DZIF R-Net Daten

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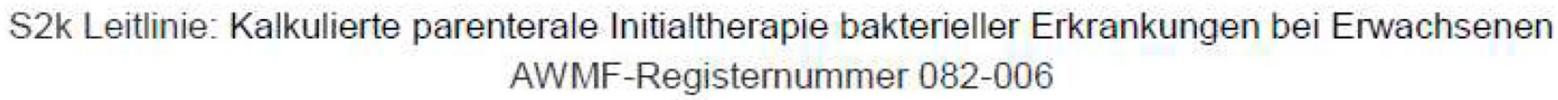
Klinik für Infektiologie und Mikrobiologie
Universität zu Lübeck / Universitätsklinikum Schleswig-Holstein
11.11.2023

Keine Interessenkonflikte

Überblick

- Pitfalls
- R-Net Studie
- Daten

Resistenzstatistik


S2k Leitlinie: Kalkulierte parenterale Initialtherapie bakterieller Erkrankungen bei Erwachsenen
AWMF-Registernummer 082-006

Kapitel 2, S. 32

„**Entscheidend für die Kalkulation einer Therapie mit Antibiotika im Einzelfall** sind vorausgehende mikrobiologische Befunde des Patienten selbst und seiner unmittelbaren Umgebung sowie **die Resistenzsituation der Abteilung, in der der Patient versorgt wird.** Sind solche Daten nicht verfügbar, kann auf regionale oder überregionale Daten zurückgegriffen werden.“

https://www.awmf.org/uploads/tx_szleitlinien/082-006l_S2k_Parenterale_Antibiotika_2019-08.pdf

Resistenzstatistik Beispiel

Beispiel: Harnwegsinfektion und Mecillinam

- Wie hoch ist die Resistenzrate von *E. coli* gegen Mecillinam in Deutschland?

Mecillinam Resistenz in DE - Pitfall

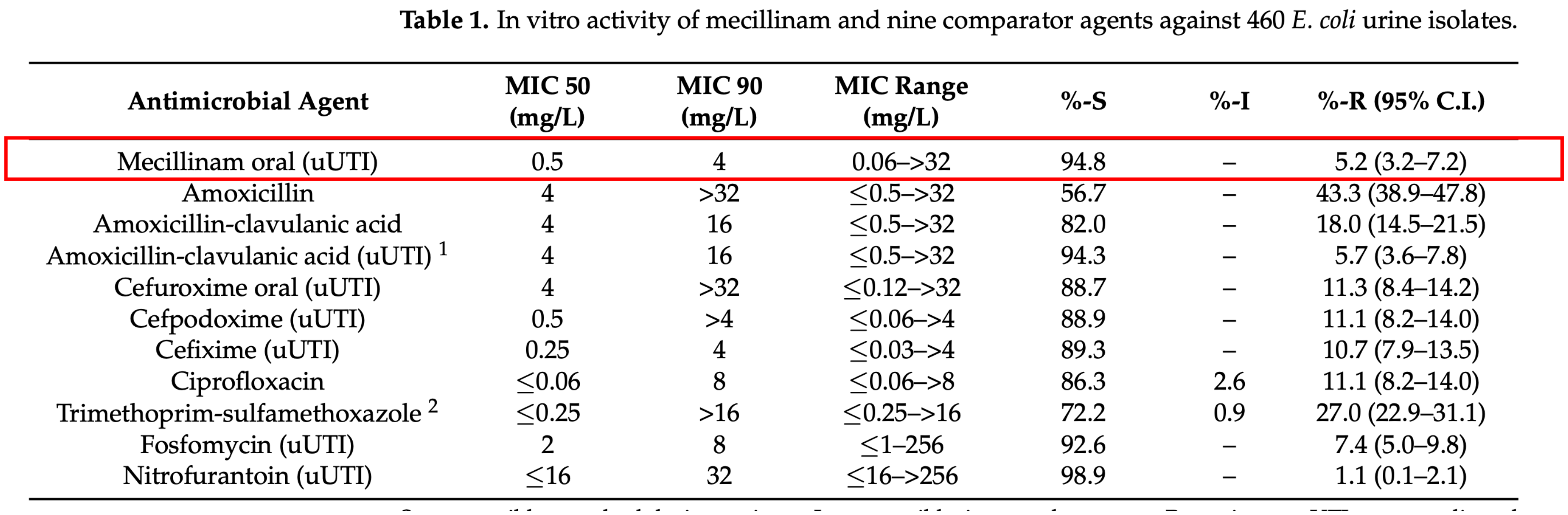


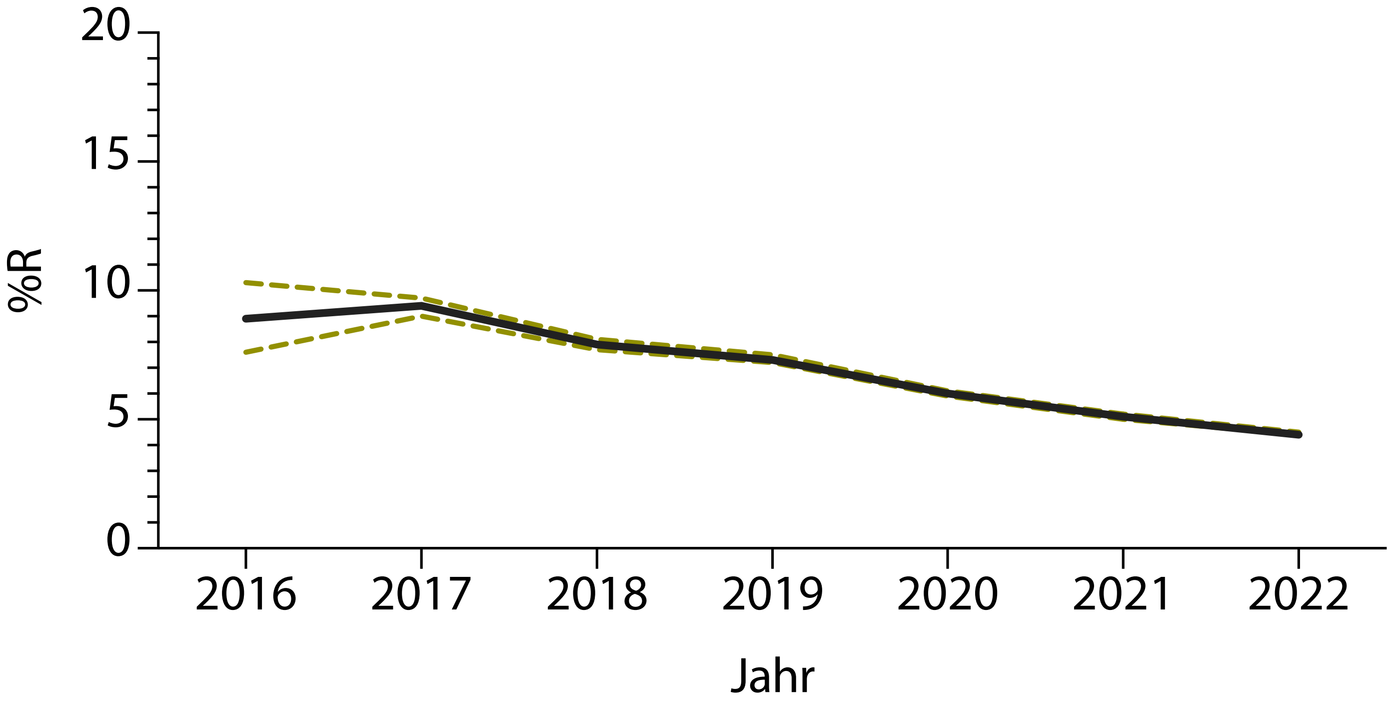
Table 1. In vitro activity of mecillinam and nine comparator agents against 460 *E. coli* urine isolates.

Antimicrobial Agent	MIC 50 (mg/L)	MIC 90 (mg/L)	MIC Range (mg/L)	%-S	%-I	%-R (95% C.I.)
Mecillinam oral (uUTI)	0.5	4	0.06–>32	94.8	–	5.2 (3.2–7.2)
Amoxicillin	4	>32	≤0.5–>32	56.7	–	43.3 (38.9–47.8)
Amoxicillin-clavulanic acid	4	16	≤0.5–>32	82.0	–	18.0 (14.5–21.5)
Amoxicillin-clavulanic acid (uUTI) [1]	4	16	≤0.5–>32	94.3	–	5.7 (3.6–7.8)
Cefuroxime oral (uUTI)	4	>32	≤0.12–>32	88.7	–	11.3 (8.4–14.2)
Cefpodoxime (uUTI)	0.5	>4	≤0.06–>4	88.9	–	11.1 (8.2–14.0)
Cefixime (uUTI)	0.25	4	≤0.03–>4	89.3	–	10.7 (7.9–13.5)
Ciprofloxacin	≤0.06	8	≤0.06–>8	86.3	2.6	11.1 (8.2–14.0)
Trimethoprim-sulfamethoxazole [2]	≤0.25	>16	≤0.25–>16	72.2	0.9	27.0 (22.9–31.1)
Fosfomycin (uUTI)	2	8	≤1–256	92.6	–	7.4 (5.0–9.8)
Nitrofurantoin (uUTI)	≤16	32	≤16–>256	98.9	–	1.1 (0.1–2.1)

Kresken et al, Antibiotics 2022

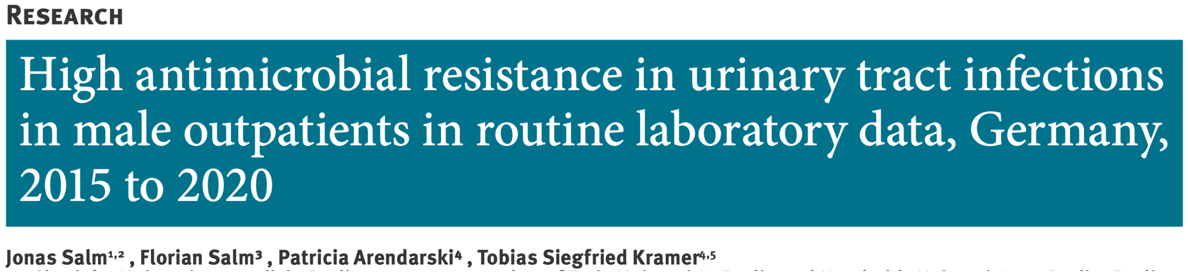
Mecillinam Resistenz in DE - Pitfall

Mecillinam-R *E. coli*



Datenquelle: ARS (RKI)
Versorgungsbereich ambulant, alle Bereiche

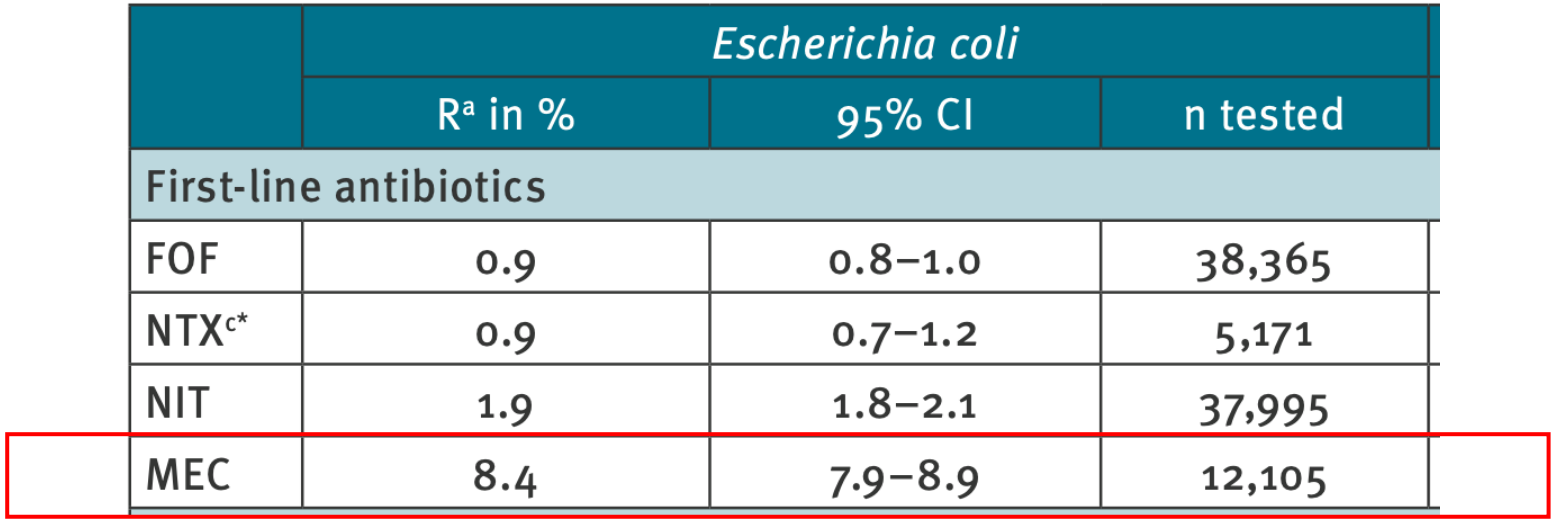
Mecillinam Resistenz in DE - Pitfall



RESEARCH

High antimicrobial resistance in urinary tract infections in male outpatients in routine laboratory data, Germany, 2015 to 2020

Jonas Salm[1,2], Florian Salm[3], Patricia Arendarski[4], Tobias Siegfried Kramer[4,5]



	Escherichia coli		
	R[a] in %	95% CI	n tested
First-line antibiotics			
FOF	0.9	0.8–1.0	38,365
NTX[c*]	0.9	0.7–1.2	5,171
NIT	1.9	1.8–2.1	37,995
MEC	8.4	7.9–8.9	12,105

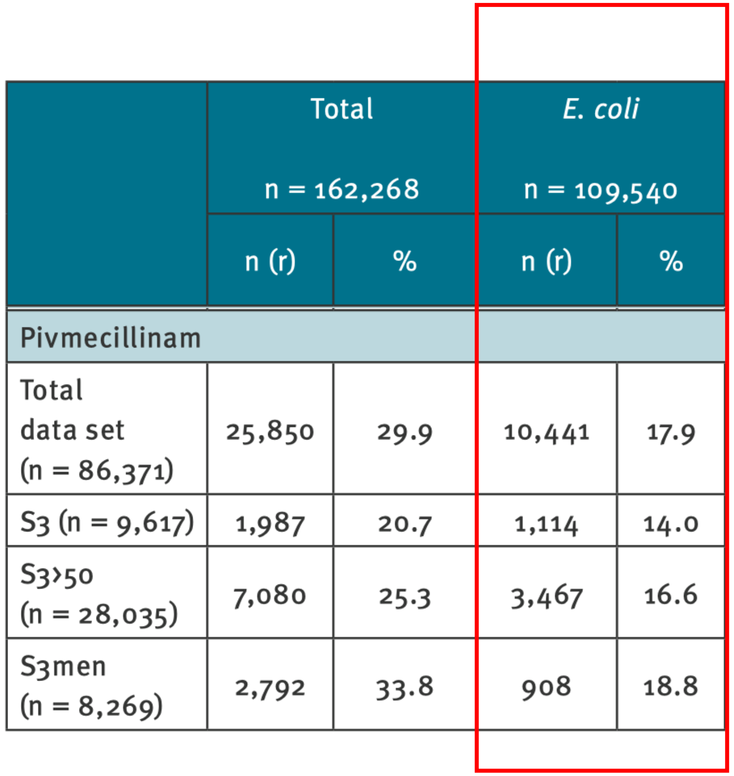
Mecillinam Resistenz in DE - Pitfall

RESEARCH

Antimicrobial resistance of clinical Enterobacterales isolates from urine samples, Germany, 2016 to 2021

Carolin Stoltidis-Claus[1,2] , Kerstin Daniela Rosenberger[3] , Falitsa Mandraka[1] , Xenia Quante[1] , Jörg Gielen[2] , Dennis Hoffmann[1] , Hilmar Wisplinghoff[1,4] , Nathalie Jazmati[1,2]
1. Wisplinghoff laboratories, Cologne, Germany
2. Institute for Medical Microbiology, Immunology and Hygiene, University of Cologne, Cologne, Germany
3. Institute of Medical Statistics and Computational Biology, Faculty of Medicine and University Hospital Cologne, University of Cologne, Cologne, Germany
4. Institute for Virology and Microbiology, Witten/Herdecke University, Witten, Germany

Correspondence: Nathalie Jazmati (n.jazmati@wisplinghoff.de)



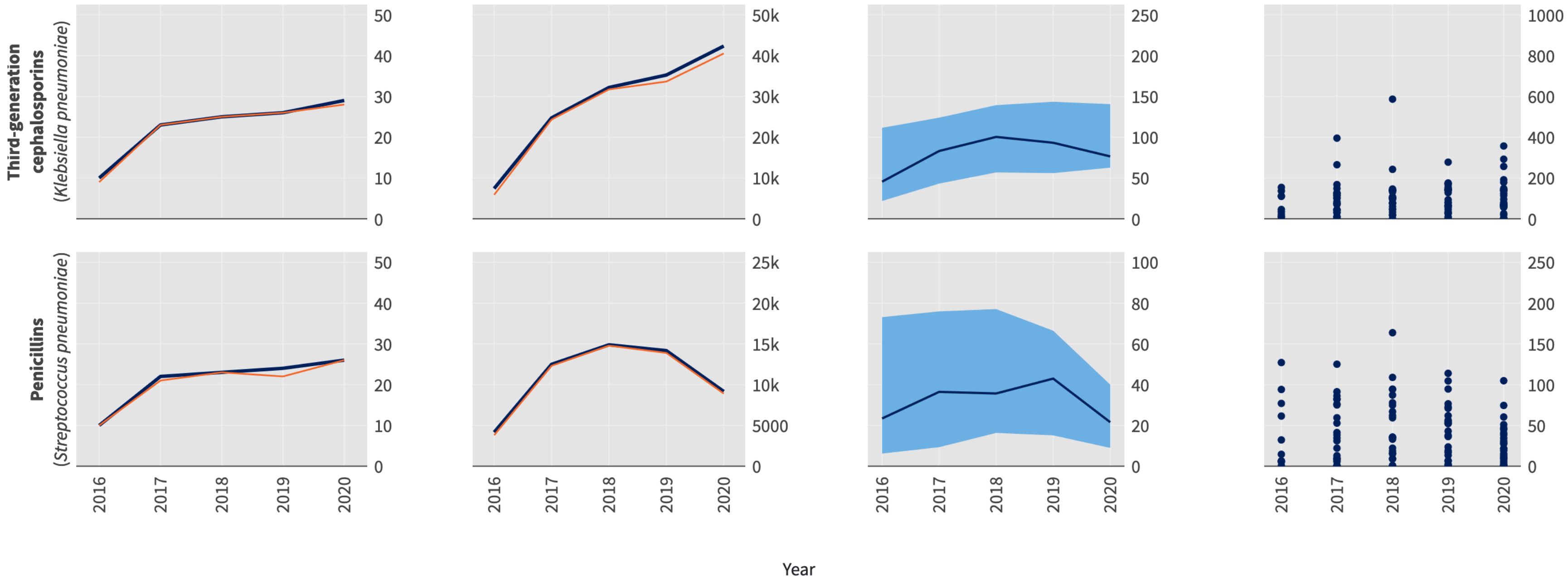
	Total		*E. coli*	
	n = 162,268		n = 109,540	
	n (r)	%	n (r)	%
Pivmecillinam				
Total data set (n = 86,371)	25,850	29.9	10,441	17.9
S3 (n = 9,617)	1,987	20.7	1,114	14.0
S3>50 (n = 28,035)	7,080	25.3	3,467	16.6
S3men (n = 8,269)	2,792	33.8	908	18.8

Wo finde ich die Resistenzdaten?

Home / Initiatives / Global Antimicrobial Resistance and Use Surveillance System (GLASS)

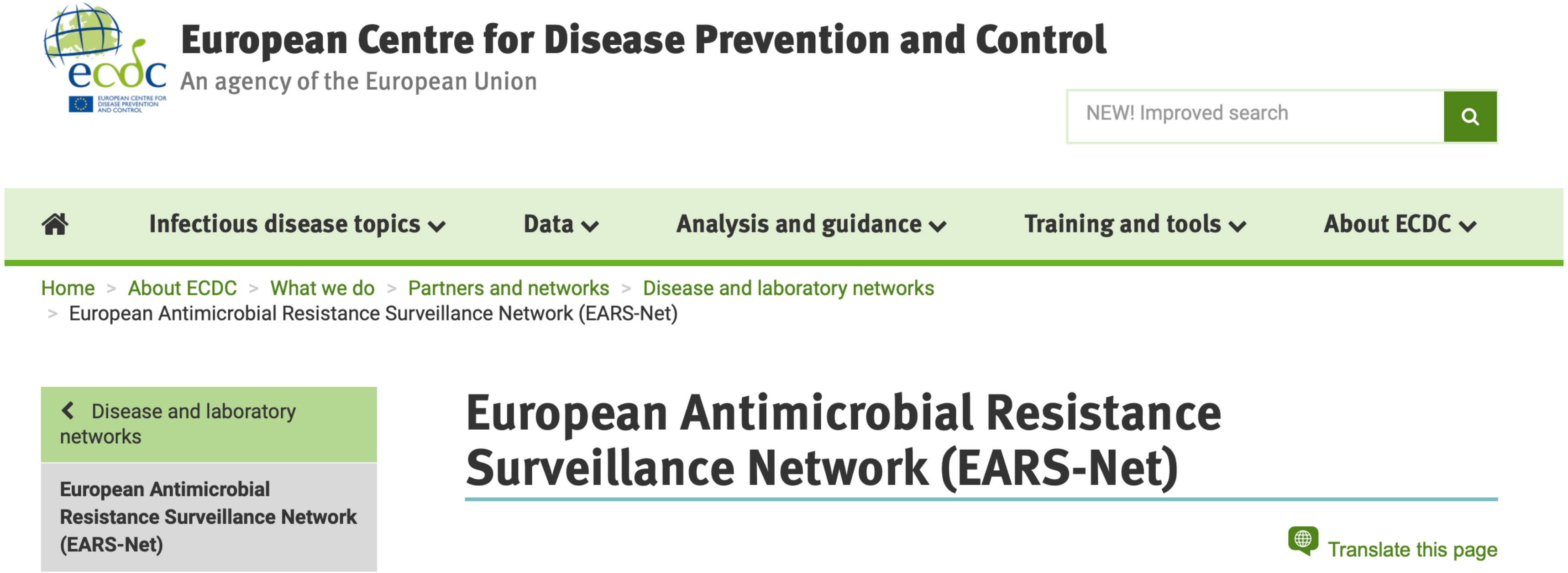
Global Antimicrobial Resistance and Use Surveillance System (GLASS)

https://www.who.int/initiatives/glass



Wo finde ich die Resistenzdaten?

https://www.ecdc.europa.eu/en/about-us/networks/disease-networks-and-laboratory-networks/ears-net-data



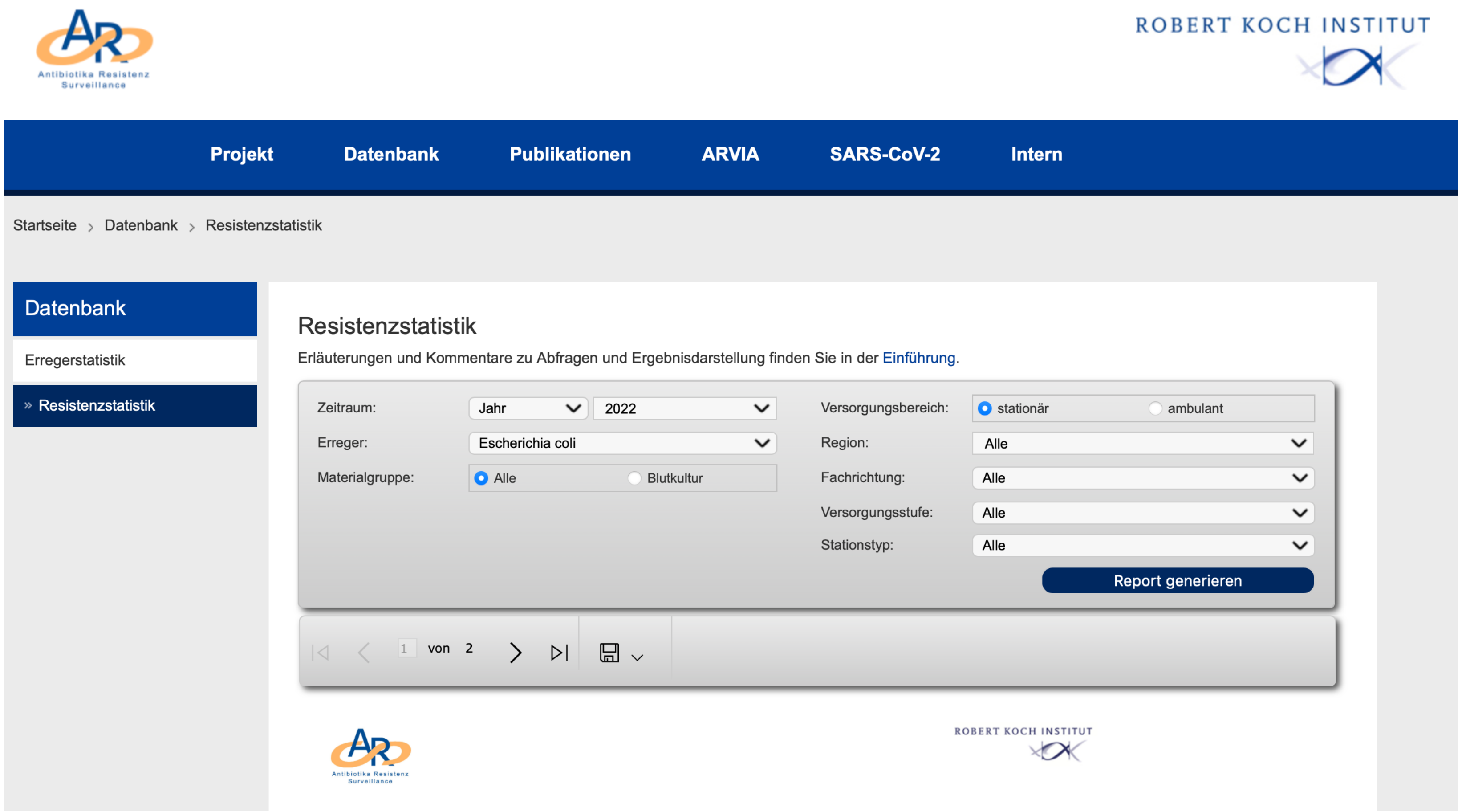
European Centre for Disease Prevention and Control

An agency of the European Union

European Antimicrobial Resistance Surveillance Network (EARS-Net)

Wo finde ich die Resistenzdaten?

https://ars.rki.de



Resistenzstatistik

Erläuterungen und Kommentare zu Abfragen und Ergebnisdarstellung finden Sie in der Einführung.

Zeitraum: Jahr 2022

Erreger: Escherichia coli

Materialgruppe: ● Alle ○ Blutkultur

Versorgungsbereich: ● stationär ○ ambulant

Region: Alle

Fachrichtung: Alle

Versorgungsstufe: Alle

Stationstyp: Alle

DZIF
Deutsches Zentrum
für Infektionsforschung

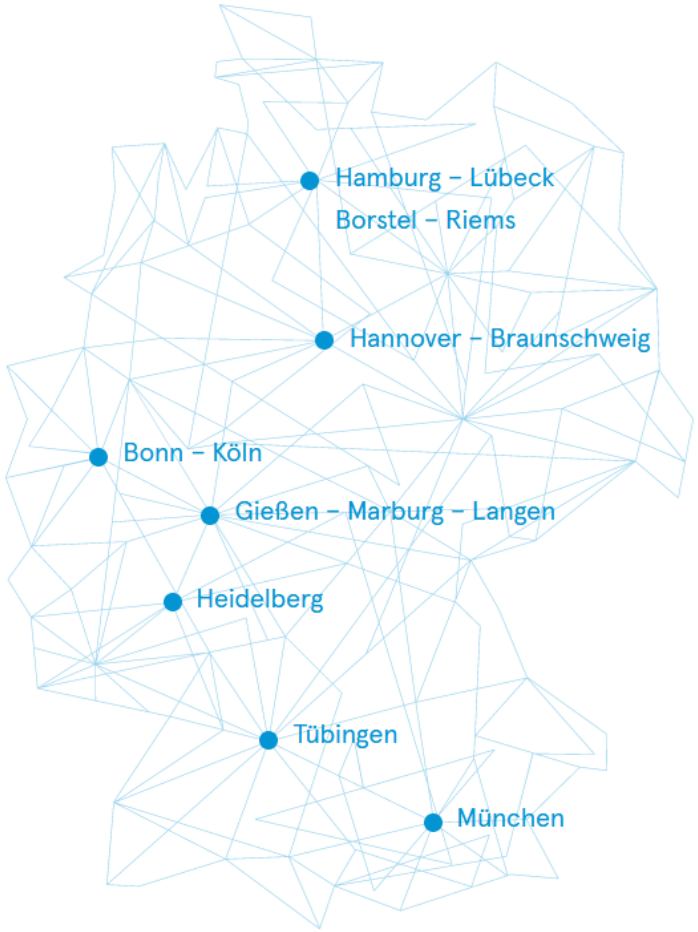
Forschungsbereich: HAARBI

Antibiotika-resistente und mit dem Gesundheitswesen assoziierte bakterielle Infektionen

Neue Strategien gegen die Entstehung und Ausbreitung von Resistenzen.

DZIF
Deutsches Zentrum
für Infektionsforschung

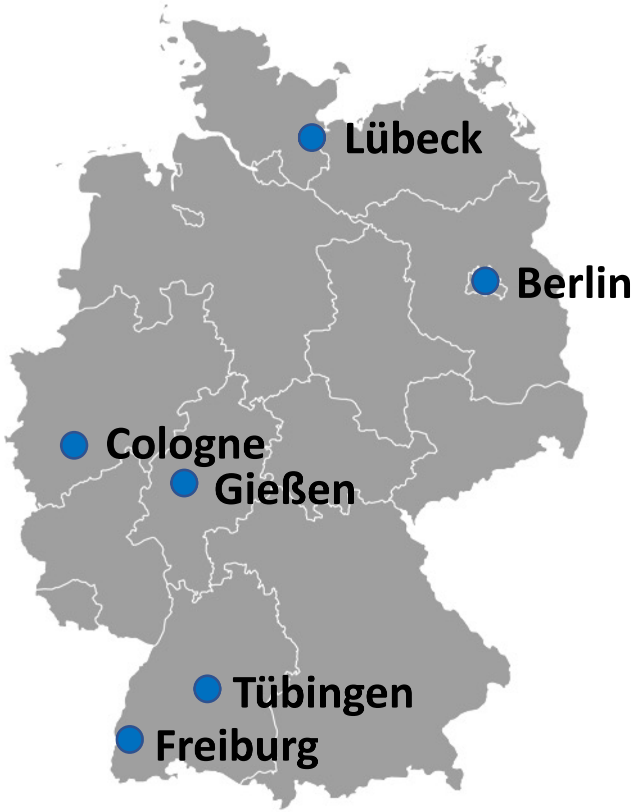
- Das **Deutsche Zentrum für Infektionsforschung (DZIF)** ist ein Zusammenschluss von über **35 Forschungsinstituten** an **7 Standorten** in ganz Deutschland, die sich der aktuellen Forschung in klar definierten thematischen Translationseinheiten (TTU) widmen.



Projekt

R-Net: Netzwerk zur Untersuchung multiresistenter Bakterien

Deutsches Zentrum für Infektionsforschung



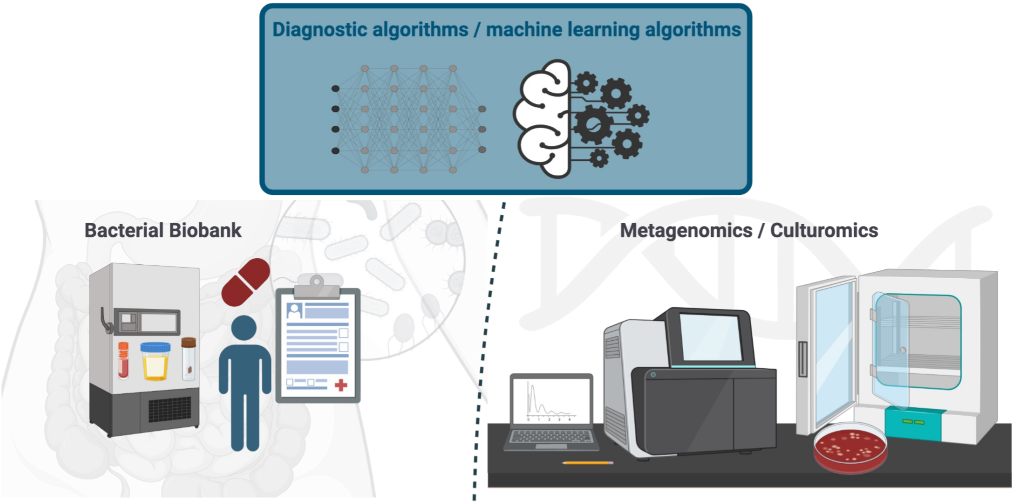
Einrichtungen

- Universität zu Köln
- Justus-Liebig-Universität Gießen
- Eberhard Karls Universität Tübingen
- Universität zu Lübeck
- Charité – Universitätsmedizin Berlin
- Universitätsklinikum Freiburg

Website:
https://www.dzif.de/en/surveillance-multidrug-resistant-bacteria-hospitals

DZIF R-Net Studie

- Resistenzdaten (Prävalenz)
- Biobank
- Datenbank/Genomische Datenbank
- Cohorte für diverse Studien



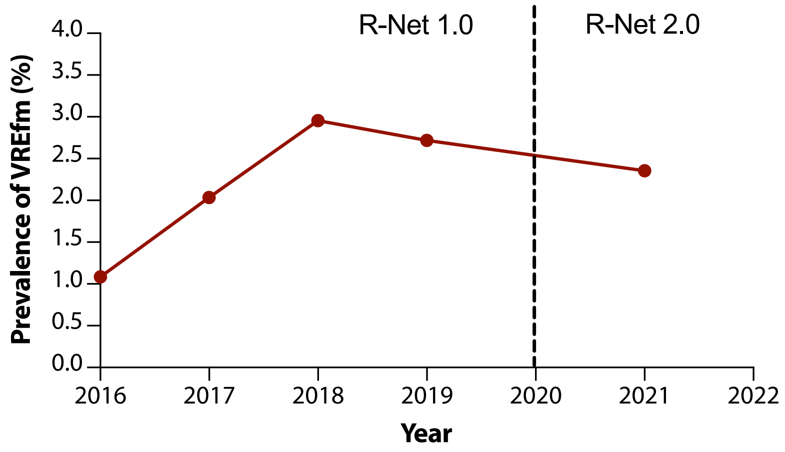
Predictions of emergence and progression of MDR and optimized treatement of patients

DZIF R-Net Studie

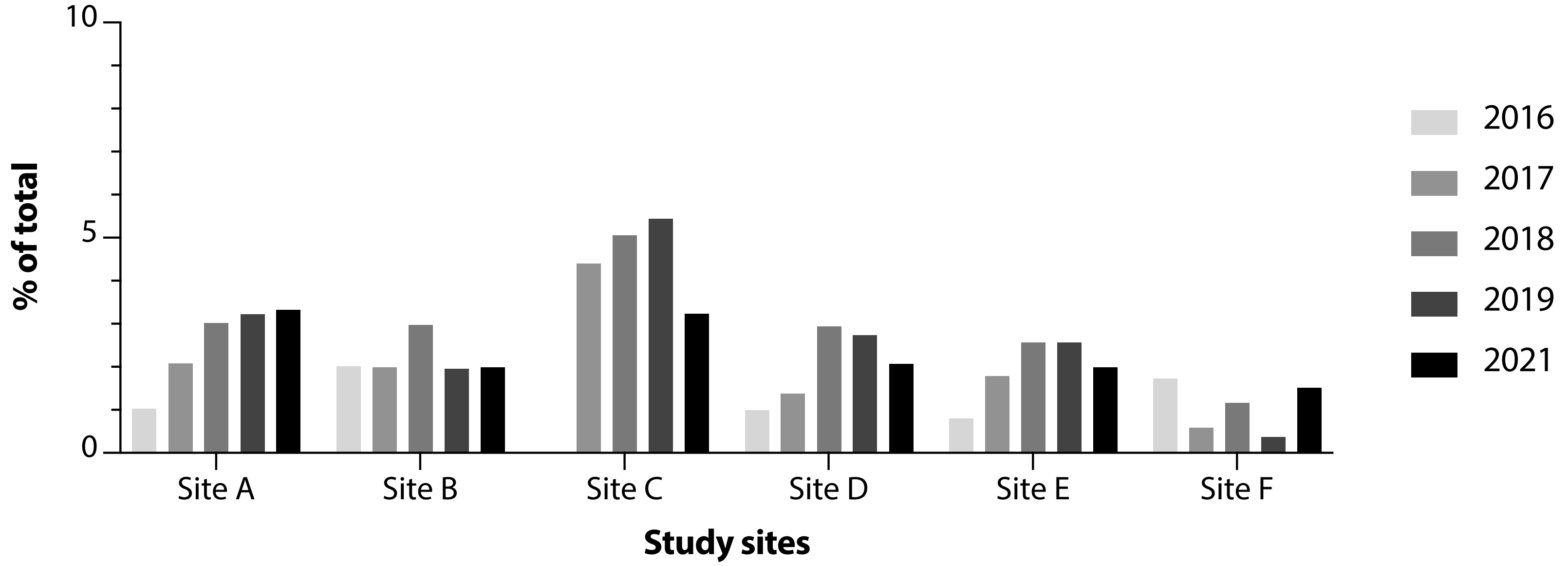
	R-Net 1.0	R-Net 2.0
Zeitraum	2016-2019	2021-2024
Ziel	MDRO Prävalenz, BSI	MDRO Prävalenz, BSI, Microbiome-Resistome
Sample size “prevalence“	• 400-500 pro Jahr pro Zentrum • 3GCREB und VRE • ≥18 J, <48 nach Aufnahme	• 400-500 pro Jahr pro Zentrum (2021 und 2023) • 3GCREB und VRE • ≥18 J, <48 nach Aufnahme
Sample size „bloodstream infection“	• 400-500 pro Jahr pro Zentrum • *S. aureus*, *Enterococcus* spp, *Enterobacter* spp, *E. coli*, *Klebsiella* spp, *P. aeruginosa* und *A. baumannii*	• 400-500 pro Jahr pro Zentrum (2022 und 2024) • *S. aureus*, *Enterococcus* spp, *Enterobacter* spp, *E. coli*, *Klebsiella* spp, *P. aeruginosa* und *A. baumannii*
Genomsequenzierung	Ausgewählte Isolate	Ausgewählte Isolate

Prävalenz / Kolonisierung bei Aufnahme

VR *E. faecium* – Trend

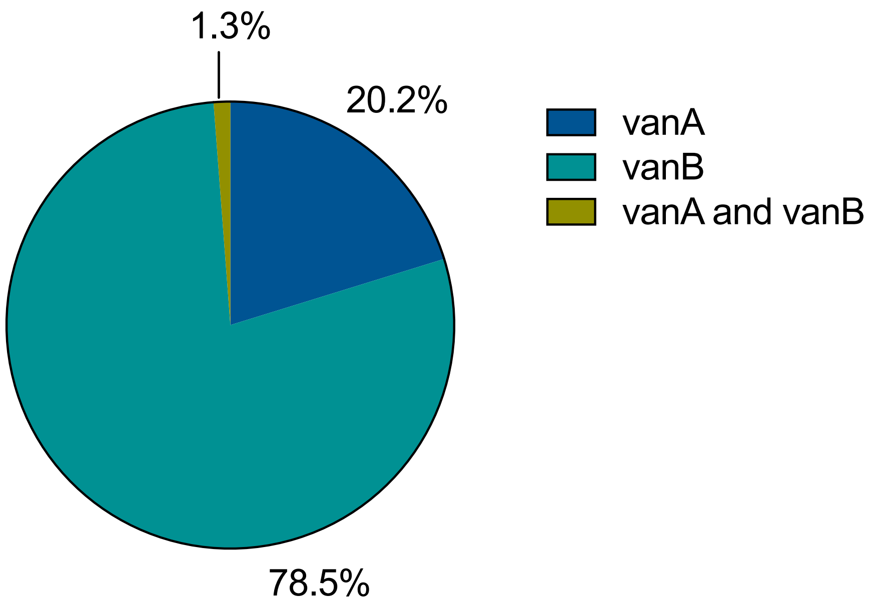


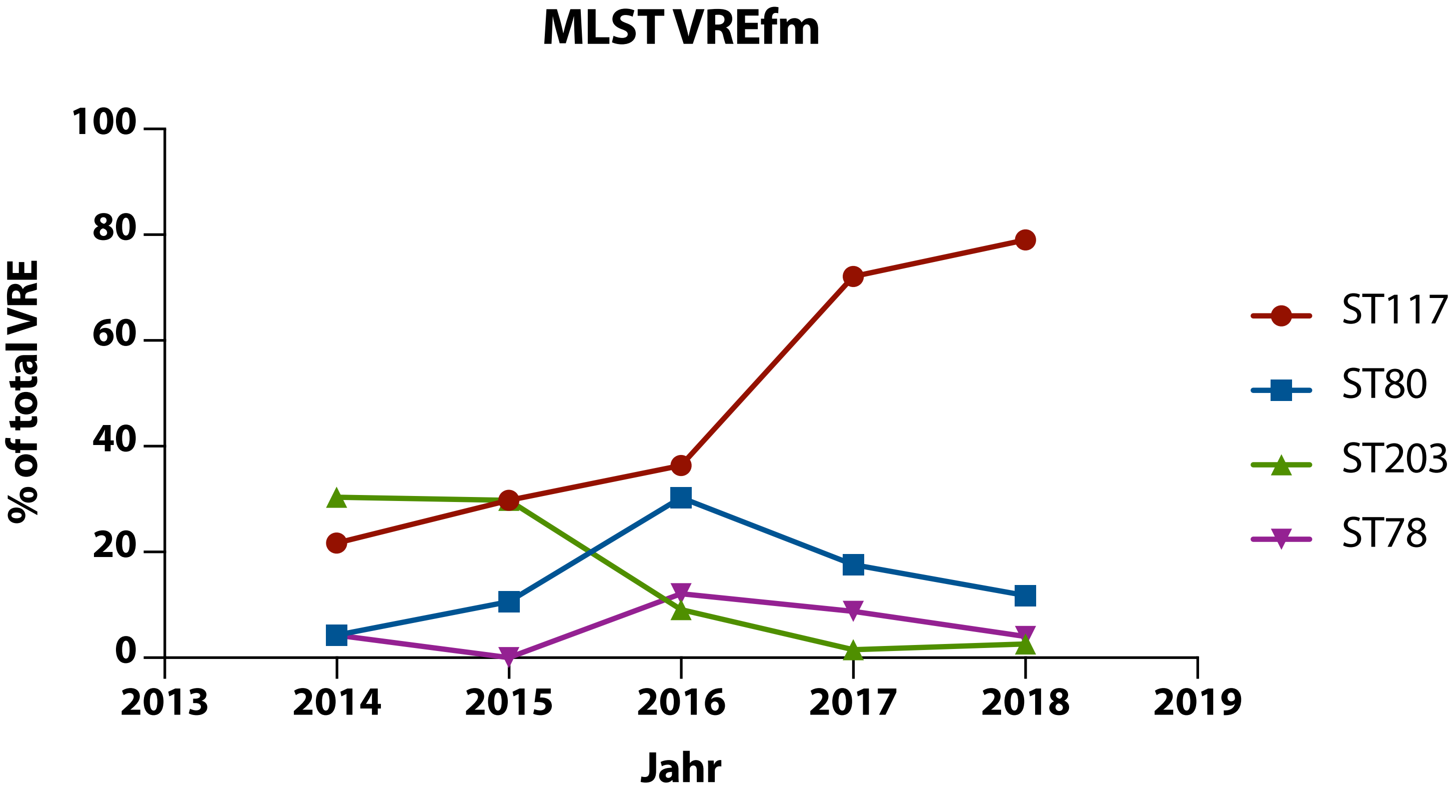
Prevalence VRE 2016-2021



DZIF R-Net, unpublished data

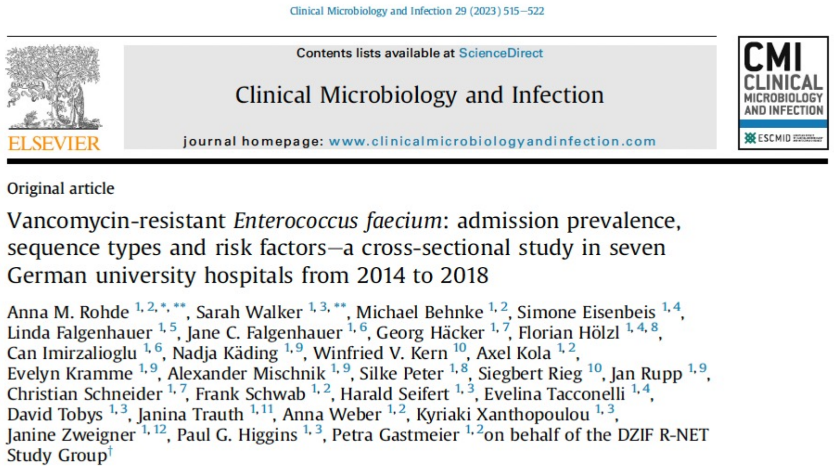
VREfm – R-Net 1.0 WGS





Modifiziert von Xanthopoulou et al, JAC 2020

VREfm – R-Net 1.0 WGS



Clinical Microbiology and Infection 29 (2023) 515–522

Contents lists available at ScienceDirect

Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com

Original article

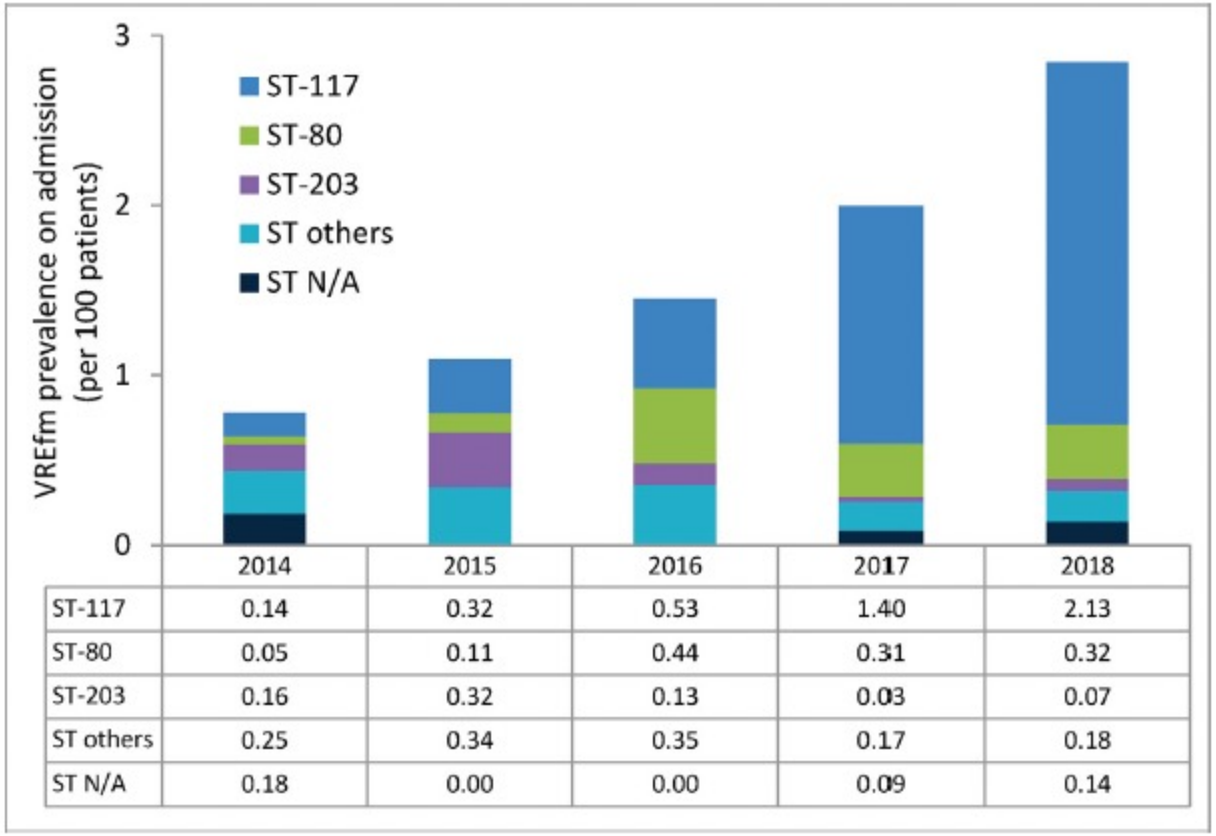
Vancomycin-resistant *Enterococcus faecium*: admission prevalence, sequence types and risk factors—a cross-sectional study in seven German university hospitals from 2014 to 2018

Anna M. Rohde [1, 2, *, **], Sarah Walker [1, 3, **], Michael Behnke [1, 2], Simone Eisenbeis [1, 4], Linda Falgenhauer [1, 5], Jane C. Falgenhauer [1, 6], Georg Häcker [1, 7], Florian Hölzl [1, 4, 8], Can Imirzalioglu [1, 6], Nadja Käding [1, 9], Winfried V. Kern [10], Axel Kola [1, 2], Evelyn Kramme [1, 9], Alexander Mischnik [1, 9], Silke Peter [1, 8], Siegbert Rieg [10], Jan Rupp [1, 9], Christian Schneider [1, 7], Frank Schwab [1, 2], Harald Seifert [1, 3], Evelina Tacconelli [1, 4], David Tobys [1, 3], Janina Trauth [1, 11], Anna Weber [1, 2], Kyriaki Xanthopoulou [1, 3], Janine Zweigner [1, 12], Paul G. Higgins [1, 3], Petra Gastmeier [1, 2] on behalf of the DZIF R-NET Study Group[†]

Risikofaktoren:
Alter
Kontakt zu Gesundheitseinrichtungen
Antibiotika
PPI/Antazida

VREfm Kolonisationsprävalenz bei Aufnahme +33% pro Jahr

→ ST117



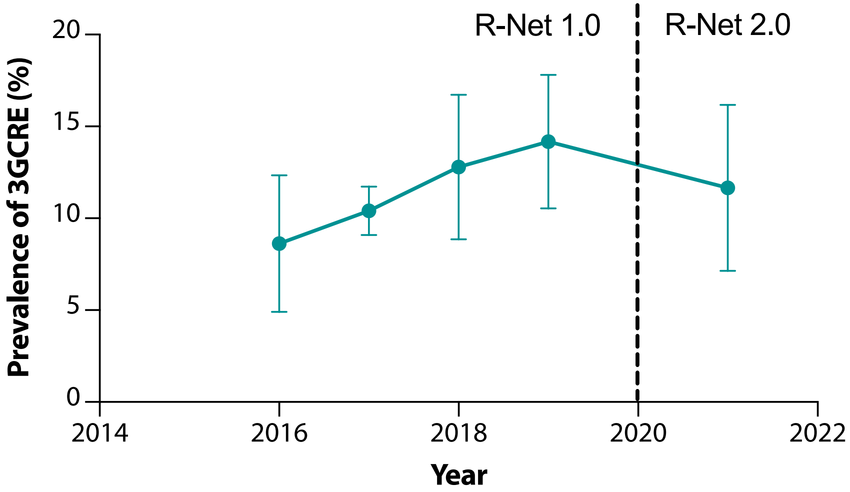
	2014	2015	2016	2017	2018
ST-117	0.14	0.32	0.53	1.40	2.13
ST-80	0.05	0.11	0.44	0.31	0.32
ST-203	0.16	0.32	0.13	0.03	0.07
ST others	0.25	0.34	0.35	0.17	0.18
ST N/A	0.18	0.00	0.00	0.09	0.14

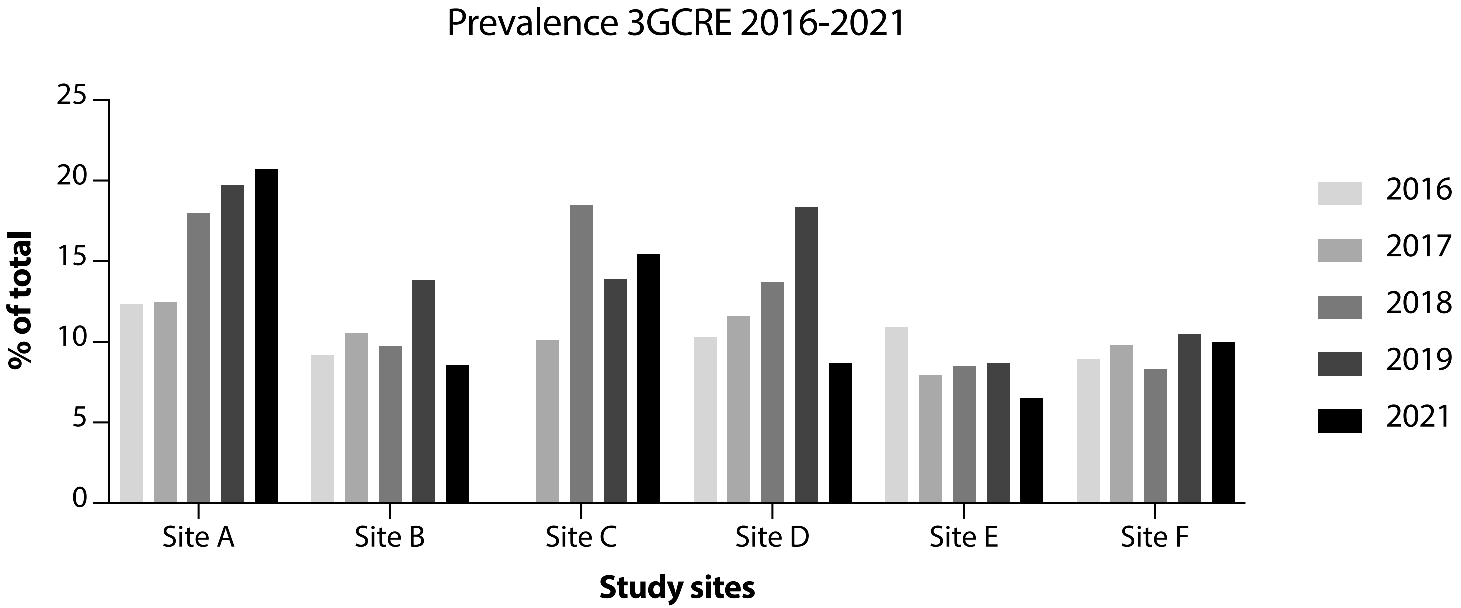
Zwischenergebnis R-Net 2.0, Prevalence 2021

Study site	**non-MDRO**		**3GCRE**		**CRGN**		**VRE**		**Total**
	n	**%**	**n**	**%**	**n**	**%**	**n**	**%**	
Site A	418	77.3%	93	17.2%	12	2.2%	18	3.3%	541
Site B	428	88.8%	38	7.9%	6	1.2%	10	2.1%	482
Site C	443	84.4%	55	10.5%	10	1.9%	17	3.2%	525
Site D	449	89.4%	40	8.0%	3	0.6%	10	2.0%	502
Site E	461	91.5%	27	5.4%	6	1.2%	10	2.0%	504
Site F	469	88.5%	45	8.5%	8	1.5%	8	1.5%	530
Total	**2,668**	**86.5%**	**298**	**9.7%**	**45**	**1.5%**	**73**	**2.4%**	**3,084**

DZIF R-Net, unpublished data

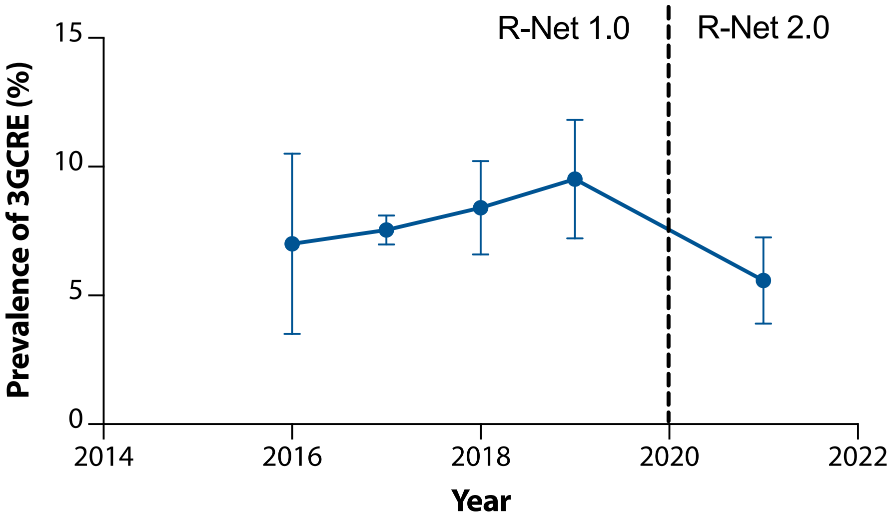
3GCRE* 2016-2021

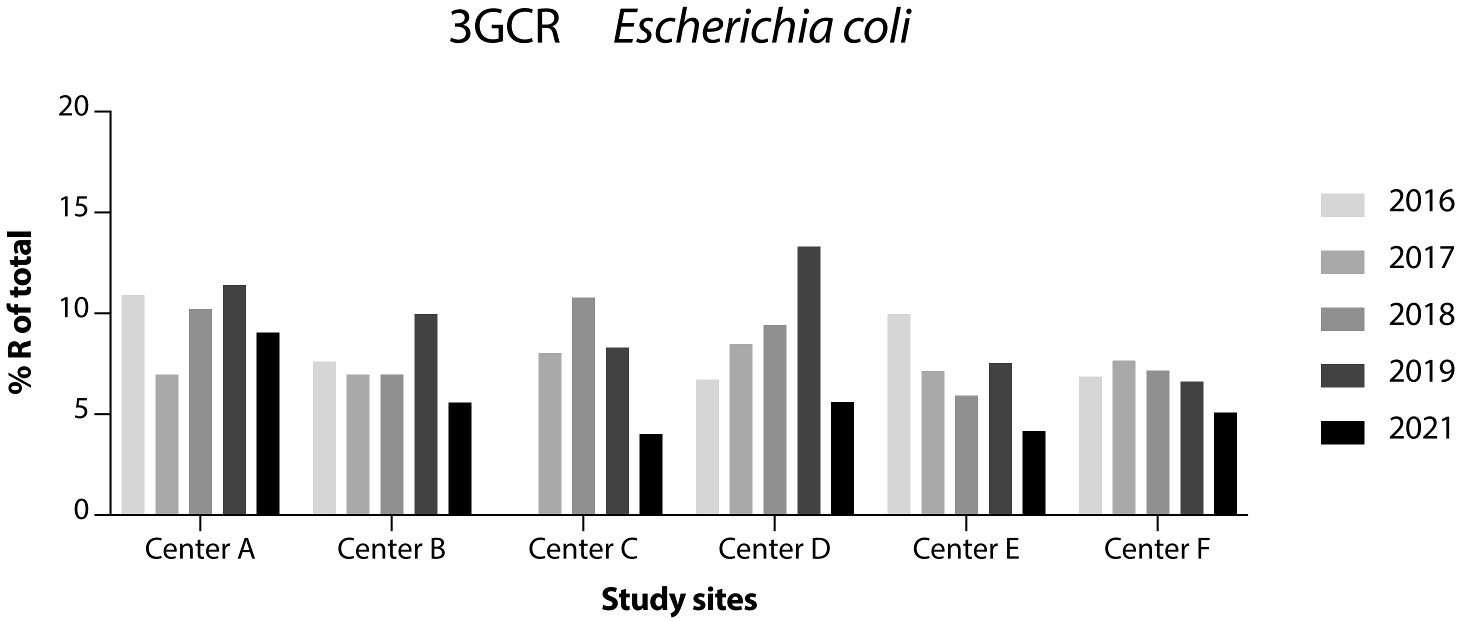




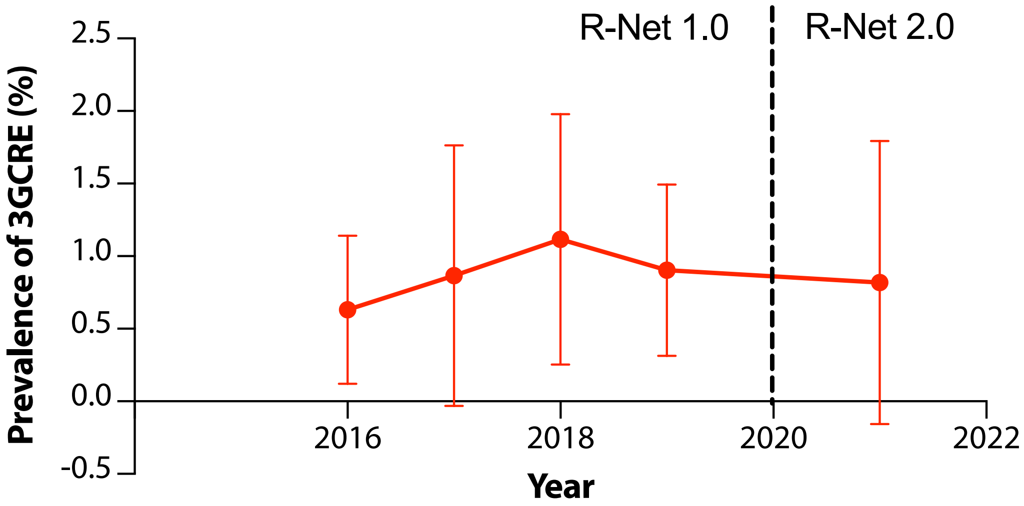
*3GCRE=3. Generation Cephalosporin-resistente Enterobacterales

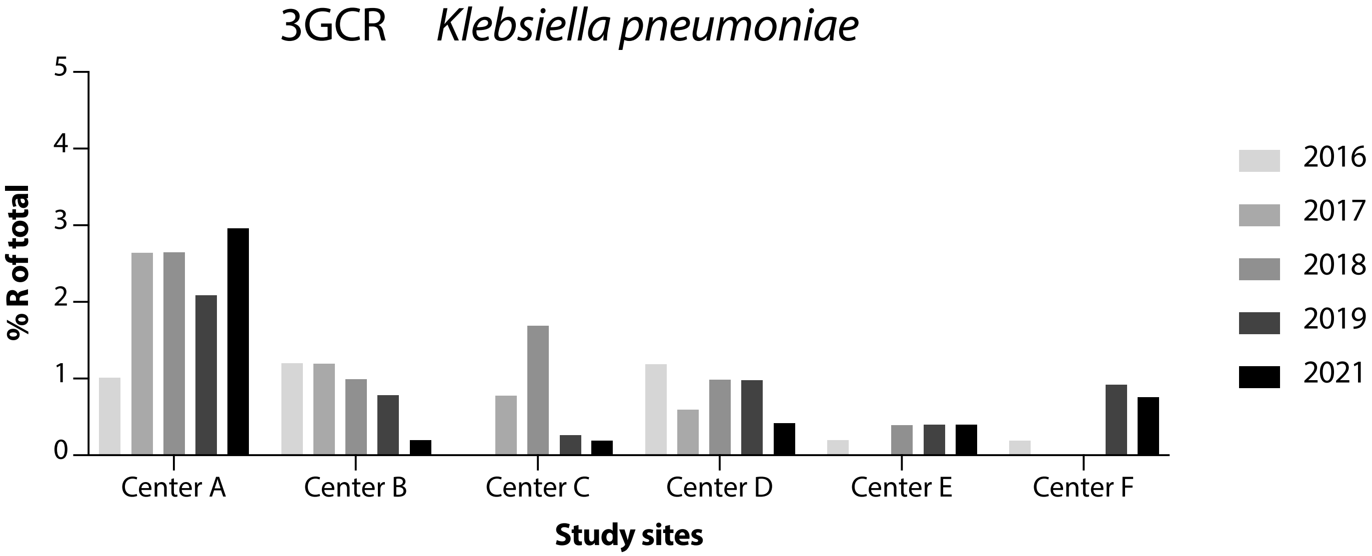
3GCR *E. coli* 2016-2021



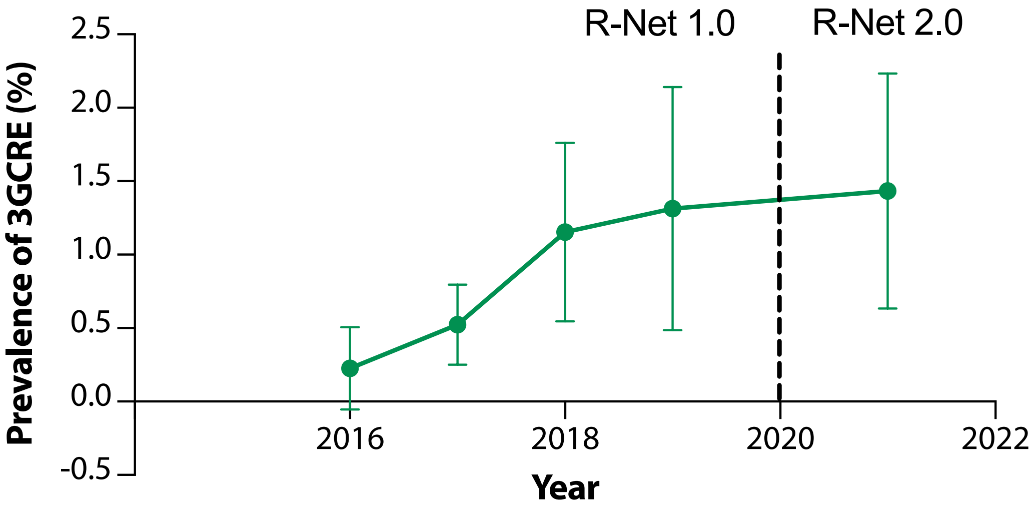


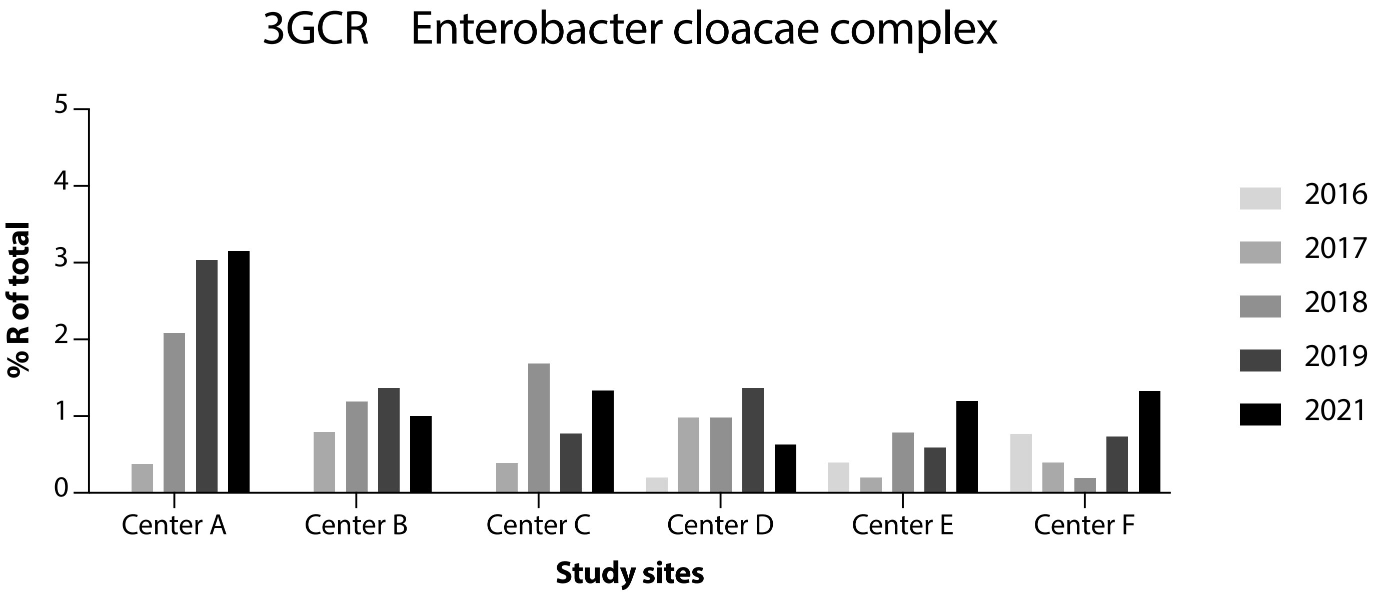
3GCR *K. pneumoniae* 2016-2021



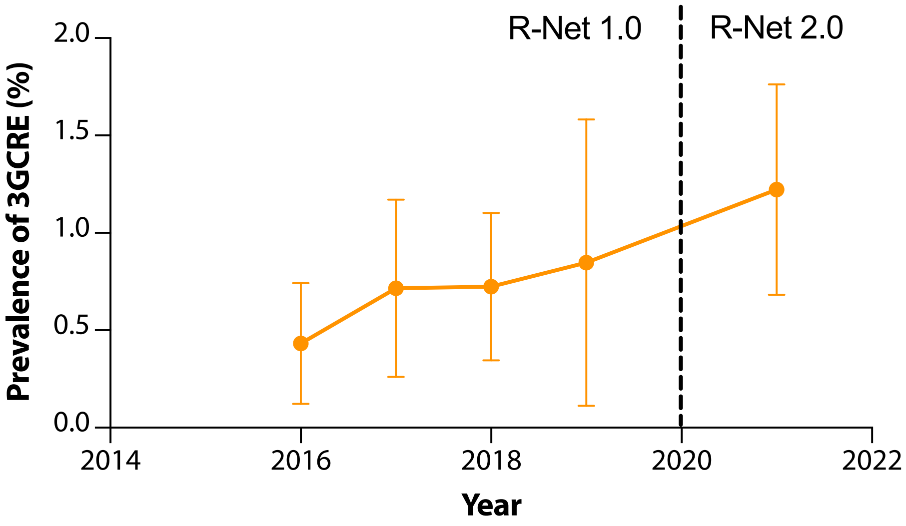


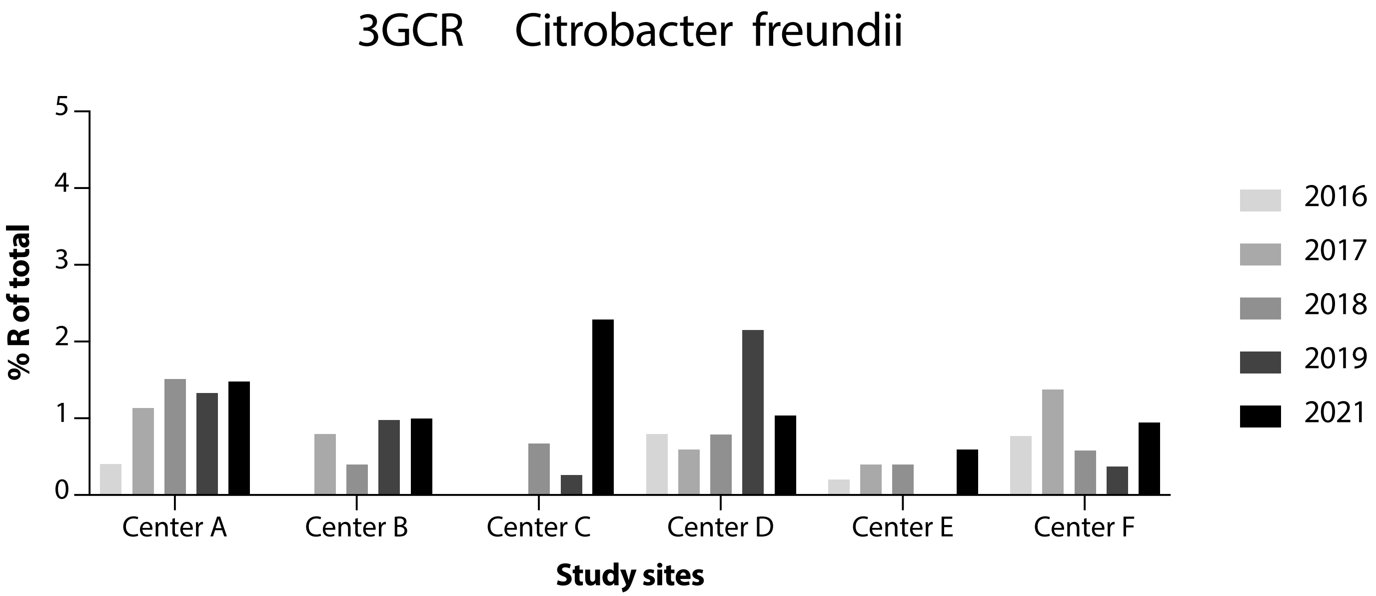
3GCR *E. cloacae* complex 2016-2021



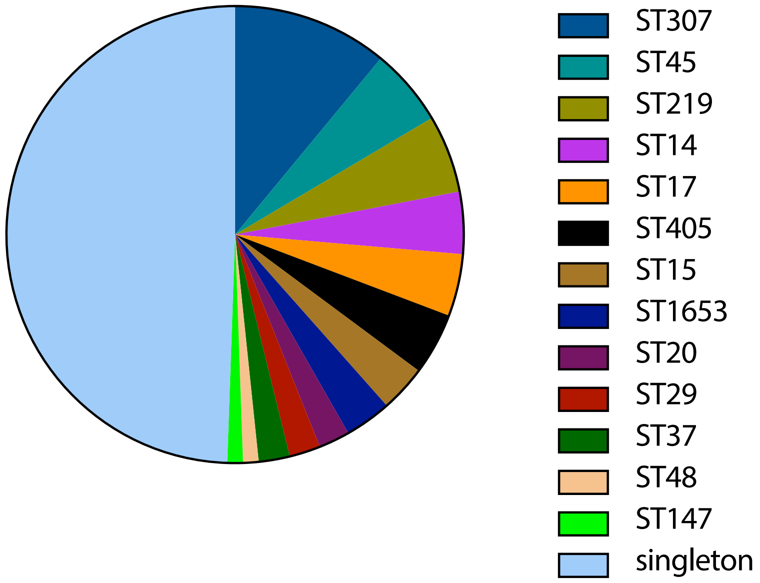


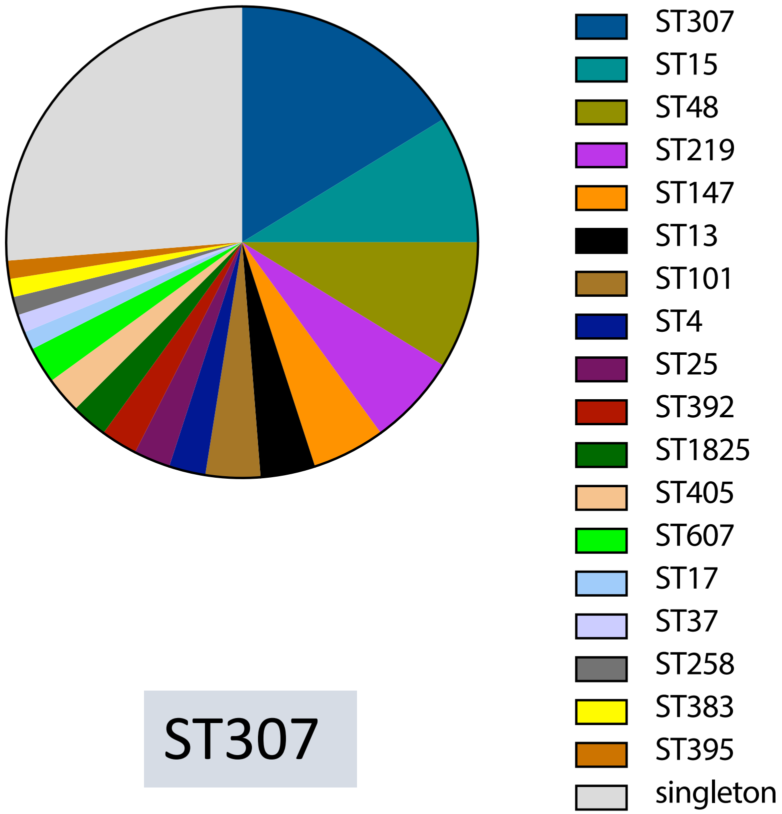
3GCR *Citrobacter freundii* 2016-2021

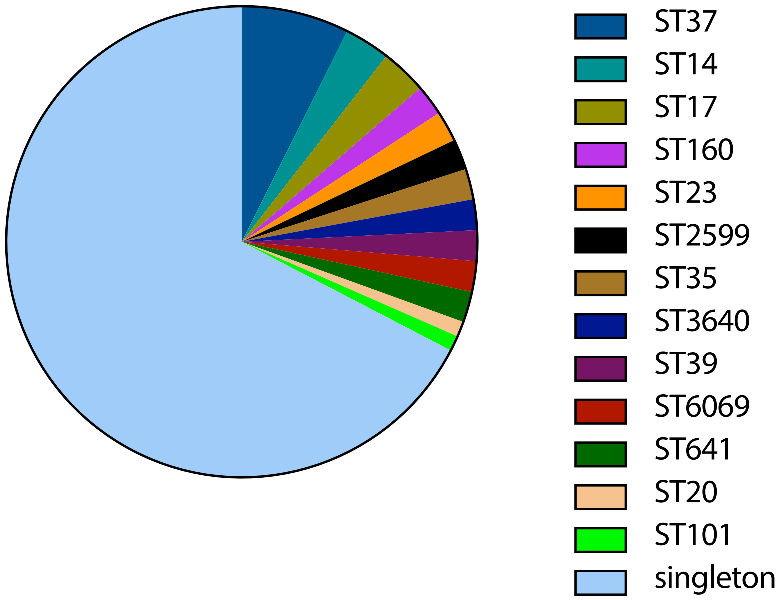




WGS *Klebsiella pneumoniae*


Kolonisierungsstämme


BSI 3GCR/CR-E


BSI 3GCs/CS-E

ST307

Modifiziert von Xanthopoulou et al, Antibiotics 2022

WGS *Klebsiella pneumoniae*

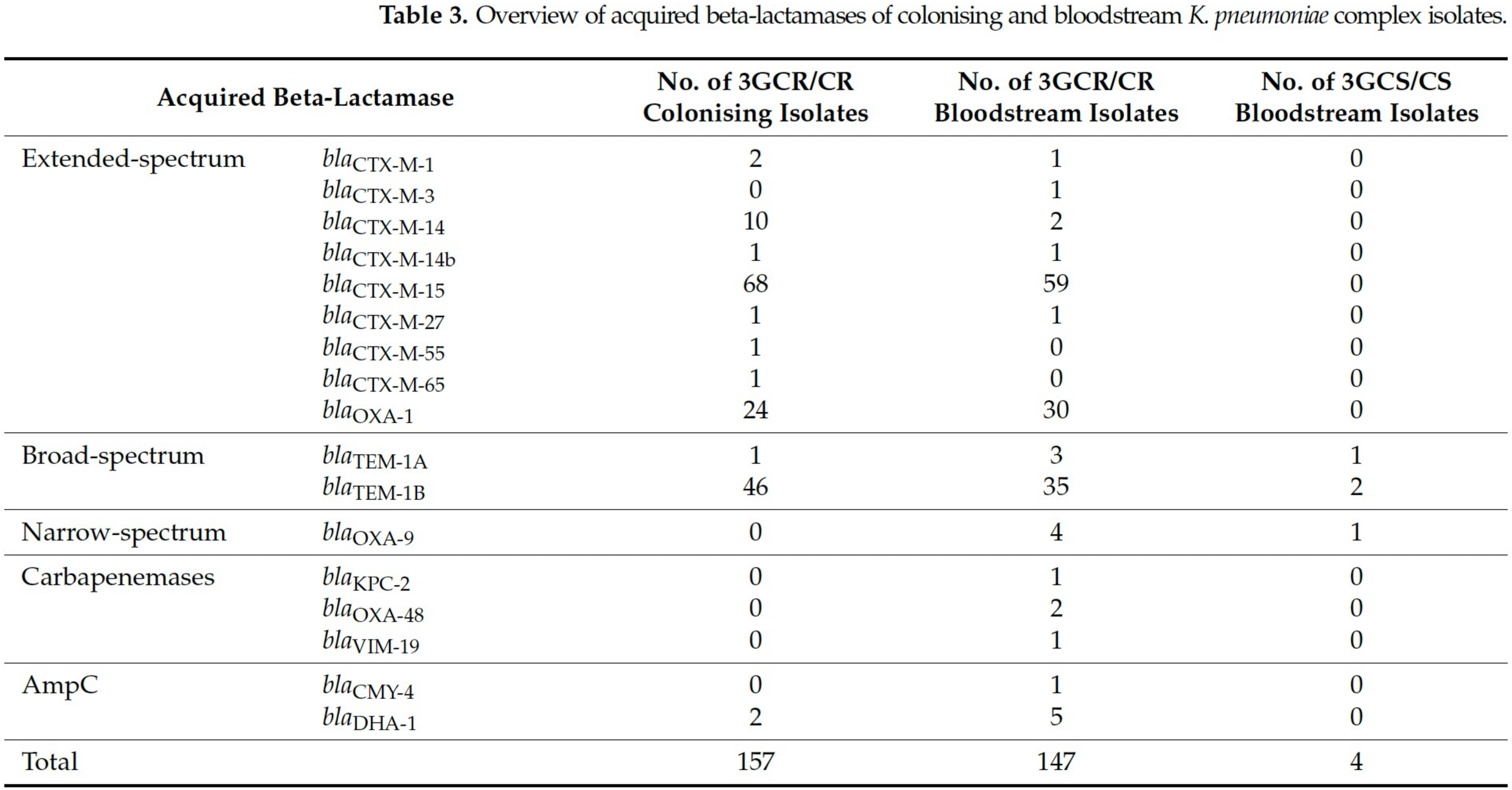
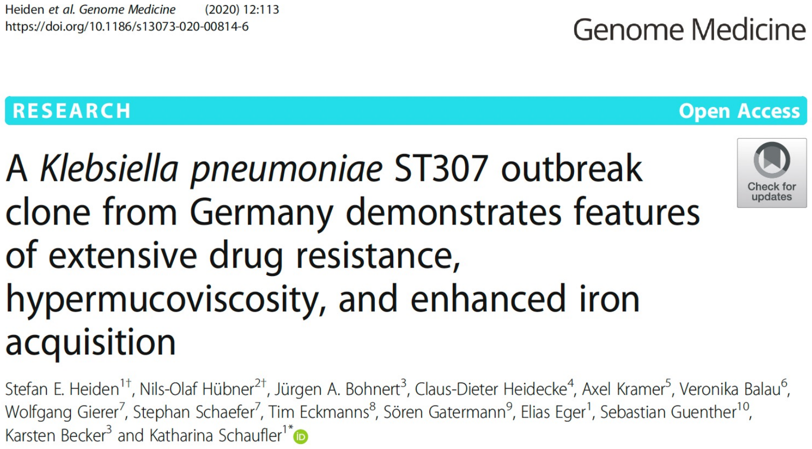


Table 3. Overview of acquired beta-lactamases of colonising and bloodstream *K. pneumoniae* complex isolates.

Acquired Beta-Lactamase		No. of 3GCR/CR Colonising Isolates	No. of 3GCR/CR Bloodstream Isolates	No. of 3GCS/CS Bloodstream Isolates
Extended-spectrum	$bla_{\text{CTX-M-1}}$	2	1	0
	$bla_{\text{CTX-M-3}}$	0	1	0
	$bla_{\text{CTX-M-14}}$	10	2	0
	$bla_{\text{CTX-M-14b}}$	1	1	0
	$bla_{\text{CTX-M-15}}$	68	59	0
	$bla_{\text{CTX-M-27}}$	1	1	0
	$bla_{\text{CTX-M-55}}$	1	0	0
	$bla_{\text{CTX-M-65}}$	1	0	0
	$bla_{\text{OXA-1}}$	24	30	0
Broad-spectrum	$bla_{\text{TEM-1A}}$	1	3	1
	$bla_{\text{TEM-1B}}$	46	35	2
Narrow-spectrum	$bla_{\text{OXA-9}}$	0	4	1
Carbapenemases	$bla_{\text{KPC-2}}$	0	1	0
	$bla_{\text{OXA-48}}$	0	2	0
	$bla_{\text{VIM-19}}$	0	1	0
AmpC	$bla_{\text{CMY-4}}$	0	1	0
	$bla_{\text{DHA-1}}$	2	5	0
Total		157	147	4

Xanthopoulou et al, Antibiotics 2022

ST307 *Klebsiella pneumoniae*



Heiden *et al. Genome Medicine* (2020) 12:113
https://doi.org/10.1186/s13073-020-00814-6

Genome Medicine

RESEARCH Open Access

A *Klebsiella pneumoniae* ST307 outbreak clone from Germany demonstrates features of extensive drug resistance, hypermucoviscosity, and enhanced iron acquisition

Stefan E. Heiden[1†], Nils-Olaf Hübner[2†], Jürgen A. Bohnert[3], Claus-Dieter Heidecke[4], Axel Kramer[5], Veronika Balau[6], Wolfgang Gierer[7], Stephan Schaefer[7], Tim Eckmanns[8], Sören Gatermann[9], Elias Eger[1], Sebastian Guenther[10], Karsten Becker[3] and Katharina Schaufler[1*]

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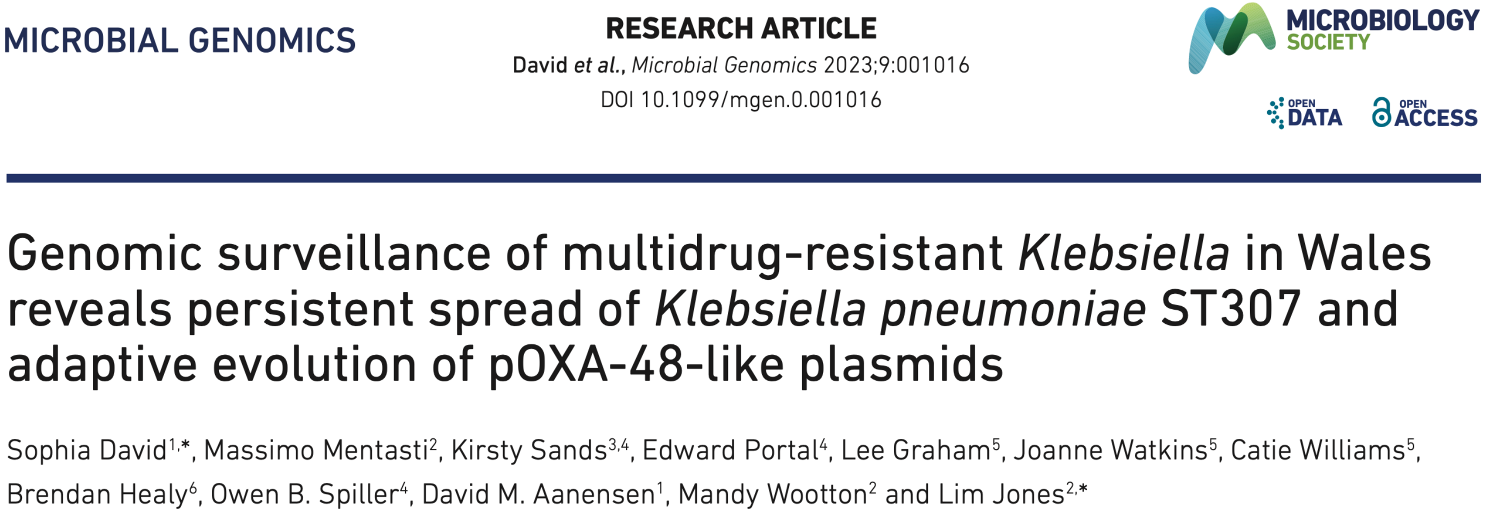
MINIREVIEW

Emerging Antimicrobial-Resistant High-Risk *Klebsiella pneumoniae* Clones ST307 and ST147

Gisele Peirano,[a,b] Liang Chen,[c,d] Barry N. Kreiswirth,[c,d] Johann D. D. Pitout[a,b,e]



MICROBIAL GENOMICS

RESEARCH ARTICLE
David *et al.*, *Microbial Genomics* 2023;9:001016
DOI 10.1099/mgen.0.001016

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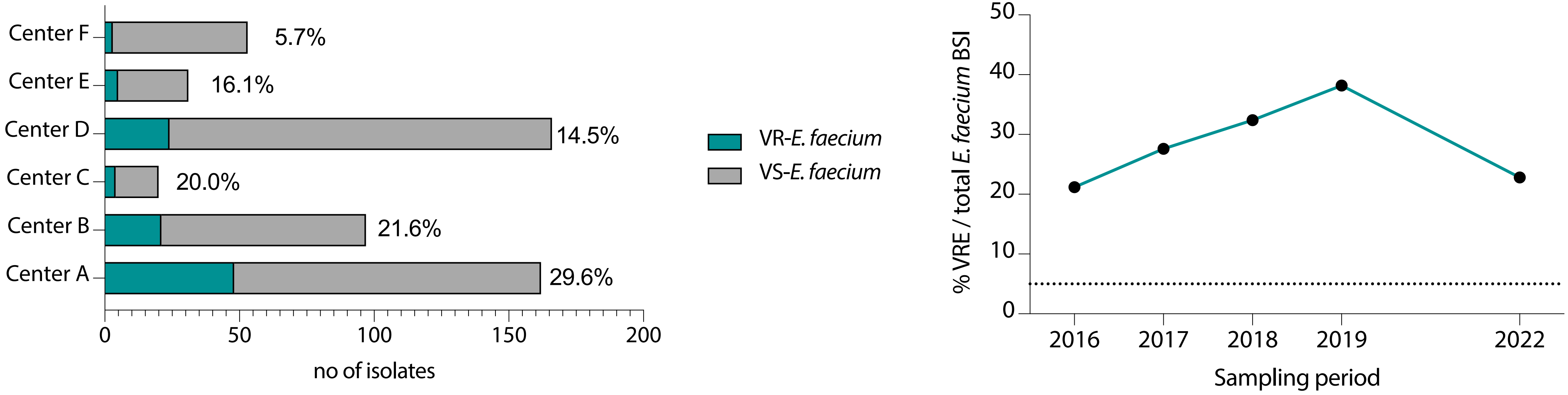
Genomic surveillance of multidrug-resistant *Klebsiella* in Wales reveals persistent spread of *Klebsiella pneumoniae* ST307 and adaptive evolution of pOXA-48-like plasmids

Sophia David[1,*], Massimo Mentasti[2], Kirsty Sands[3,4], Edward Portal[4], Lee Graham[5], Joanne Watkins[5], Catie Williams[5], Brendan Healy[6], Owen B. Spiller[4], David M. Aanensen[1], Mandy Wootton[2] and Lim Jones[2,*]

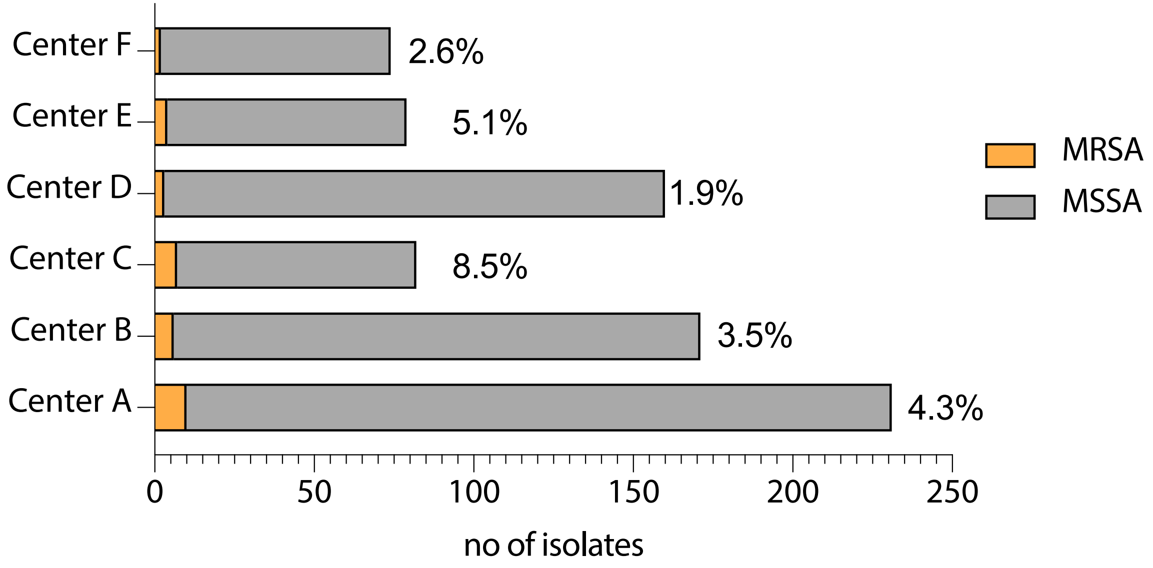
Blutstrominfektionen (BSI)

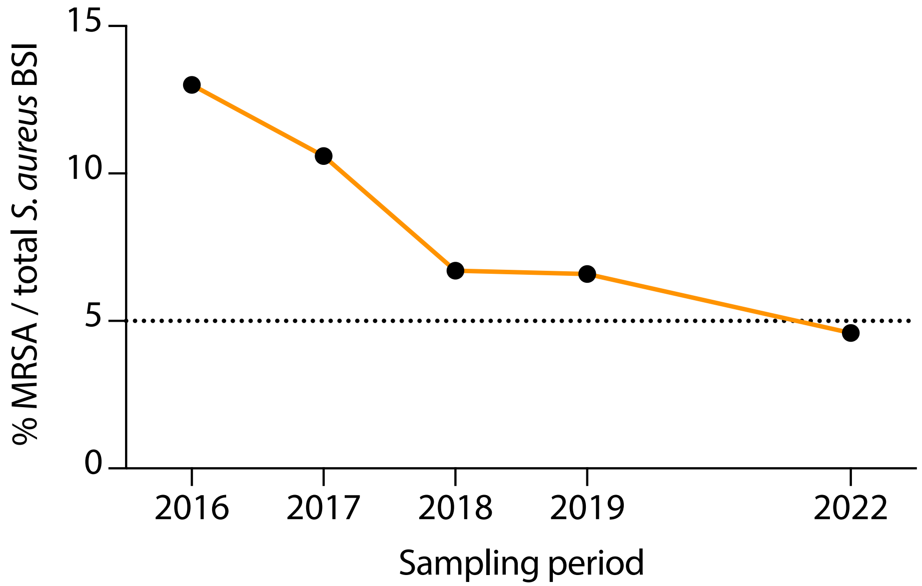
Enterococcus faecium – BSI



DZIF R-Net, unpublished data

Staphylococcus aureus – BSI





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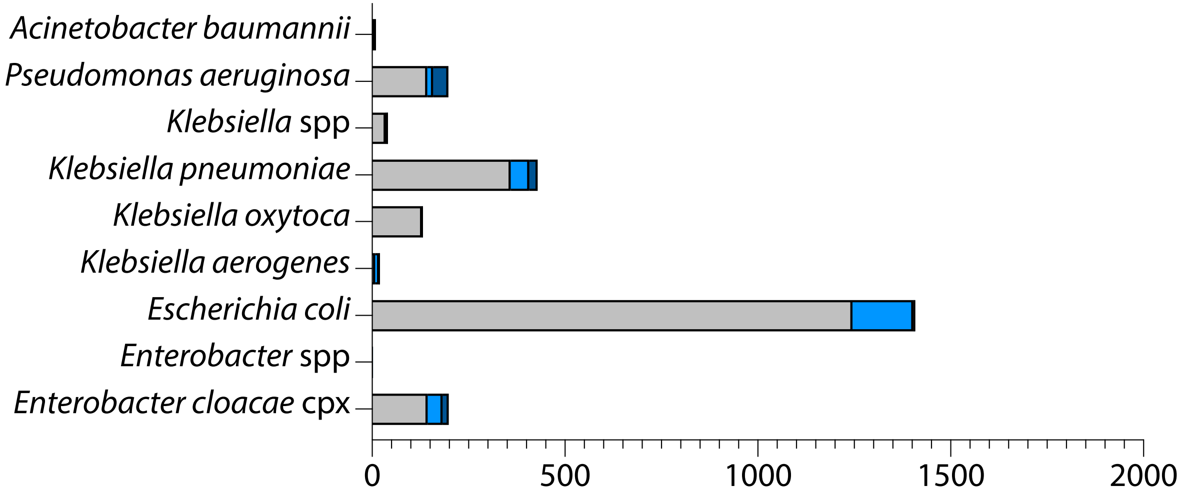
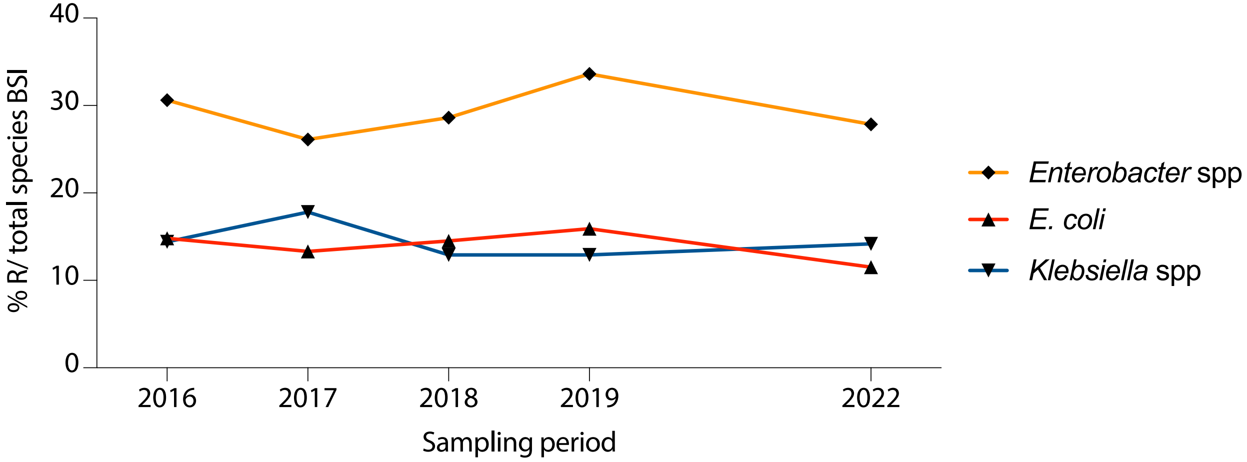
Enterobacterales – BSI





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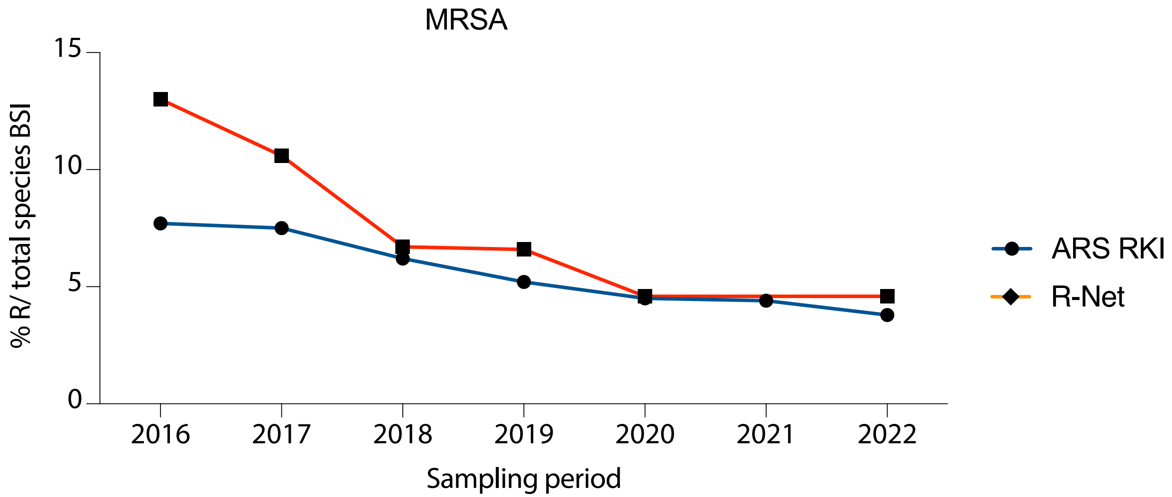
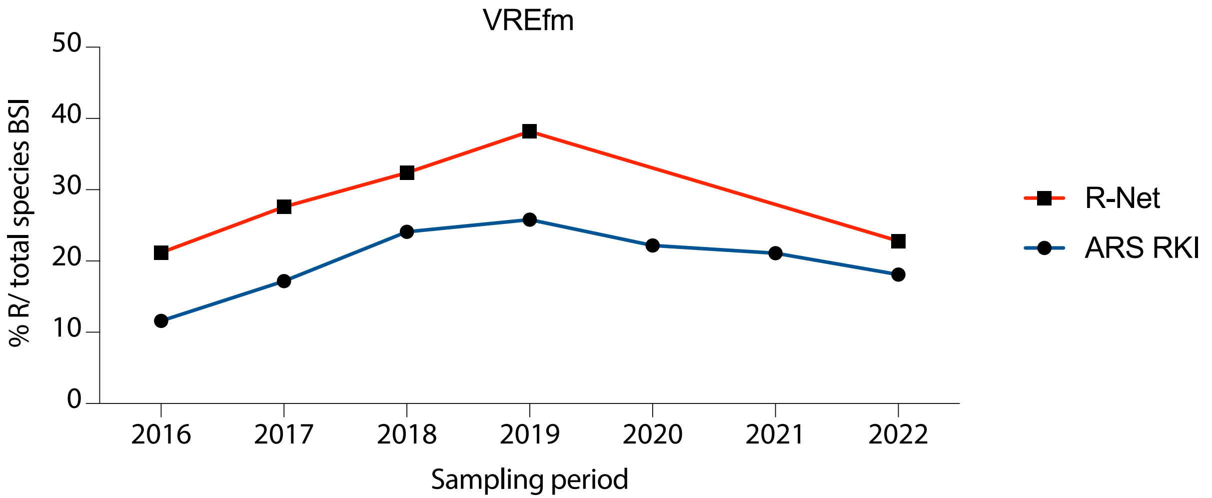
ARS (RKI) vs R-Net





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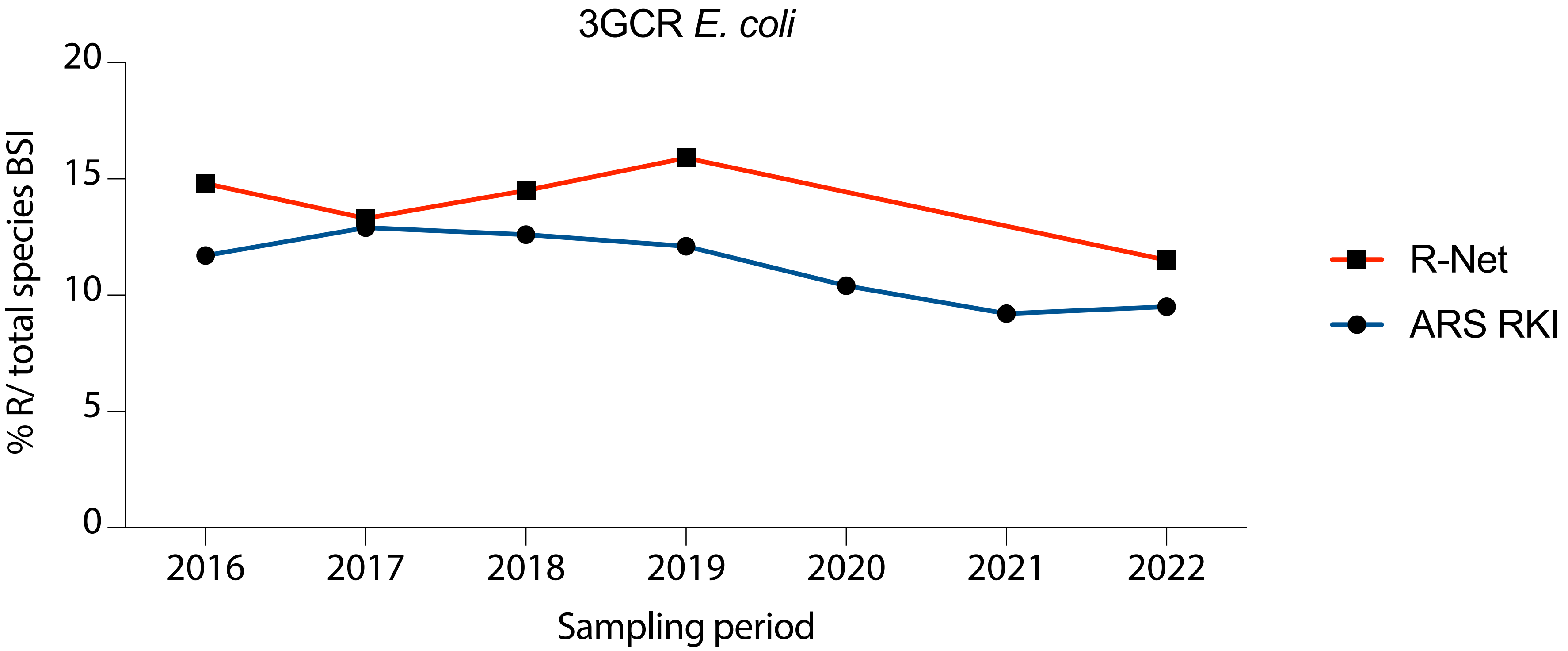

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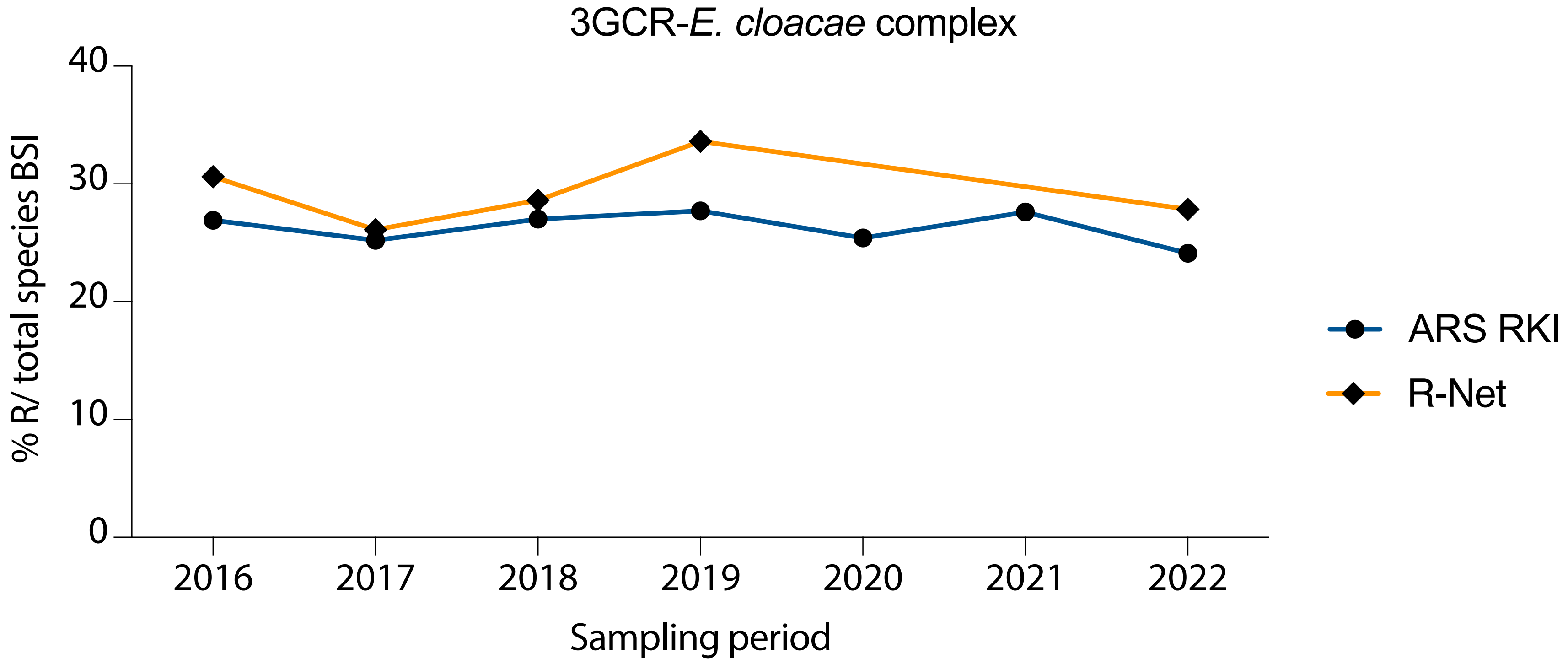

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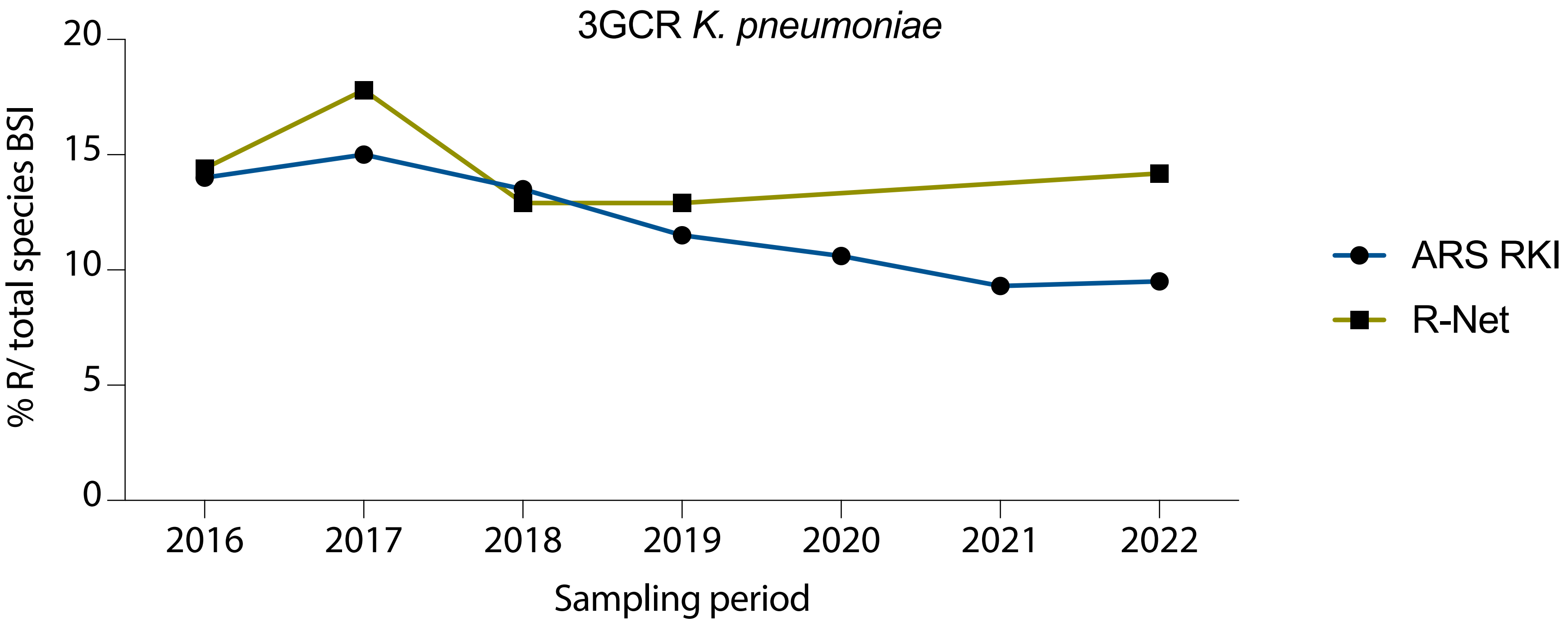
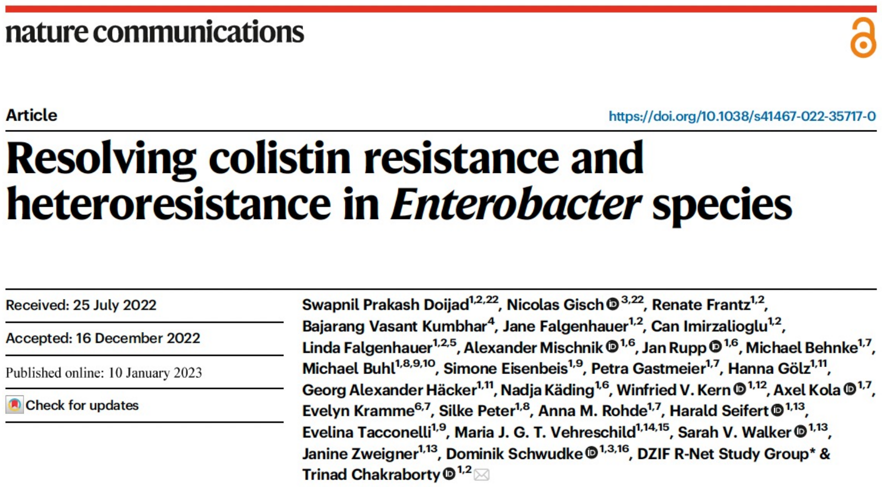


ARS (RKI) vs R-Net



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Resolving colistin resistance and heteroresistance in *Enterobacter* species

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Check for updates

Swapnil Prakash Doijad[1,2,22], Nicolas Gisch[3,22], Renate Frantz[1,2], Bajarang Vasant Kumbhar[4], Jane Falgenhauer[1,2], Can Imirzalioglu[1,2], Linda Falgenhauer[1,2,5], Alexander Mischnik[1,6], Jan Rupp[1,6], Michael Behnke[1,7], Michael Buhl[1,8,9,10], Simone Eisenbeis[1,9], Petra Gastmeier[1,7], Hanna Gölz[1,11], Georg Alexander Häcker[1,11], Nadja Käding[1,6], Winfried V. Kern[1,12], Axel Kola[1,7], Evelyn Kramme[6,7], Silke Peter[1,8], Anna M. Rohde[1,7], Harald Seifert[1,13], Evelina Tacconelli[1,9], Maria J. G. T. Vehreschild[1,14,15], Sarah V. Walker[1,13], Janine Zweigner[1,13], Dominik Schwudke[1,3,16], DZIF R-Net Study Group* & Trinad Chakraborty[1,2] ✉

JOURNAL ARTICLE

Association of ward-level antibiotic consumption with healthcare-associated *Clostridioides difficile* infections: an ecological study in five German university hospitals, 2017–2019

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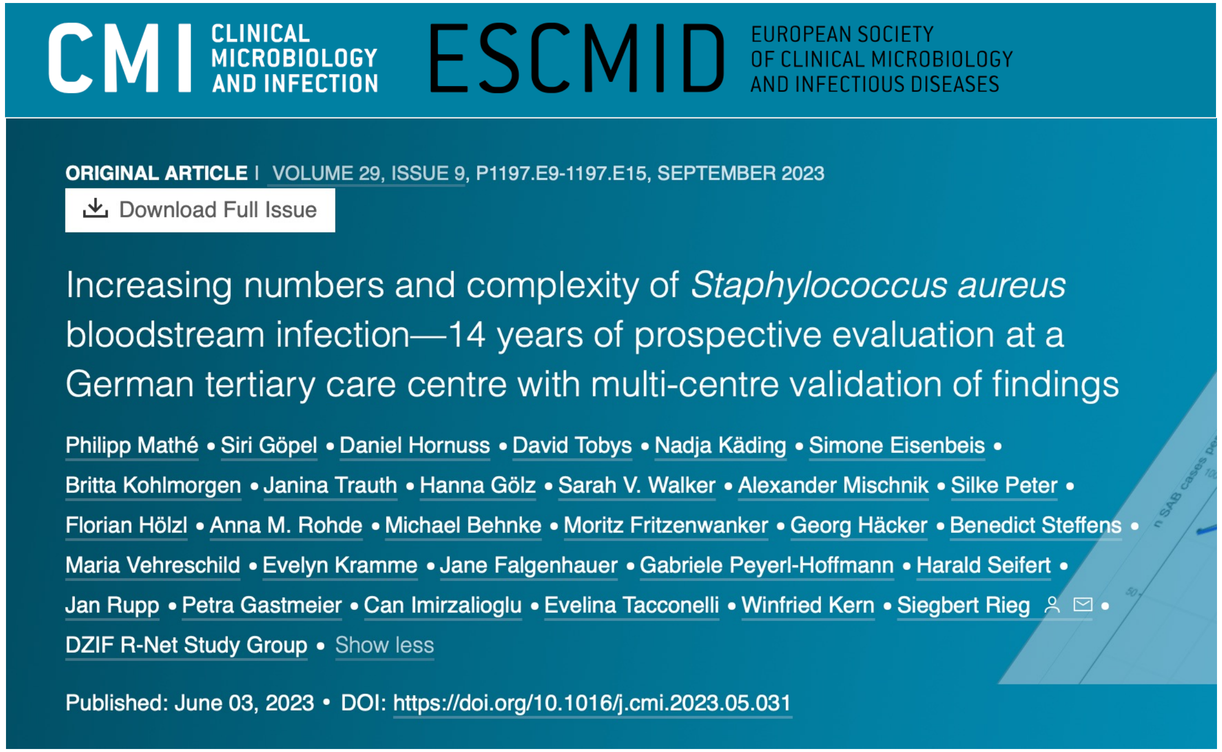

CMI CLINICAL MICROBIOLOGY AND INFECTION ESCMID EUROPEAN SOCIETY OF CLINICAL MICROBIOLOGY AND INFECTIOUS DISEASES

ORIGINAL ARTICLE | VOLUME 29, ISSUE 9, P1197.E9-1197.E15, SEPTEMBER 2023

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Increasing numbers and complexity of *Staphylococcus aureus* bloodstream infection—14 years of prospective evaluation at a German tertiary care centre with multi-centre validation of findings

Philipp Mathé • Siri Göpel • Daniel Hornuss • David Tobys • Nadja Käding • Simone Eisenbeis • Britta Kohlmorgen • Janina Trauth • Hanna Gölz • Sarah V. Walker • Alexander Mischnik • Silke Peter • Florian Hölzl • Anna M. Rohde • Michael Behnke • Moritz Fritzenwanker • Georg Häcker • Benedict Steffens • Maria Vehreschild • Evelyn Kramme • Jane Falgenhauer • Gabriele Peyerl-Hoffmann • Harald Seifert • Jan Rupp • Petra Gastmeier • Can Imirzalioglu • Evelina Tacconelli • Winfried Kern • Siegbert Rieg ✉ • DZIF R-Net Study Group • Show less

Published: June 03, 2023 • DOI: https://doi.org/10.1016/j.cmi.2023.05.031

Zusammenfassung

- Fallstricke – Resistenzstatistik / Nenner / Bias

- DZIF R-Net Prävelenzdaten (Kolonisierung):
  - Zunahme VREfm → ST117
  - 3GCRE: *Enterobacter* spp und *Citrobacter* spp
  - CRE: Prävalenz sehr niedrig

- Isolate verfügbar → Nutzungsvereinbarung DZIF

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Gießen-Marburg-Langen: Torsten Hain, Can Imirzaglioglu

Berlin: Petra Gastmeier

Tübingen: Silke Peter, Siri Göpel

Freiburg: Siegbert Rieg

Vielen Dank an die R-Net Study Sites

Fragen?

Vielen Dank für Ihre Aufmerksamkeit