the aggregated MIC distributions encompass the variation between different investigators and between different methods.

Inhibition zone diameter distributions

The website gives inhibition zone diameter distributions for individual organisms and antimicrobial agents in tables and histograms. The distributions are based on collated data from an increasing number of sources worldwide. The data are representative of results obtained

<http://www.eucast.org>

Distribución de CMLs y ECOFFs



EUCAST

EUROPEAN COMMITTEE
ON ANTIMICROBIAL
SUSCEPTIBILITY TESTING

European Society of Clinical Microbiology and Infectious Diseases

Antimicrobial wild type distributions of microorganisms

Search

Method: ☒ MIC ☐ Disk diffusion

Antimicrobial:

Species:

Species: **Pseudomonas aeruginosa** (Method: **MIC**)

MIC distributions include collated data from multiple sources, geographical areas and time periods and can never be used to infer resistance

	0.002	0.004	0.008	0.016	0.032	0.064	0.125	0.25	0.5	1	2	4	8	16	32	64	128	256	512	ECOFF
Amikacin	0	0	0	0	0	0	0	93	369	963	5440	6280	2974	997	104	152	19	5	0	16.0
Ampicillin-sulbactam (ratio)	0	0	0	0	0	0	0	1	21	3	5	7	16	24	80	3468	0	0	0	ND
Aztreonam	0	0	0	0	1	2	6	8	62	87	510	1244	509	430	229	61	41	1	0	16.0
Cefepime	0	0	0	1	1	1	99	152	793	3787	10519	7295	6110	4438	3779	113	38	12	0	8.0
Cefotaxime	0	0	0	0	2	3	2	2	10	13	21	93	412	419	274	155	79	14	0	32.0
Cefpirome	0	0	0	0	0	0	0	1	9	135	262	154	77	38	16	6	6	0	0	ND
Cefpodoxime	0	0	0	0	0	0	8	0	3	1	0	0	1	2	2	7	414	0	0	ND
Ceftazidime	0	0	0	1	4	8	31	292	966	5975	12322	6271	2738	1712	815	751	167	117	106	8.0
Ceftobiprole	0	0	0	1	4	11	11	67	446	2209	2134	1437	1373	1435	98	168	0	0	0	ND
Ceftriaxone	0	0	0	0	0	0	0	79	135	239	374	868	2008	2961	4489	21738	9	11	0	ND
Ciprofloxacin	0	0	19	42	535	3046	9340	4559	3234	1882	1501	876	928	516	499	720	137	28	105	0.5
Clinafloxacin	0	0	0	0	12	36	147	336	165	104	51	36	27	0	0	0	0	0	104	ND
Colistin	0	0	0	0	1	5	18	100	913	1818	1146	112	25	45	6	1	12	0	6	4.0
Doripenem	0	0	0	9	80	587	1667	2194	2196	1439	795	878	662	596	45	7	0	0	0	1.0
Ertapenem	0	0	1	2	2	1	21	21	72	178	304	319	286	267	208	218	104	0	105	ND

<http://www.eucast.org>

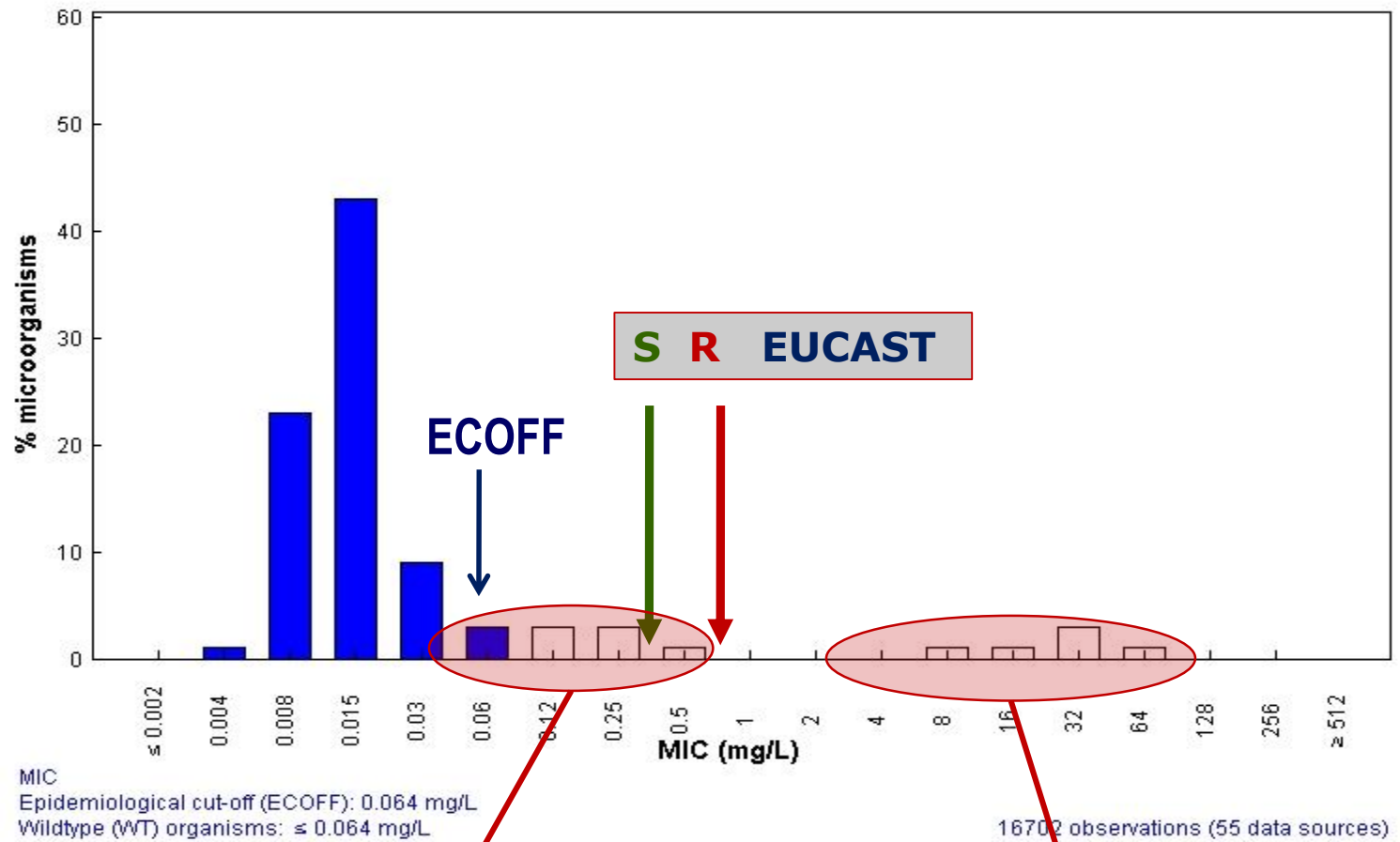
Do we need MIC values in surveillance programs for Public Health?

THE ROLE OF THE MIC VALUE: Not just a number!

- More information can be obtained with MICs than when only use clinical breakpoints
- Breakpoints can be modified by different committees over time (resistance rates can be reinterpreted when MICs are available)
- MICs explain differences between different breakpoints
- Clinical breakpoints might be ineffective to detect resistance mechanisms and MICs are useful for this purpose
- MICs can simplify complex resistance mechanisms
- MICs are relevant when using molecular methods for surveillance

Ciprofloxacin / Escherichia coli
International MIC Distribution - Reference Database 2018-02-17

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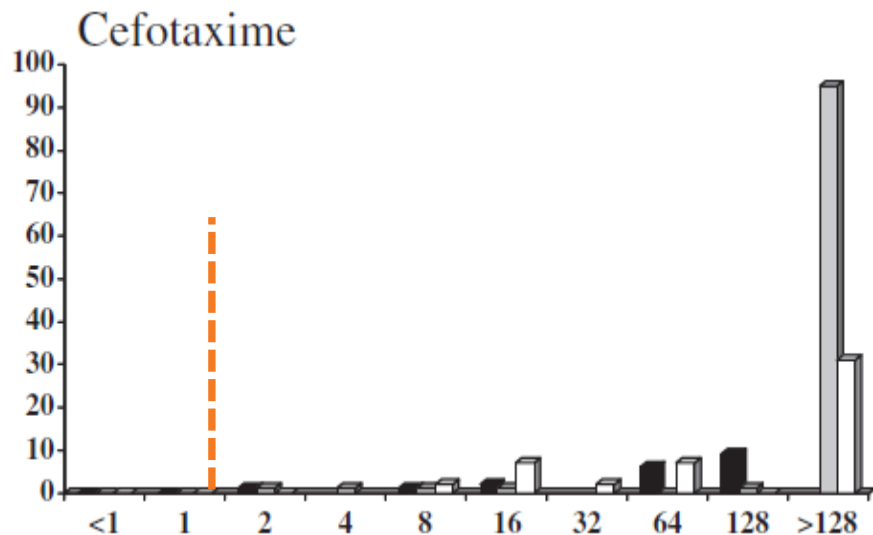
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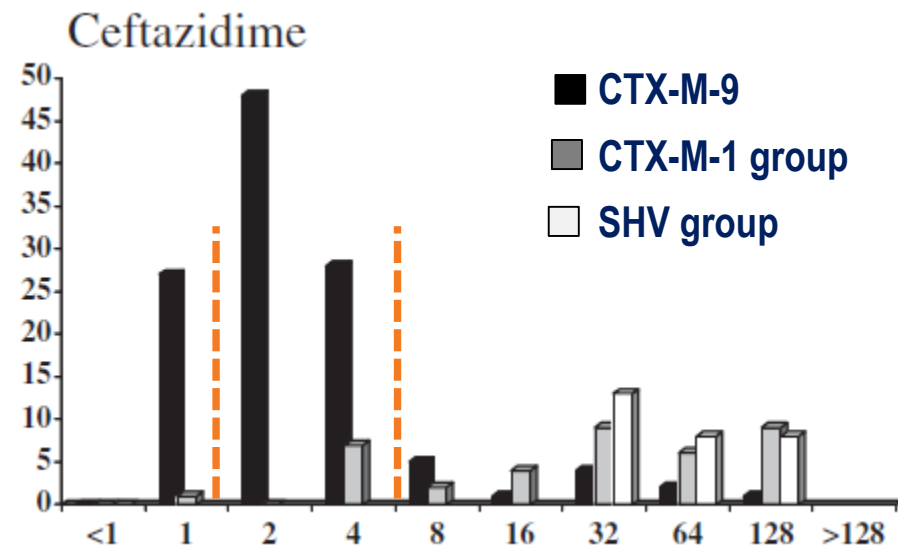
Cephalosporin breakpoints and Enterobacteriaceae

- Impact of CLSI & EUCAST breakpoints in ESBL-*E. coli* blood isolates



S-EUCAST
S-CLSI
0%

MIC (mg/L)



S-EUCAST
14.7%

S-CLSI
35.1%

MIC (mg/L)

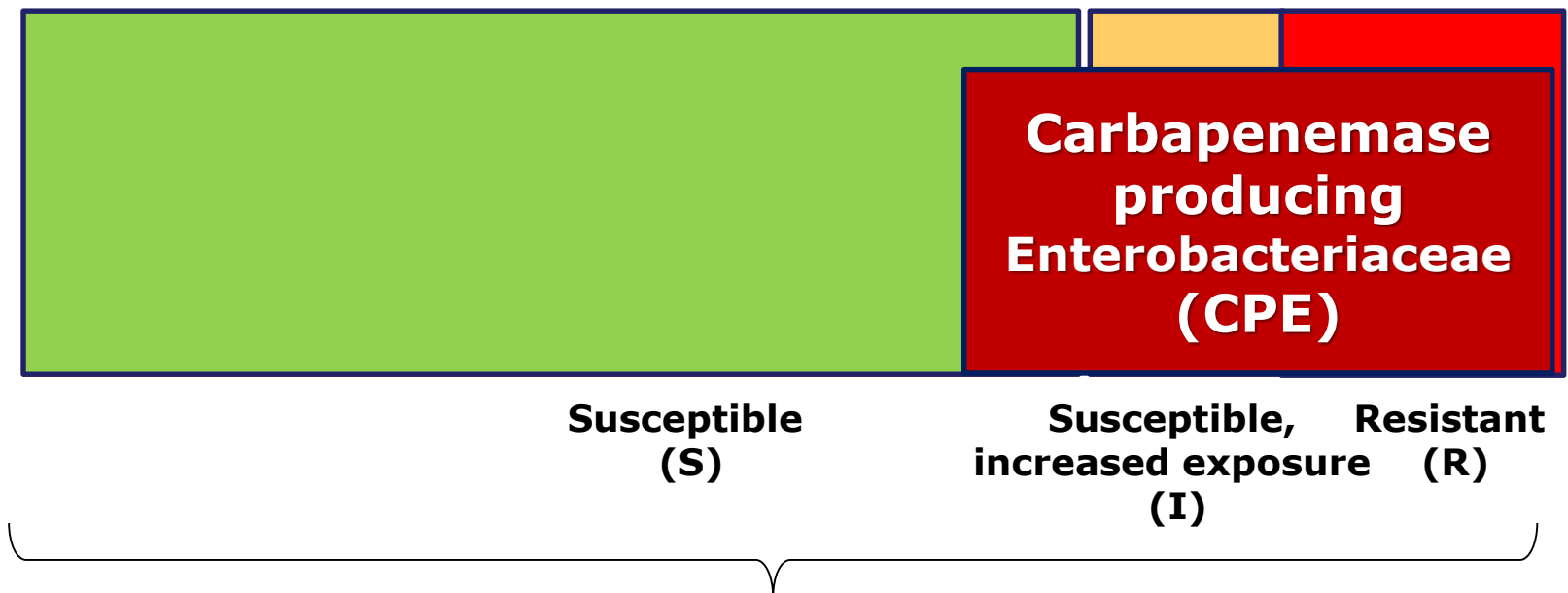
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Clinical breakpoints and detection of resistance

- Most carbapenemase producing Enterobacteriaceae are considered resistant (R) to carbapenems but can be also susceptible (S) or intermediate (I)



Clinical response to carbapenems



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Guidelines for detection of resistance mechanisms and specific resistances of clinical and/or epidemiological importance



Clinical breakpoints and screening cut-off values for carbapenemase-producing Enterobacteriaceae

Carbapenem	MIC (mg/L)		Disk diffusion zone diameter (mm)	
	S/I breakpoint	Screening cut-off	S/I breakpoint	Screening cut-off
Meropenem ¹	≤2	>0.125	≥22	<25 ²
Imipenem	≤2	>1	≥22	<23
Ertapenem ³	≤0.5	>0.125	≥25	<25

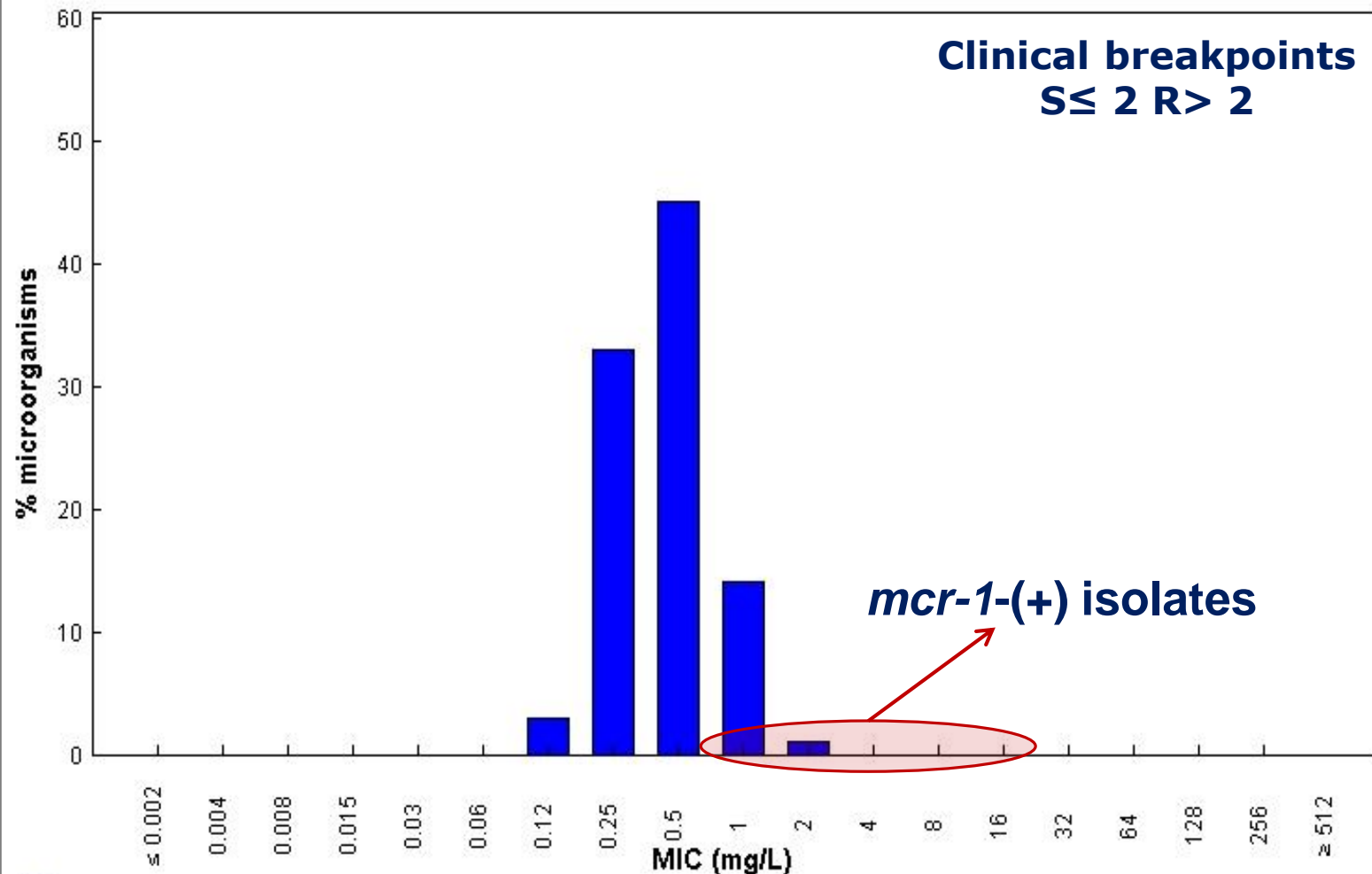
¹Best balance of sensitivity and specificity.

²In rare cases OXA-48-producers have zone diameters of 24-26 mm, so 27 mm may be used as a screening cut-off during outbreaks, but with significant reduction in specificity.

³High sensitivity, but low specificity and therefore not recommended.

Colistin / Escherichia coli
International MIC Distribution - Reference Database 2016-06-17

MIC distributions include collated data from multiple sources, geographical areas and time periods and can never be used to infer rates of resistance



MIC

Epidemiological cut-off (ECOFF): 2 mg/L

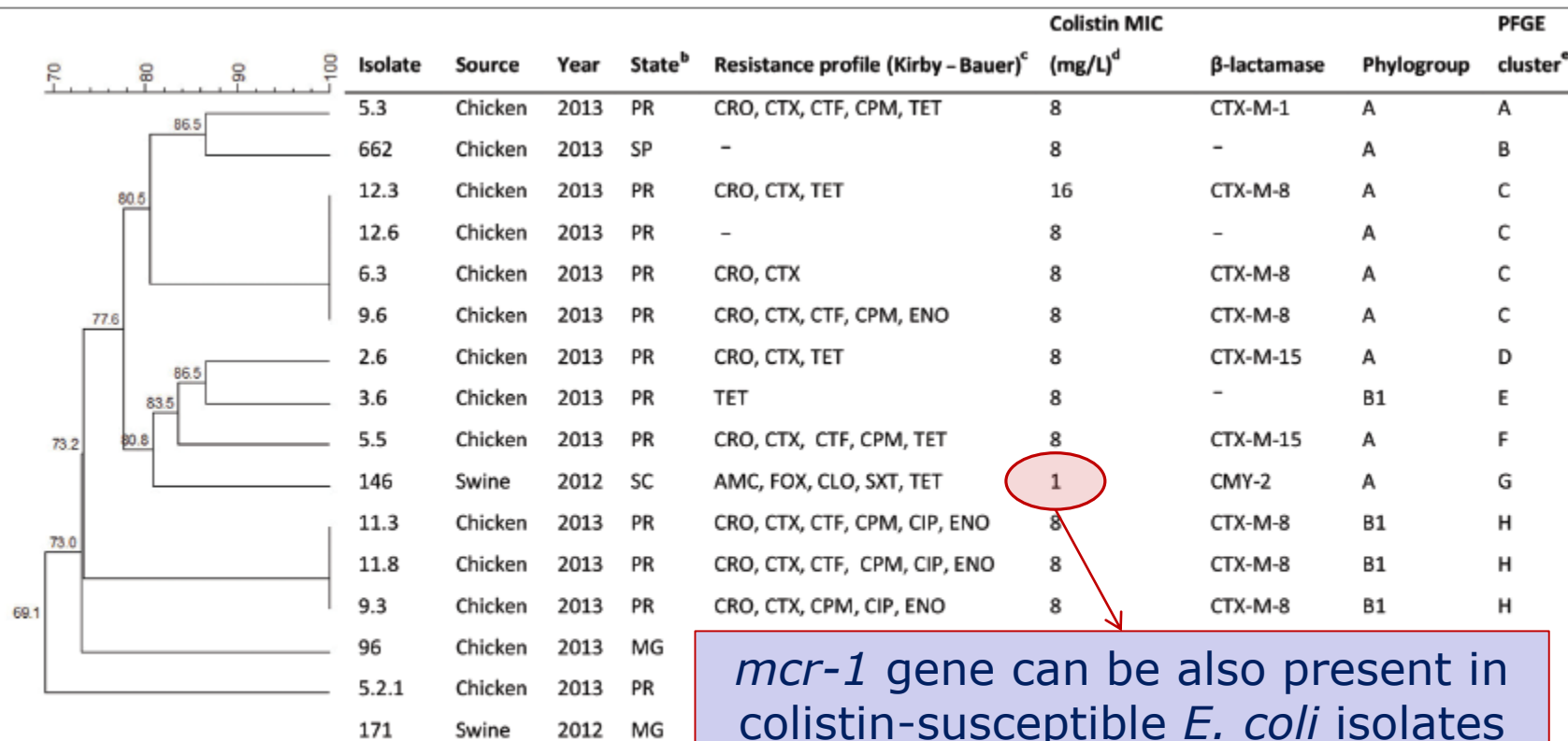
Wildtype (WT) organisms: ≤ 2 mg/L

6090 observations (15 data sources)

Silent dissemination of colistin-resistant *Escherichia coli* in South America could contribute to the global spread of the *mcr-1* gene

Eurosurveillance; 28 April 2016

MR Fernandes¹, Q Moura², L Sartori¹, KC Silva³, MP Cunha³, F Esposito¹, R Lopes², LK Otutumi⁴, DD Gonçalves⁴, M Dropa⁵, MH Matté⁵, DF Monte⁶, M Landgraf⁶, GR Francisco⁷, MF Bueno⁷, D de Oliveira Garcia⁷, T Knöbl³, AM Moreno³, N Lincopan¹

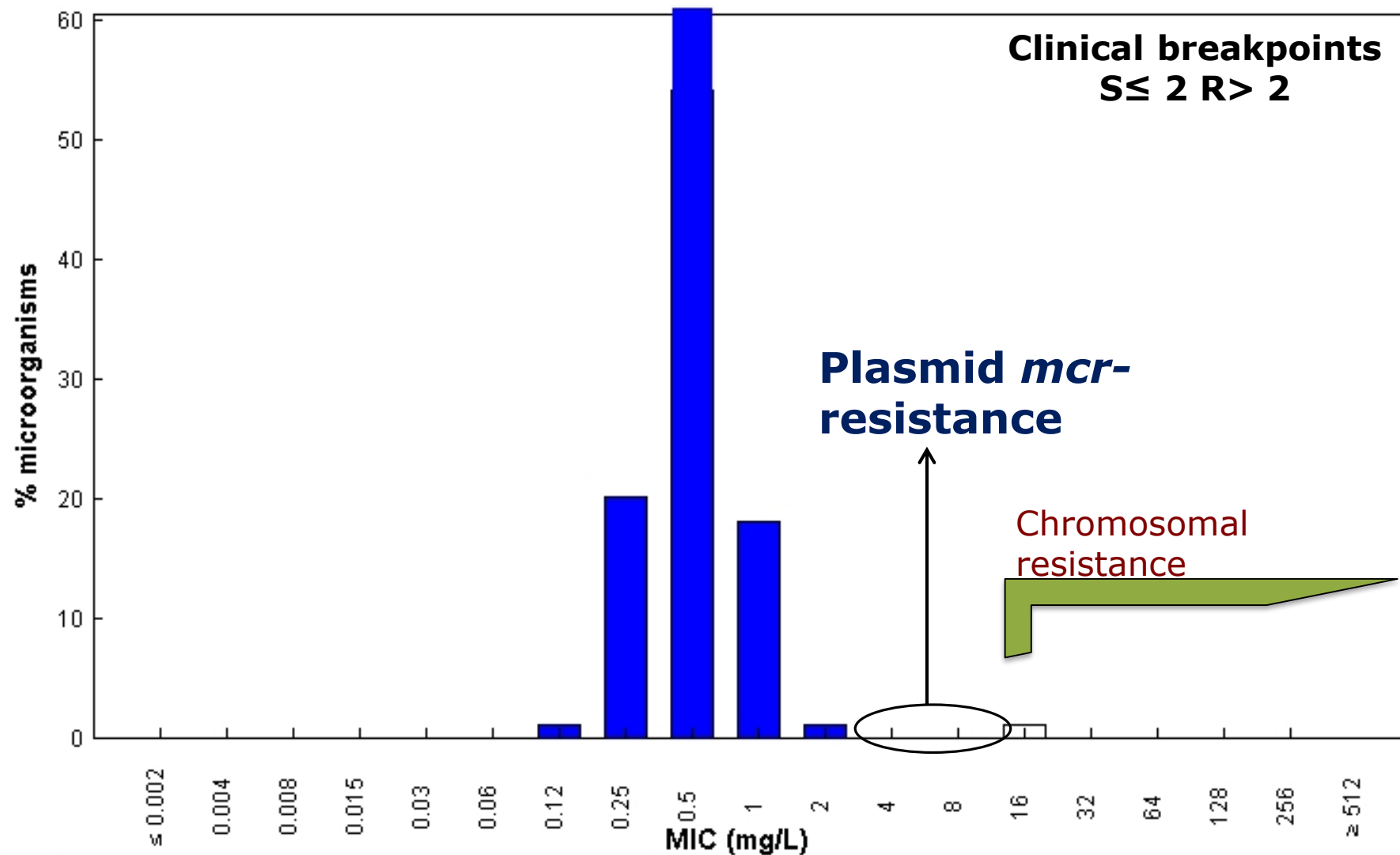


MIC: minimum inhibitory concentration; nt: non typeable by PFGE.

GenBank accession number for *mcr-1* genes identified in this study: KU750813, KU928239–42, KU935441–9, KX01152–1.

Colistin / *Klebsiella pneumoniae*
International MIC Distribution - Reference Database 2017-12-10

MIC distributions include collated data from multiple sources, geographical areas and time periods and can never be used to infer rates of resistance



MIC

Epidemiological cut-off (ECOFF): 2 mg/L

Wildtype (WT) organisms: ≤ 2 mg/L

2237 observations (10 data sources)



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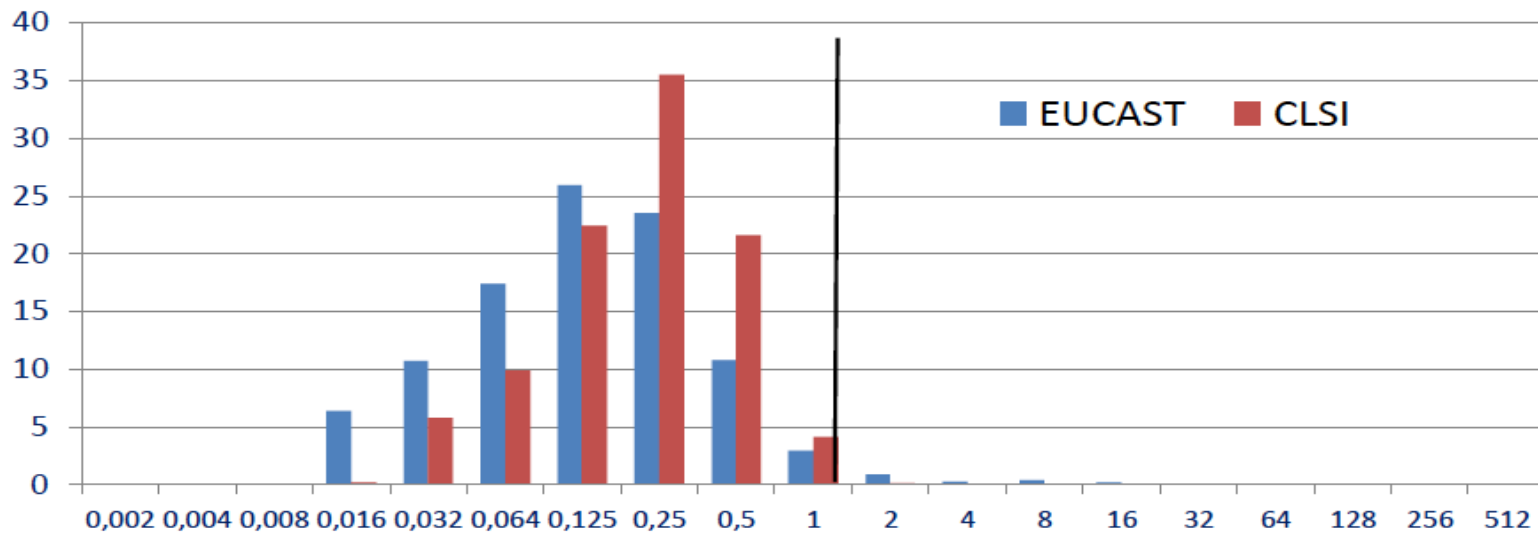
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Neisseria gonorrhoeae and azithromycin

CLSI and EUCAST data base



Criteria	Breakpoint			ECV - ECOFF	
	CLSI	EUCAST		CLSI	EUCAST
S	-	≤ 0.25			
I	-	0.5			
R	-*	> 0.5		≤1	≤1

* NWT: 2 mg/L

Food safety

Kirkcaldy *et al.* Antimicrob Agents Chemother 2015; 59: 998-1003
 CLSI M100-S27
www.eucast.org



***Neisseria gonorrhoeae* and azithromycin**

Resistance mechanisms

- Different levels of resistance caused by different resistance mechanisms

High level resistance (MICs ≥ 256 mg/L)

- 23S rRNA gene mutations (A2059G) (3 or 4 of the 4 alleles)

Low to moderate level (MICs 2-32 mg/L)

- 23S rRNA gene mutations (C2611T) (3 or 4 of the 4 alleles)
- 23S rRNA methylases (*ermA*, *ermB*, *ermC*, and *ermF*)
- Efflux pumps:
 - MtrCDE overexpression (35A deletion in the promoter of *mtrR* repressor)
 - MtrR A39T and G45D mutations
 - MacAB
 - *mef*
- mutations in the ribosomal genes: *rplD*, *rplV*

- Presence of different resistance mechanisms

Chisholm *et al.* AAC. 2010; 54: 3812-6
Demczuk *et al.* JCM. 2016; 54: 1304-13
Kirkcaldy *et al.* AAC 2015; 59: 998-1003



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Review

The role of whole genome sequencing in antimicrobial susceptibility testing of bacteria: report from the EUCAST Subcommittee

M.J. Ellington^{1,†}, O. Ekelund^{2,†}, F.M. Aarestrup³, R. Canton⁴, M. Doumith¹, C. Giske⁵, H. Grundman⁶, H. Hasman⁷, M.T.G. Holden⁸, K.L. Hopkins¹, J. Iredell⁹, G. Kahlmeter², C.U. Köser¹⁰, A. MacGowan¹¹, D. Mevius^{12,13}, M. Mulvey¹⁴, T. Naas¹⁵, T. Peto¹⁶, J.-M. Rolain¹⁷, Ø. Samuelsen¹⁸, N. Woodford^{1,*}

...**the MIC**... reflects more than gene presence / absence; ... multiple and complex interplays between different systems including cellular permeability, influx/efflux, target availability and binding as well as enzymatic expression levels and activities.

... the primary AST comparator for WGS-based prediction should be the **ECOFF**, wherever possible, in order to assess WGS-inferred 'antibiograms' (based on gene positivity) against phenotypically-defined categories of wild-type or non-wild-type.



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