SITA

11° CONGRESSO NAZIONALE

FIRENZE | 3 dicembre 2021

Epidemiologia dei germi MDR e stewardship diagnostica in era COVID-19

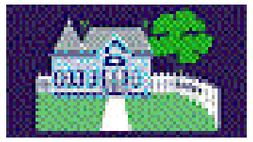
Tommaso Giani

Dip. Medicina Sperimentale e Clinica
Università di Firenze

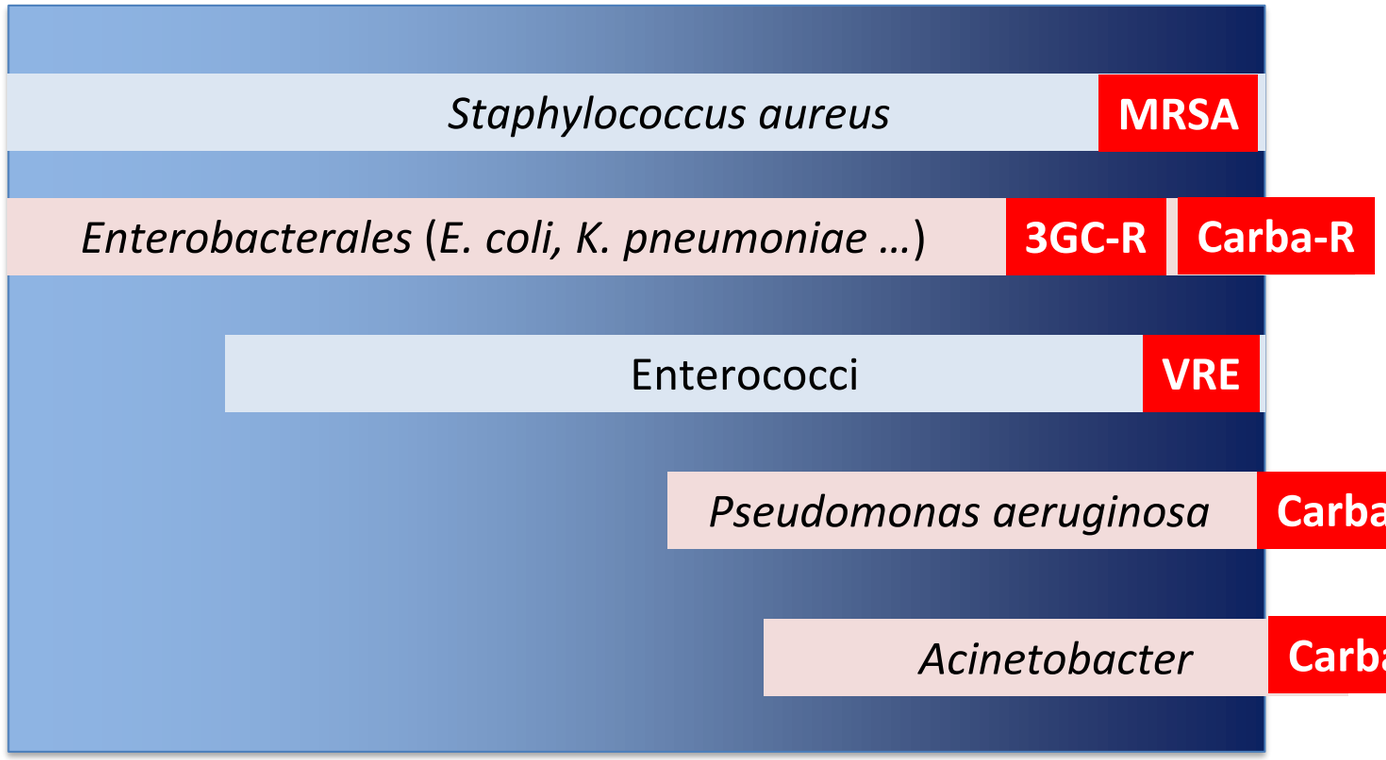
SODc Microbiologia e Virologia
A.O.U. Careggi, Firenze

Dichiarazione su potenziali conflitti di interesse
Consulenze, partecipazione *advisory boards*, *speaker's bureau*, contratti/contributi di ricerca e di eventi studio: Accelerate Diagnostics, Alifax, Becton Dickinson, Biomerieux, Thermofischer Scientific, Venetorx

I patogeni multiresistenti più frequenti nella pratica clinica



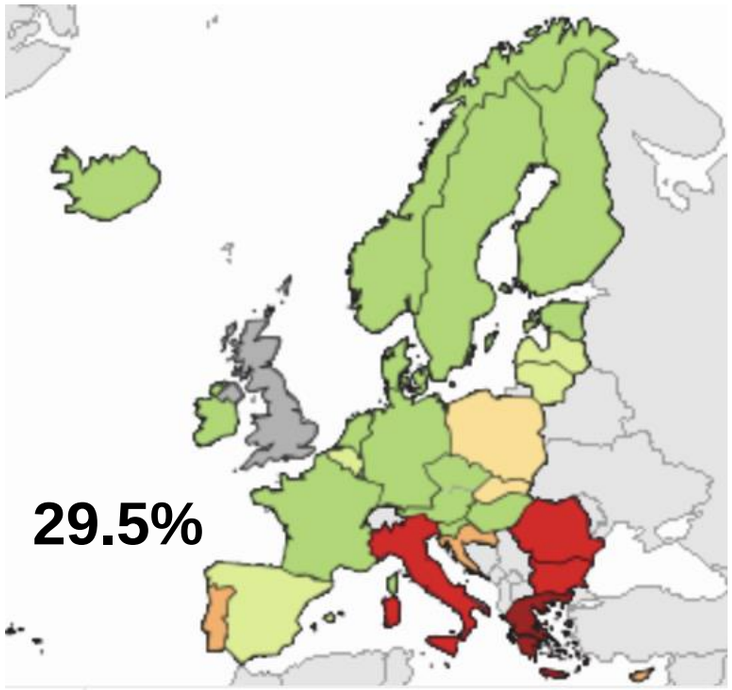
Comunità



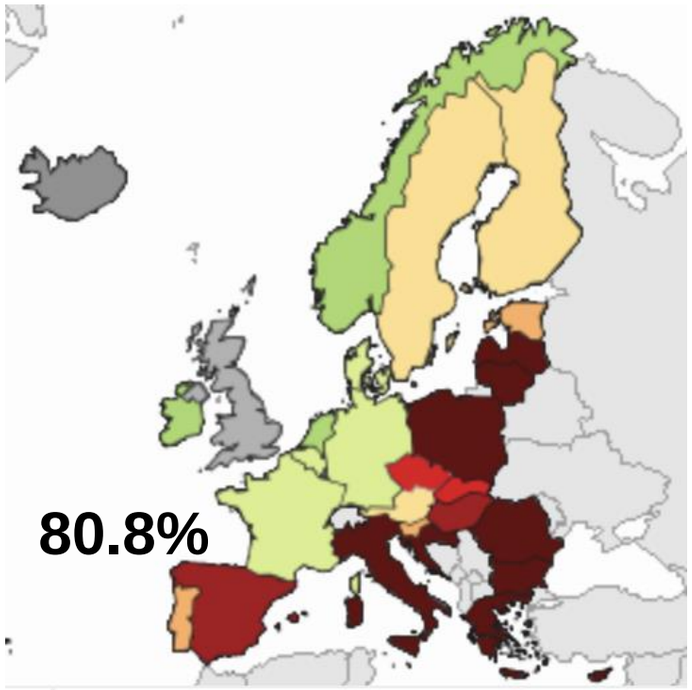
Ospedali
Long-term care facilities

I patogeni multiresistenti più frequenti nella pratica clinica

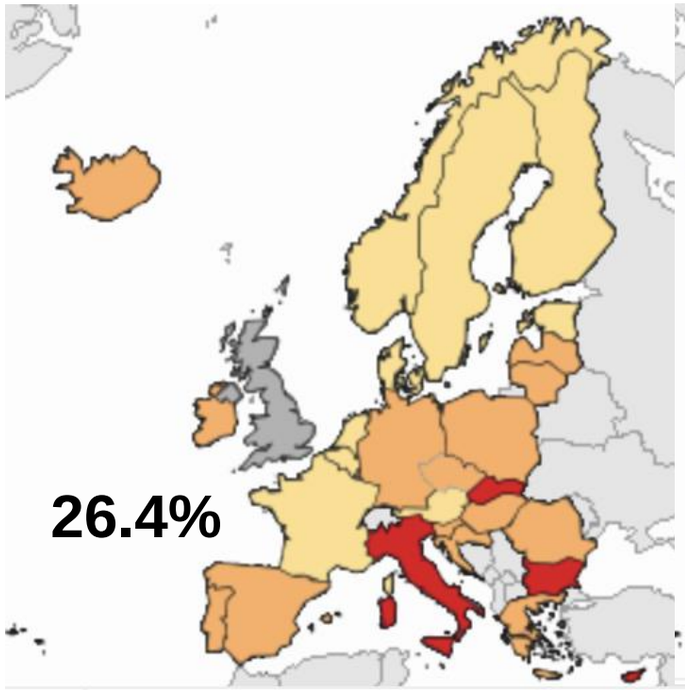
***K. pneumoniae* Carba-R**



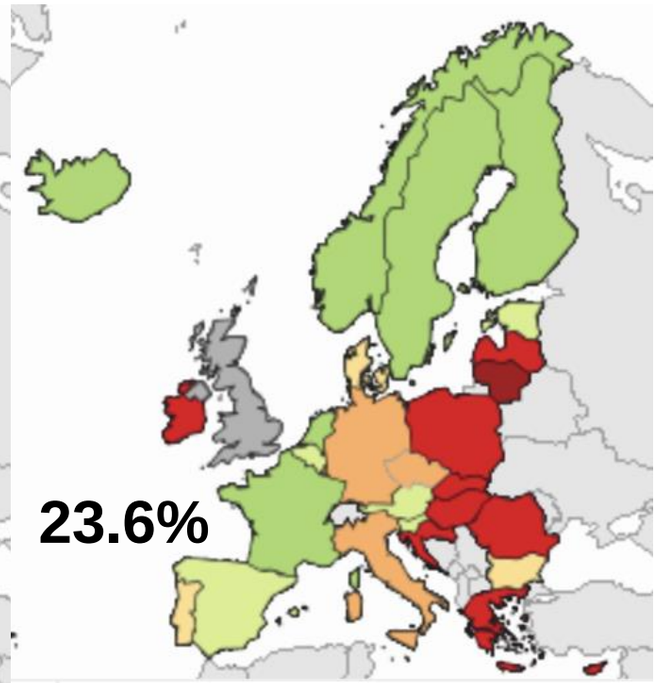
***A. baumannii* Carba-R**



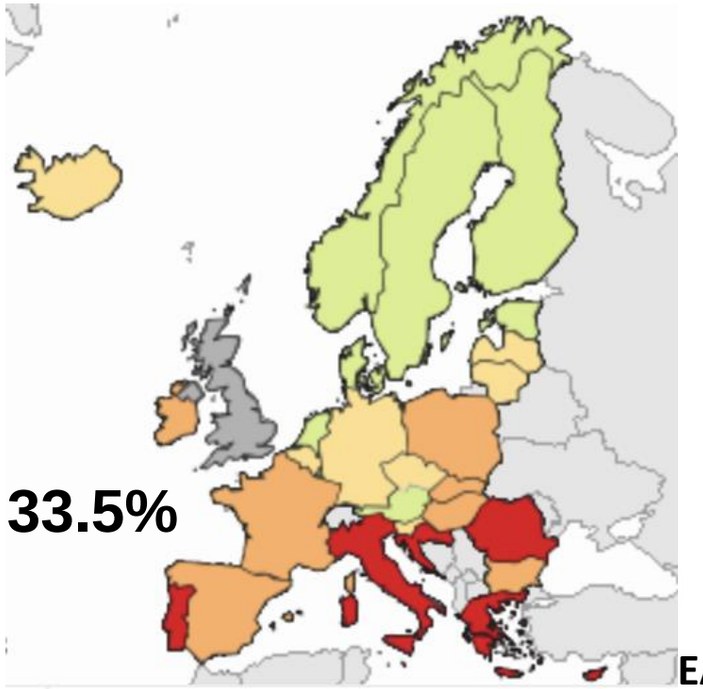
***E. coli* 3rd gen Ceph-R**



***E. faecium* Vanco-R**



MRSA

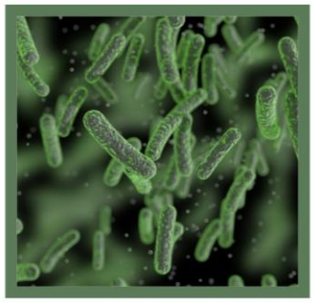


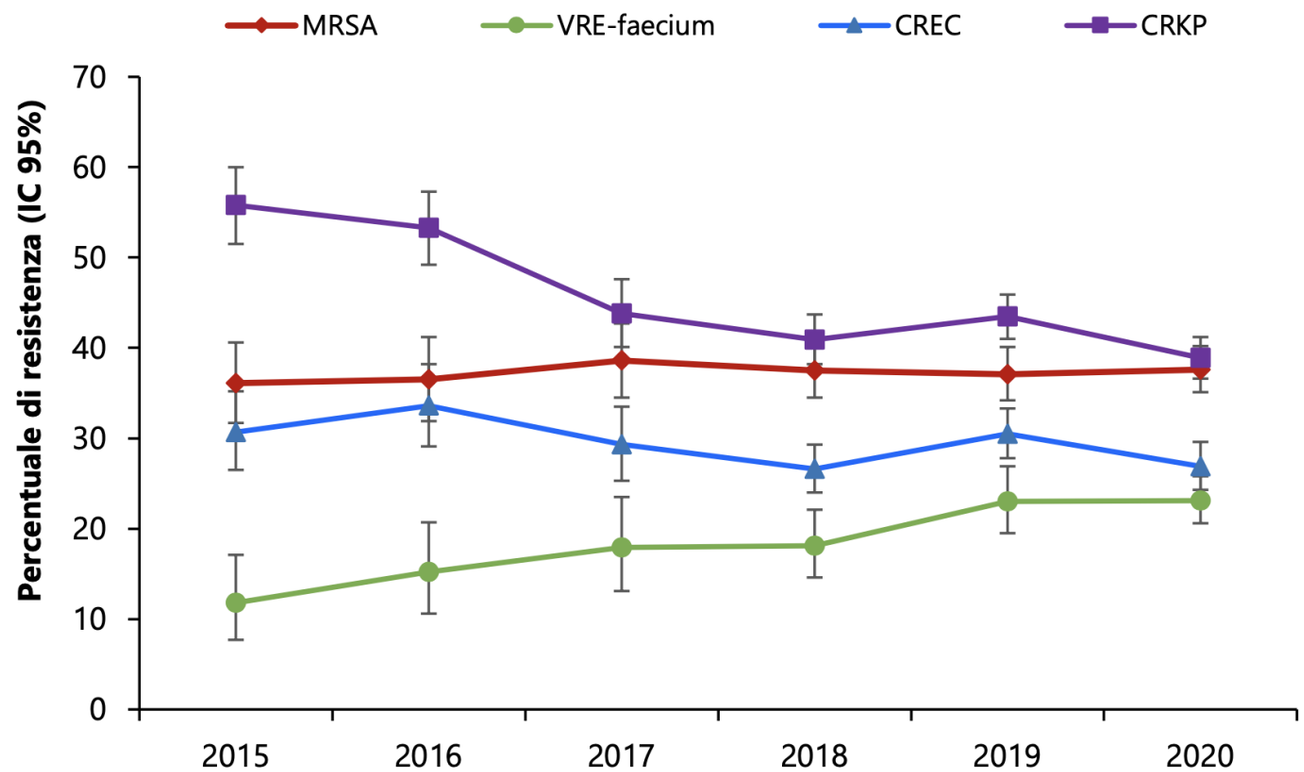
EARS-NET, 2020

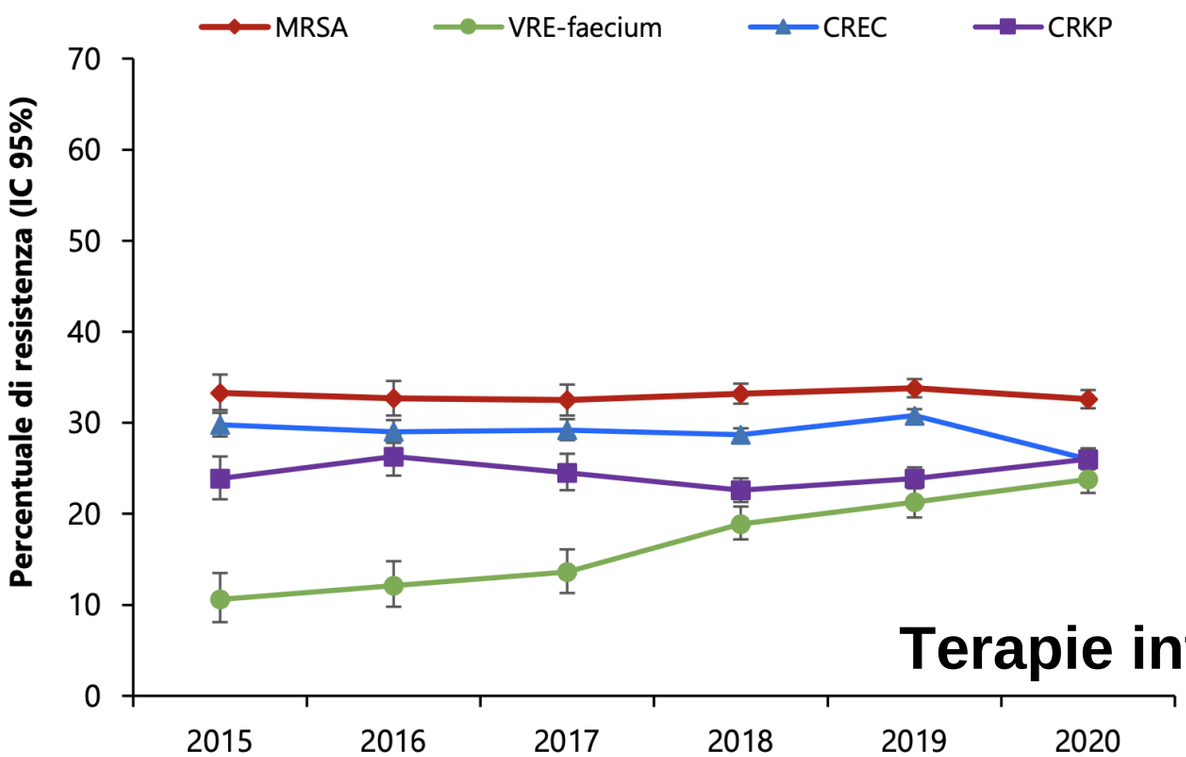
Prevalenza patogeni multiresistenti più frequenti nella pratica clina: rapport AR-ISS 2021

AR-ISS:
sorveglianza nazionale
dell'Antibiotico-Resistenza

Dati 2020







Terapie intensive

MRSA *S. aureus* resistente alla meticillina
VRE-*faecium* *E. faecium* resistente alla vancomicina
CREC *E. coli* resistente alle cefalosporine di terza generazione
CRKP *K. pneumoniae* resistente ai carbapenemi

Fattori che condizionano AMR durante la pandemia da COVID-19

- **Overuse / uso non corretto antibiotici (ospedale e comunità)**
- **Diminuzione pratiche di *antimicrobial stewardship***
- **Cambiamenti nella pratiche di *infection control***
- **Ridotta sorveglianza AMR**

+

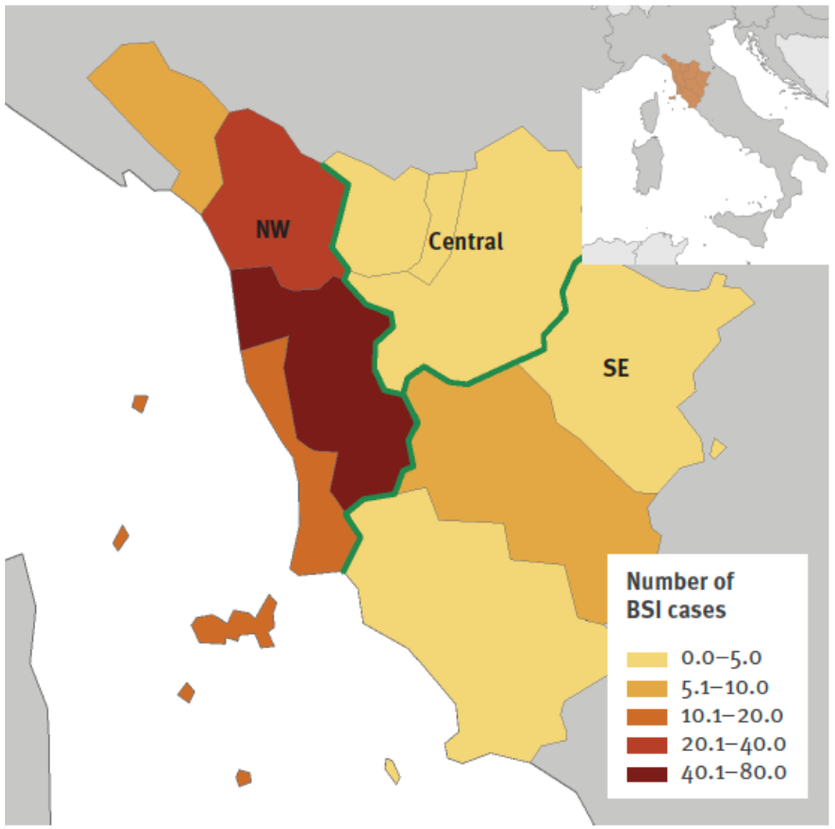
- **Ridotta mobilità della popolazione**
- **Minor numero di trasferimenti pazienti**

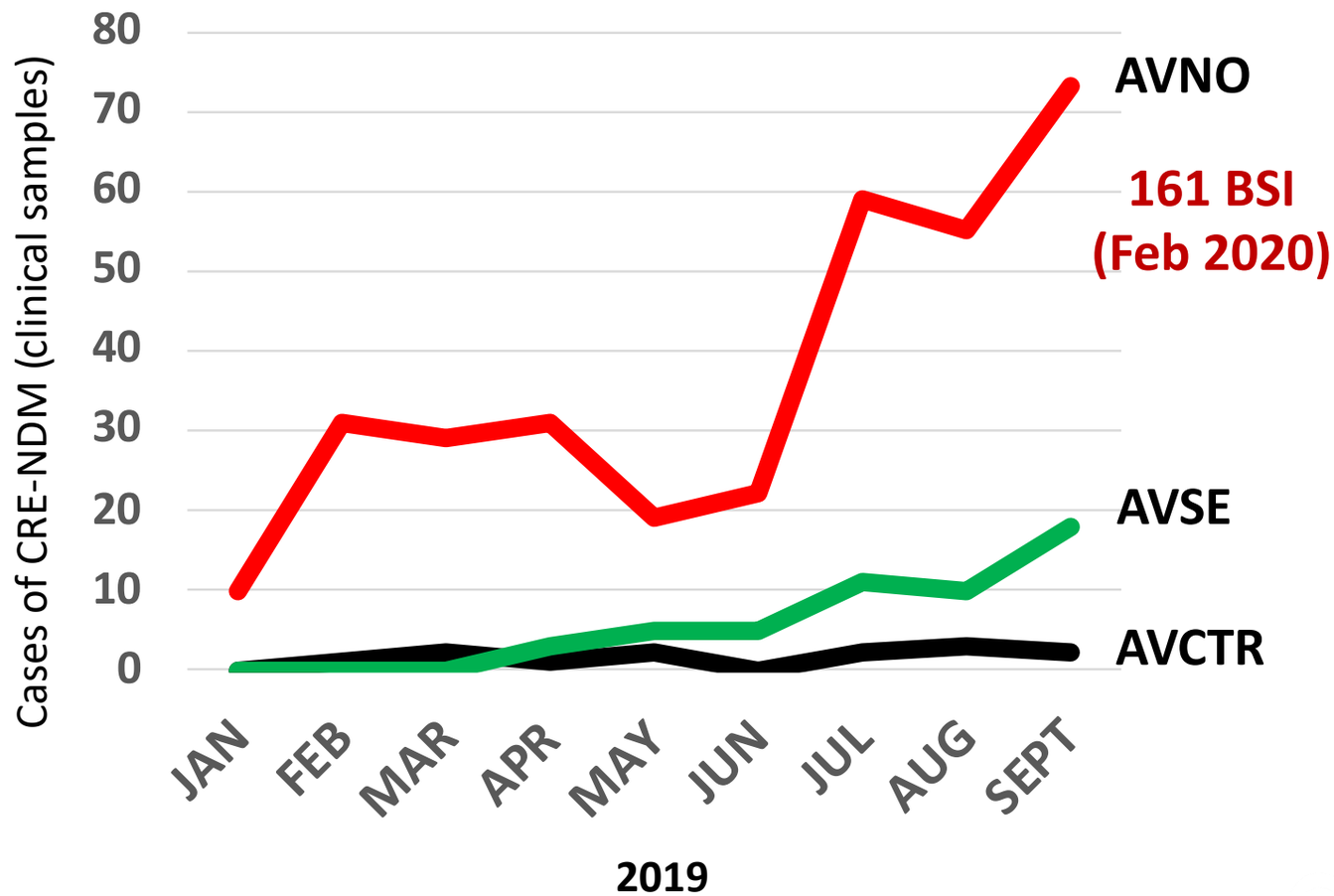
−

RAPID COMMUNICATION

Prolonged outbreak of New Delhi metallo-beta-lactamase-producing carbapenem-resistant Enterobacterales (NDM-CRE), Tuscany, Italy, 2018 to 2019

Lara Tavoschi[1], Silvia Forni[2], Andrea Porretta[1,5], Lorenzo Righi[3], Filippo Pieralli[4], Francesco Menichetti[5], Marco Falcone[5], Giulia Gemignani[5], Spartaco Sani[6], Paola Vivani[7], Tommaso Bellandi[8], Danilo Tacconi[9], Lucia Turini[10], Giulio Toccafondi[3], Gaetano Privitera[1,5], Pierluigi Lopalco[1,5], Angelo Baggiani[1,5], Fabrizio Gemmi[2], Grazia Luchini[5], Maurizio Petrillo[11], Lorenzo Roti[10], Patrizio Pezzotti[12], Annalisa Pantosti[12], Stefania Iannazzo[13], Maria Teresa Mechi[3], Gian Maria Rossolini[4,14], on behalf of the Tuscan Clinical Microbiology Laboratory Network[15]





www.ars.toscana.it

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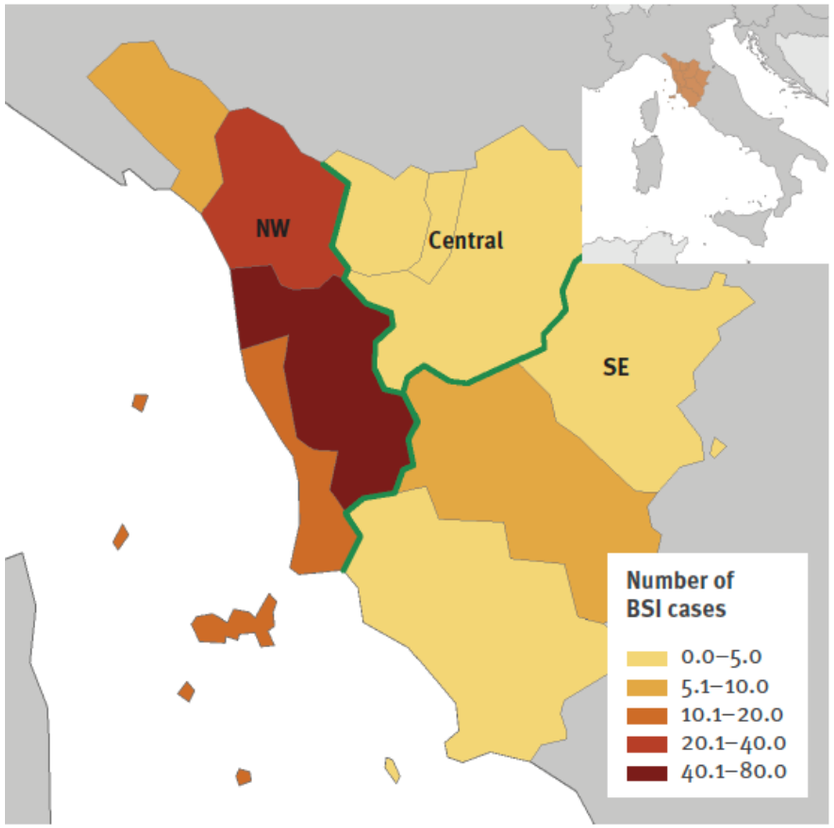
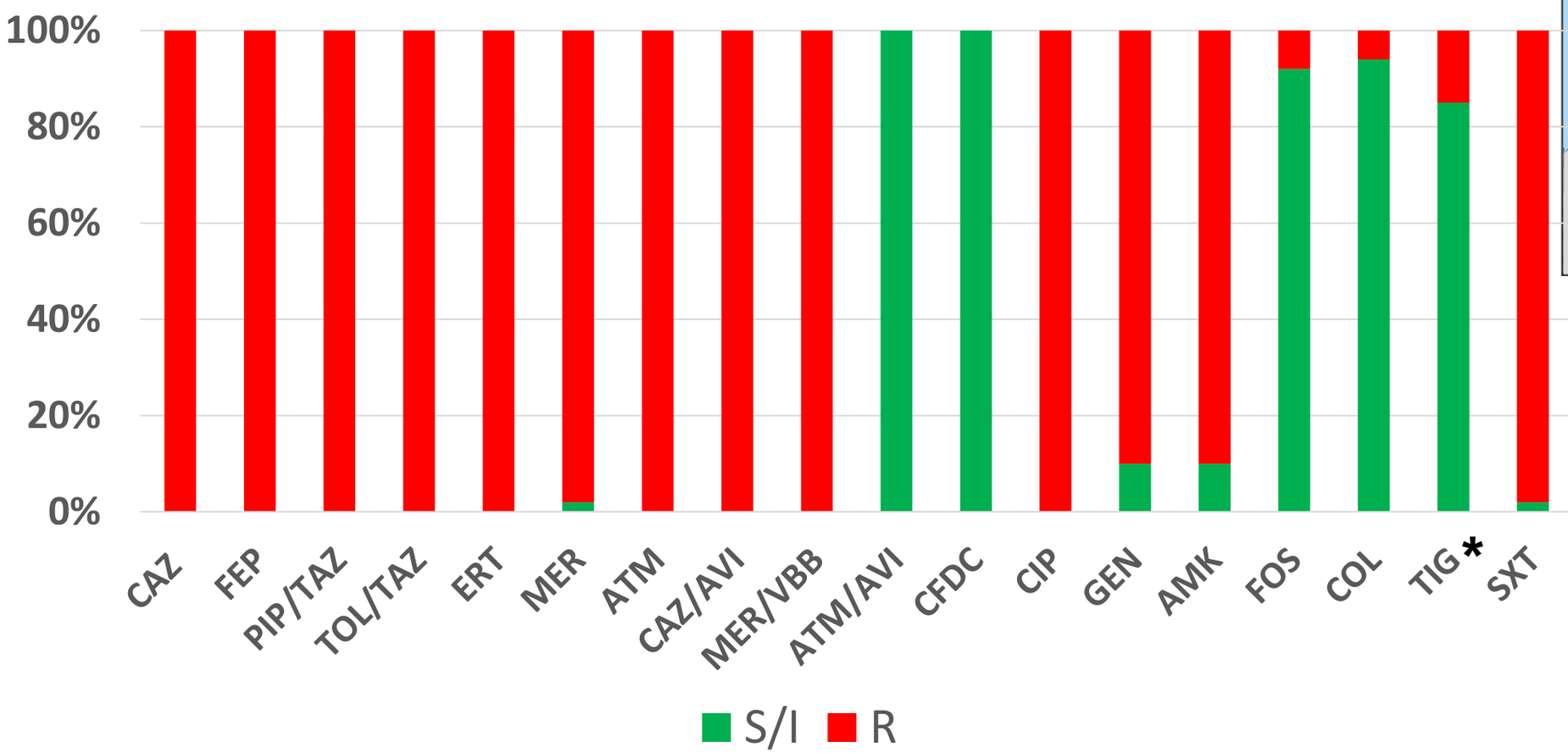
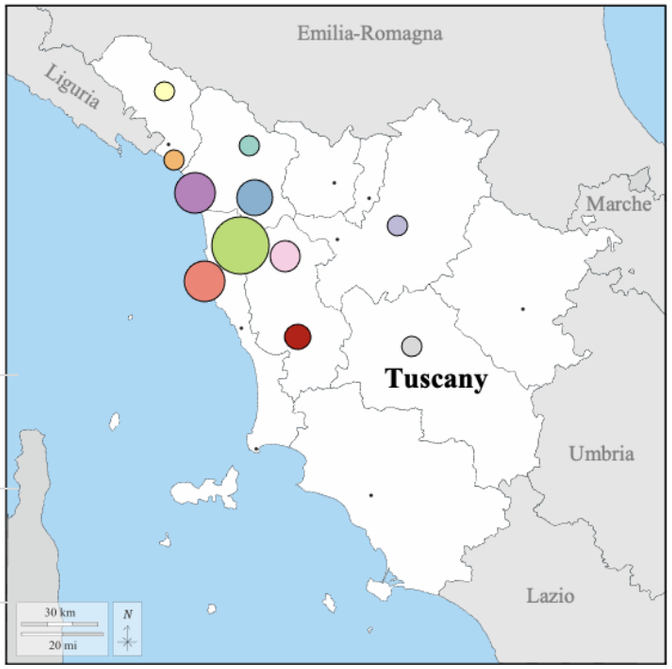


Outbreak **causato in larga parte da espansione clonale di un singolo clone di *K. pneumoniae* (ST147) «clone toscano»**

CRE-NDM outbreak Toscano : resistenza agli antibiotici

N = 48 isolati di *K. pneumoniae* ST147 NDM-1+ (BSI)

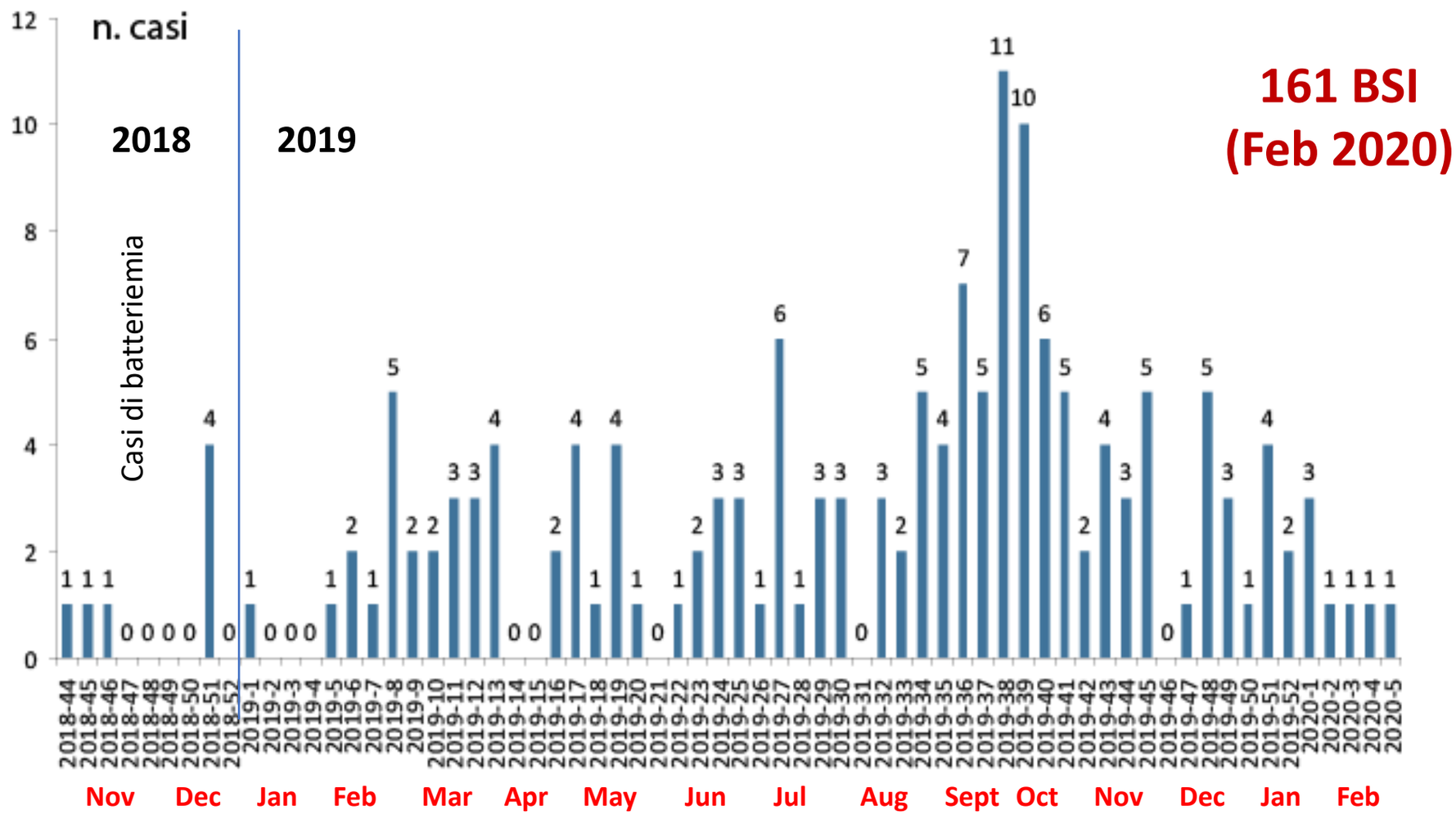




* tigecycline rates calculated based on EUCAST breakpoints for *E. coli*

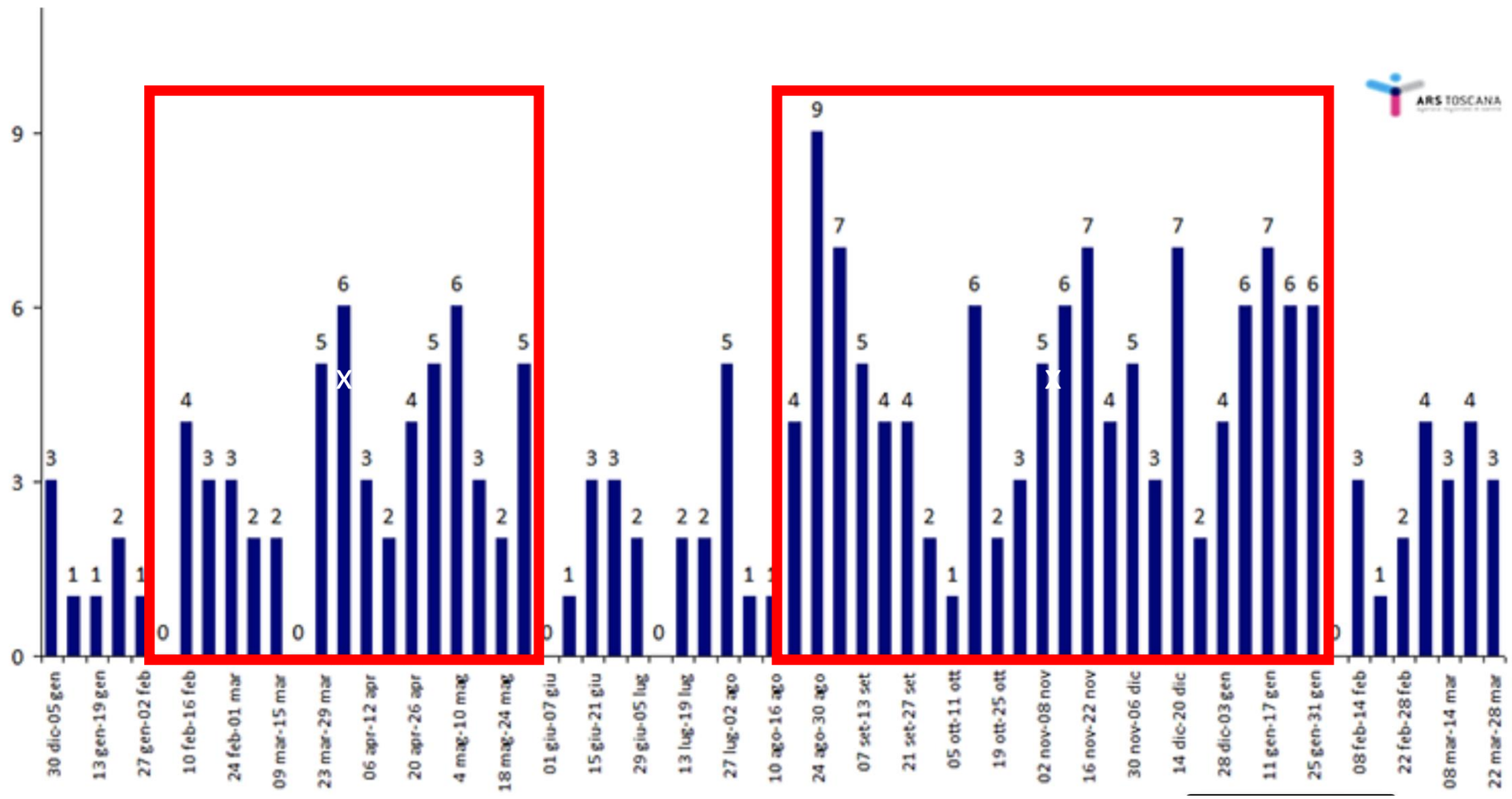
Di Pilato V *et al.*, Lancet Microbe *on press*

Trend BSI da NDM-CRE in Toscana: Nov 2018 – Feb 2020



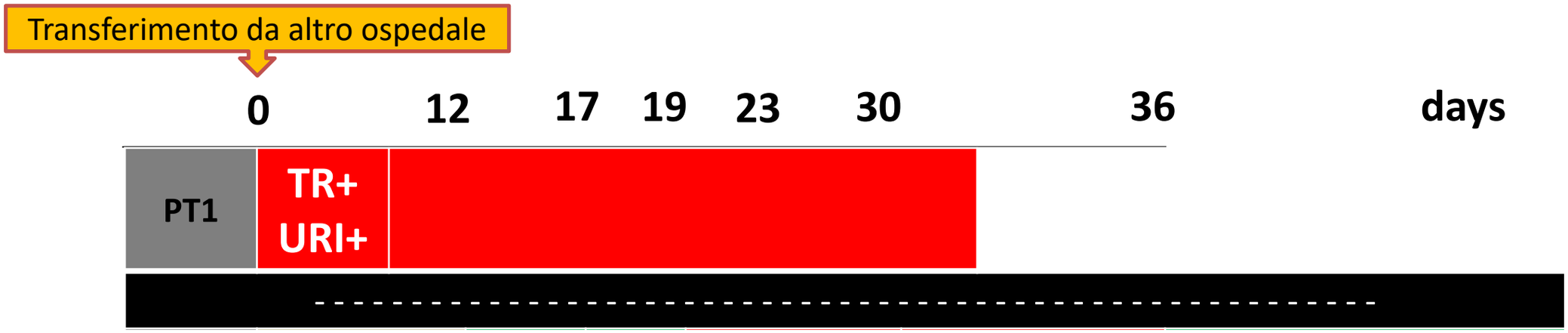
www.ars.toscana.it

Trend di BSI causate da NDM-CRE in Toscana: Gen 2020 – Mar 2021



www.ars.toscana.it

Outbreak di CPE-NDM in una ICU



Tutti gli isolati appartenevano al «clone toscano» ST147

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Contents lists available at ScienceDirect

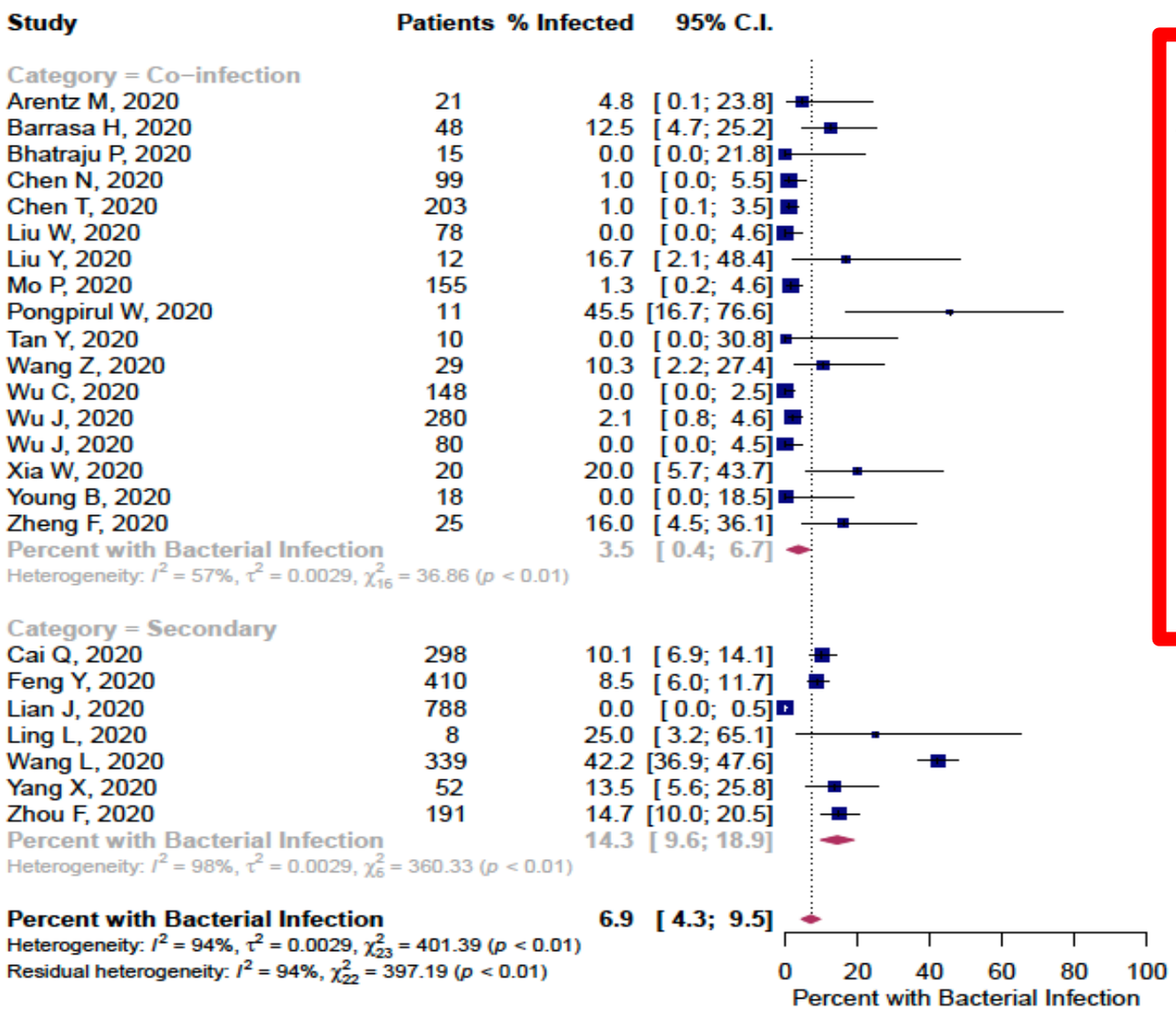
Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com

Systematic Review

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]



A low proportion of COVID-19 patients have a bacterial co-infection. These findings do not support the routine use of antibiotics in the management of confirmed COVID-19 infection

Infezioni secondarie batteriche e fungine in pazienti COVID

Chong *et al*, Infection 2021

State-of-the-art review of secondary pulmonary infections in patients with COVID-19 pneumonia

Incidenza infezioni secondarie: 16%

The widespread use of empirical antibiotics during the current pandemic ***may contribute to the development of multidrug-resistant microorganisms***, and antimicrobial stewardship programs are required for minimizing and de-escalating antibiotics

Grasselli *et al*, Chest 2021

Hospital-Acquired Infections in Critically Ill Patients With COVID-19

Incidenza infezioni secondarie: 46%

Critically ill patients with COVID-19 are at high risk of HAIs from **MDR organisms (35%)**. HAIs prolong mechanical ventilation and hospitalization, and HAIs complicated by septic shock almost double mortality.

Infezioni secondarie batteriche e fungine in pazienti COVID @AOUC

	Secondary infections		**No secondary infections**		P-value
	No.	%	N.	%	
Total	106	22	376	88	

Giani-Spinicci *et al* – in preparation

Infezioni secondarie batteriche e fungine in pazienti COVID @AOUC

pazienti COVID-19 con coinfezione (n=106)

Infezioni dopo le 48h dal ricovero= 88%

UTI (38%)	***LRTI (32%)***	***BSI (29%)***
E. coli (21.4%)	*P. aeruginosa (35.4%)*	CONS (25.7%)
E. faecalis (18.4%)	*K. pneumoniae (13.4%)*	*E. faecalis (13.5%)*
K. pneumoniae (15.3%)	*E. coli (12.2%)*	*K. pneumoniae (9.5%)*
E. faecium (14.3%)	*A. baumannii (8.5%)*	*E. coli (9.5%)*

***Enterobacterales*: 35% ESBL; 15% DTR**

***P. aeruginosa:* 22.5% DTR**

***A. baumannii*: 100% DTR**

Giani-Spinicci *et al* – in preparation

La diagnostica delle infezioni del tratto respiratorio al tempo del COVID-19

- **COVID o NO-COVID?**
- **NO-COVID: altri patogeni?**
- **COVID: coinfezioni/sovrainfezioni?**
- **Necessaria la rapidità (*fast microbiology*)**
  - percorso COVID
  - *Antimicrobial stewardship*
  - *Infection prevention and control*

Pannelli Sindromici per LRTI con SARS-CoV-2

QIAGEN

QIAstat-Dx Respiratory SARS-CoV-2 Panel

TTR, 1 h

Bacterial

- *Mycoplasma pneumoniae*
- *Legionella pneumophila*
- *Bordetella pertussis*

Viral

- Influenza A
- Influenza A subtype H1N1/2009
- Influenza A subtype H1
- Influenza A subtype H3
- Influenza B
- Coronavirus 229E
- Coronavirus HKU1
- Coronavirus NL63
- Coronavirus OC43
- Parainfluenza virus 1
- Parainfluenza virus 2
- Parainfluenza virus 3
- Parainfluenza virus 4
- Adenovirus
- Respiratory Syncytial virus A/B
- Human Metapneumovirus A/B
- Bocavirus
- Rhinovirus/Enterovirus*
- **SARS-CoV-2**

RANDOX BIOSCIENCES

VIVALYTIC VIRAL RESPIRATORY TRACT INFECTION ARRAY (VRI)

TTR, 2.5 h

VIRUSES
SARS-CoV-2 (COVID-19)
Sarbecovirus (SARS, SARS like, SARS-CoV-2)
Coronavirus 229E/NL63
Coronavirus OC43/HKUI
Middle East Respiratory Syndrome Coronavirus (MERS-CoV)
Adenovirus A/B/C/D/E
Enterovirus A/B/C
Influenza A
Influenza B
Rhinovirus A/B

BioFire® Respiratory 2.1 (RP2.1) Panel with SARS-CoV-2

BIOMÉRIEUX

VIRUSES:

- Adenovirus
- Coronavirus HKU1
- Coronavirus NL63
- Coronavirus 229E
- Coronavirus OC43
- **Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)**
- Human Metapneumovirus
- Human Rhinovirus/Enterovirus
- Influenza A
- Influenza A/H1
- Influenza A/H3
- Influenza A/H1-2009
- Influenza B

BACTERIA:

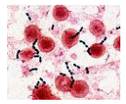
- *Bordetella parapertussis*
- *Bordetella pertussis*
- *Chlamydia pneumoniae*
- *Mycoplasma pneumoniae*

TTR, 1 h

Tecnologie diagnostiche molecolari per LRTI

Campioni respiratori (es. BAL)

Gram



ID MALDI

Incubazione | **AST** | **>=3 giorni**

16 - 48 h

Parziale

Parziale

Definitivo

TTR: 70 min

- Ricerca dei più comuni patogeni responsabili delle infezioni in quel distretto
- Ricerca di determinanti di resistenza rilevanti per l'uso di alcuni antibiotici (ANTIBIOGRAMMA MOLECOLARE)

ID/AST Molecolare (panelli sindromici)

Più rapida / più accurata revisione della terapia empirica

Possibilità di attendere per selezionare terapia (quasi) targeted

Esempio di “pannello sindromico” per diagnostica molecolare di polmonite

Bacterial Targets:

Acinetobacter calcoaceticus-baumannii complex
Enterobacter aerogenes
Enterobacter cloacae complex
Escherichia coli
Haemophilus influenzae
Klebsiella oxytoca
Klebsiella pneumoniae group
Moraxella catarrhalis
Proteus spp.
Pseudomonas aeruginosa
Serratia marcescens
Staphylococcus aureus
Streptococcus agalactiae
Streptococcus pneumoniae
Streptococcus pyogenes

Atypical Bacterial:

Chlamydia pneumoniae
Legionella pneumophila
Mycoplasma pneumoniae

Viruses:

Adenovirus
Coronavirus
Human Metapneumovirus
Human Rhinovirus/Enterovirus
Influenza A
Influenza B
Parainfluenza Virus
Respiratory Syncytial Virus

Antimicrobial Resistance Genes:

CTX-M (ESBL; resistance to specific classes of beta lactam antibiotics)
IMP (Carbapenem resistance)
KPC (Carbapenem resistance)
mecA/C and MREJ (Methicillin resistance)
NDM (Carbapenem resistance)
Oxa48-like (Carbapenem resistance)
VIM (Carbapenem resistance)

Principali batteri e virus causa di LRTI

non-CPE / CPE (+ tipo di CPE)

MRSA / MSSA

Risultati in 70 minuti da campione clinico
Alto valore predittivo negativo
Semiquantitativo

L'importanza di individuare correttamente il tipo di carbapenemasi

Attività dei nuovi antibiotici anti-Gram-negativi nei confronti di ceppi produttori di diversi tipi di carbapenemasi

Enzima	CAZ/AVI	MER/VAB	IMI/REL	CFDC	*ATM/AVI*	*FEP/TNB*
KPC	+	+	+	+	+	+
OXA-48	+	-	-	+	+	+
VIM	-	-	-	+	+	+
NDM	-	-	-	+	+	+
IMP	-	-	-	+	+	-

CAZ/AVI = ceftazidime/avibactam
MER/VAB = meropenem/vaborbactam
IMI/REL = imipenem/relebactam
CFDC = cefiderocol
ATM/AVI = aztreonam/avibactam
FEP/TNB = cefepime/taniborbactam

Conclusioni

- AMR è alimentata da diversi fattori correlati alla pandemia COVID-19
- Il problema ha evoluzioni peggiori nei contesti epidemiologici dove la AMR è più alta
- È necessario mantenere alta la attenzione sulla diffusione dei ceppi MDRO e sulla *antimicrobial stewardhip*, per evitare ulteriori danni generati da AMR+COVID
- La *stewardship* diagnostica è essenziale per implementare programmi di *antimicrobial stewardship* e *infection control*

GRAZIE

per

l' ATTENZIONE

tommaso.giani@unifi.it