



# Linezolid-resistente *S. epidermidis* in Deutschland

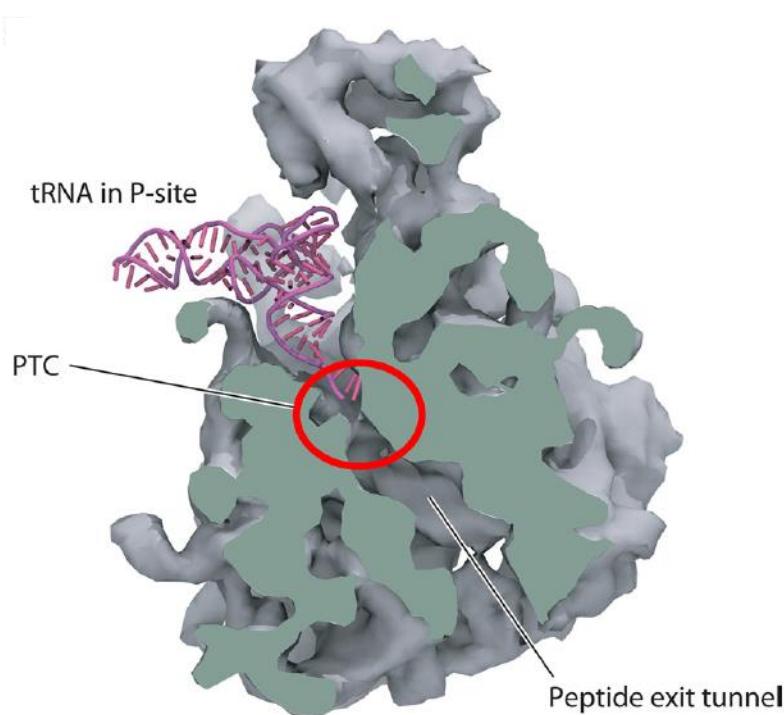
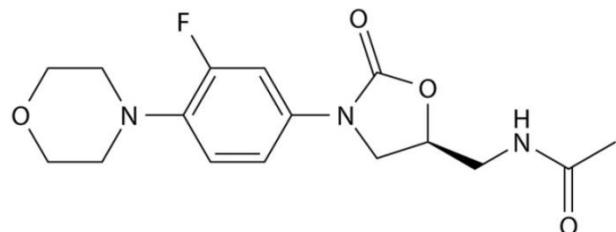
Franziska Layer

NRZ für Staphylokokken und Enterokokken  
FG 13 Nosokomiale Infektionserreger und  
Antibiotikaresistenzen, Abt. Infektionskrankheiten  
Robert Koch-Institut, Bereich Wernigerode

Bonn, 26.03.2018



# Linezolid



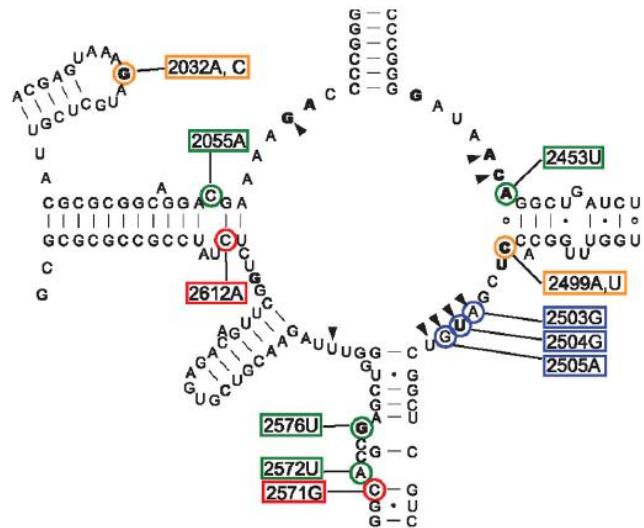
Long & Vester, Antimicrob. Agents Chemother. 2012

- Reserveantibiotikum aus der Klasse der Oxazolidinone
- Hemmung der Proteinsynthese
- bindet spezifisch an die 23S rRNA der 50S-Untereinheit des bakteriellen Ribosoms  
(PTC Peptidyl-Transferase-Center)

# Linezolidresistenz

- verursacht durch Mutationen und/ oder den Erwerb von Genen

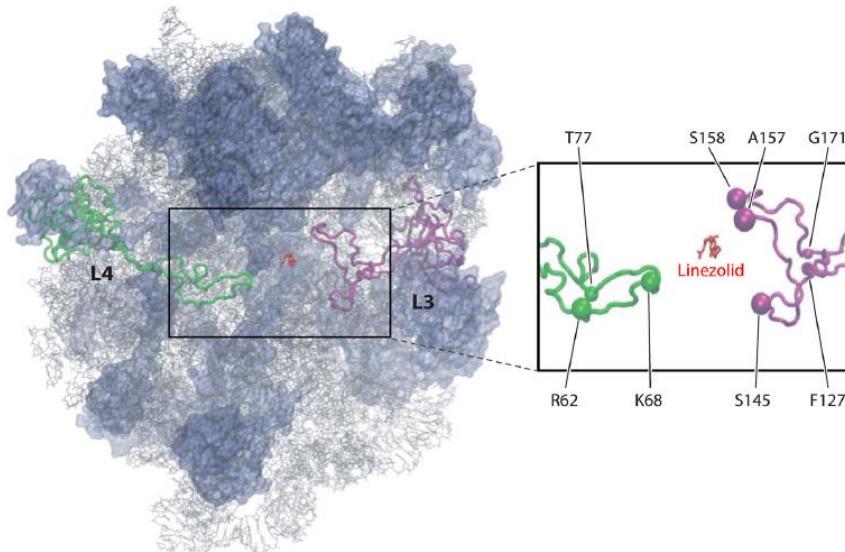
➤ **Mutationen in der 23S rRNA Bindungsstelle**



Long et al., Antimicrob. Agents Chemother. 2010

Secondary structure of the 23S rRNA Peptidyltransferase loop; colored mutations indicate 1st (blue), 2nd (green), 3rd (orange) and outer layer (red) nucleotides with respect to linezolid

➤ **Mutationen in den ribosomalen Proteinen L3, L4, L22 des PTC**



Long & Vester, Antimicrob. Agents Chemother. 2012

Illustration how parts of L3 and L4 extend toward the PTC where linezolid is bound.

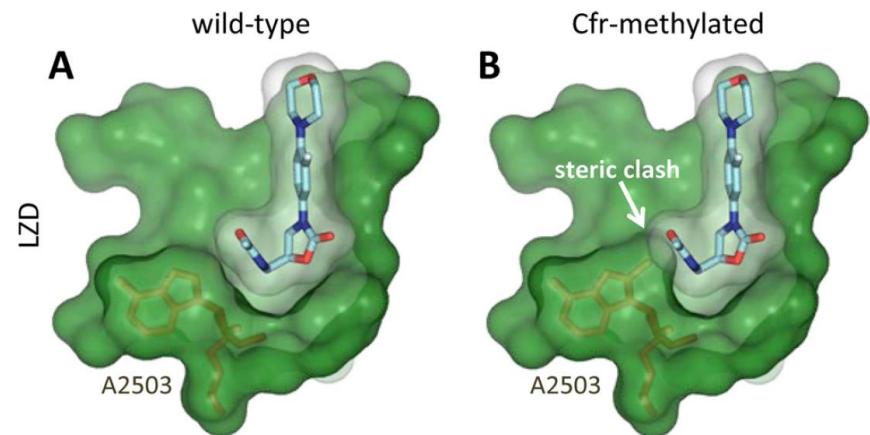
# Linezolidresistenz

- **cfr kodiert eine Methyltransferase**  
(Methylierung von Adenin an der Position A2503)

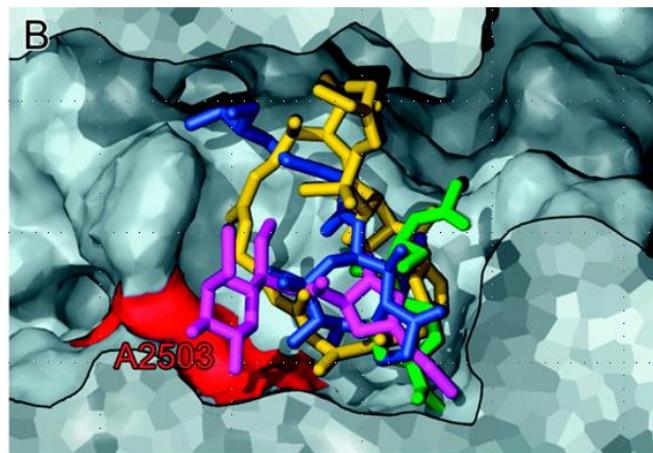
vermittelt Kreuzresistenzen  
(PhLOPS<sub>A</sub>) durch Methylierung eines zentralen Antibiotika-Angriffspunktes

PhLOPSA phenotype (resistance to Phenicols, Lincosamides, Oxazolidinones, Pleuromutilins and Streptogramin A Antibiotics)

meistens Plasmid vermittelt und teilweise übertragbar



Locke et al., Antimicrob. Agents Chemother. 2010



Long K S et al. Antimicrob. Agents Chemother. 2006

Binding of Chloramphenicol (green), Clindamycin (pink), Tiamulin (blue) and Dalfopristin (yellow) to overlapping sites at the ribosomal peptidyl transferase center.



# Hospital-assoziierte Koagulase-negative Staphylokokken mit Resistenz gegenüber Linezolid werden weltweit beschrieben

(b)



(b) Linezolid-resistant CoNS reported in North America (USA, Mexiko), South America (Brazil), Europe (Greece, Spain, Italy, France, Ireland) and Asia (India).

Gu et al., J Antimicrob Chemother. 2013

[J Antimicrob Chemother. 2018 Jan 1;73\(1\):41-51. doi: 10.1093/jac/dkx370.](#)

## Long-lasting successful dissemination of resistance to oxazolidinones in MDR *Staphylococcus epidermidis* clinical isolates in a tertiary care hospital in France.

Dortet L<sup>1,2,3,4</sup>, Glaser P<sup>4,5</sup>, Kassis-Chikhani N<sup>6</sup>, Girlich D<sup>2,3,4</sup>, Ichai P<sup>7</sup>, Boudon M<sup>7</sup>, Samuel D<sup>7</sup>, Creton E<sup>2,3,4</sup>, Imanci D<sup>8</sup>, Bonnin R<sup>2,3,4</sup>, Fortineau N<sup>1,2,3,4</sup>, Naas T<sup>1,2,3,4</sup>.

[J Antimicrob Chemother. 2017 Dec 1;72\(12\):3252-3257. doi: 10.1093/jac/dkx292.](#)

## Novel multiresistance cfr plasmids in linezolid-resistant methicillin-resistant *Staphylococcus epidermidis* and vancomycin-resistant *Enterococcus faecium* (VRE) from a hospital outbreak: co-location of cfr and optrA in VRE.

Lazaris A<sup>1</sup>, Coleman DC<sup>1</sup>, Kearns AM<sup>2</sup>, Pichon B<sup>2</sup>, Kinnevey PM<sup>1</sup>, Earls MR<sup>1</sup>, Boyle B<sup>3</sup>, O'Connell B<sup>3,4</sup>, Brennan GI<sup>4</sup>, Shore AC<sup>1</sup>.

[J Antimicrob Chemother. 2018 Feb 9. doi: 10.1093/jac/dky010. \[Epub ahead of print\]](#)

## Emergence and control of linezolid-resistant *Staphylococcus epidermidis* in an ICU of a German hospital.

Weßels C<sup>1</sup>, Strommenger B<sup>2</sup>, Klare I<sup>2</sup>, Bender J<sup>2</sup>, Messler S<sup>3</sup>, Mattner F<sup>1</sup>, Krakau M<sup>4</sup>, Werner G<sup>2</sup>, Layer E<sup>2</sup>

[Infect Control Hosp Epidemiol. 2018 Feb 12:1-3. doi: 10.1017/ice.2018.5. \[Epub ahead of print\]](#)

## Dissemination of *Staphylococcus epidermidis* ST22 With Stable, High-Level Resistance to Linezolid and Tedizolid in the Greek-Turkish Region (2008-2016).

Freitas AR<sup>1</sup>, Dilek AR<sup>2</sup>, Peixe L<sup>1</sup>, Novais C<sup>1</sup>.



# Einsendungen von Linezolid-resistenten Staphylokokken an das NRZ

...Fragen der Einsender

"Kann das NRZ die Resistenz bestätigen?"

"Inwieweit sind Isolate verwandt?" (Aufklärung von Transmissionsketten)

...Routinediagnostik

Bestimmung der MHK mittels Mikrodilution

PCR zum Nachweis des *cfr*-Gens

*Sma*I-Makrorestriktion

Multilocus Sequenztypisierung (MLST)

...Forschung

Bestimmung der ribosomalen Mutationen

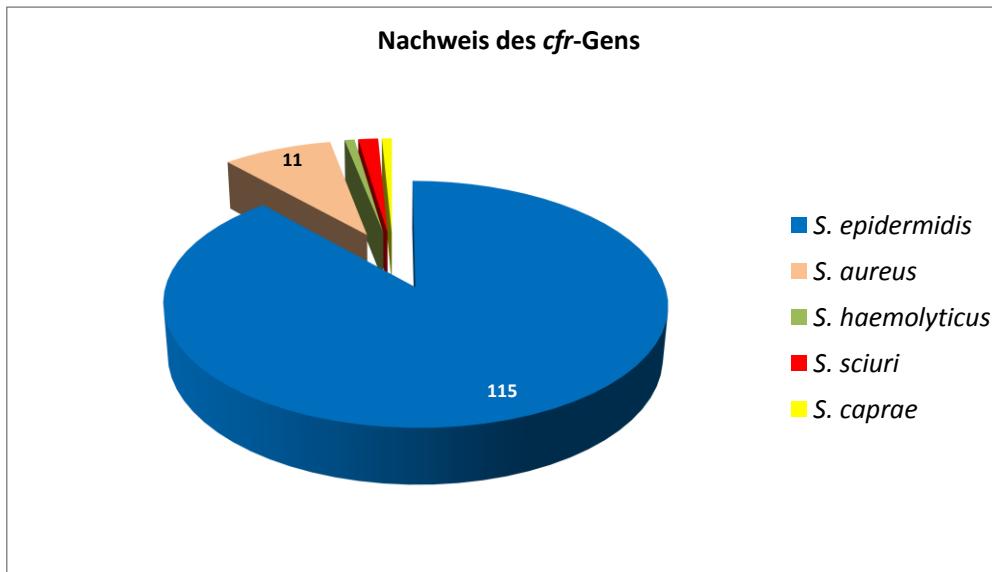
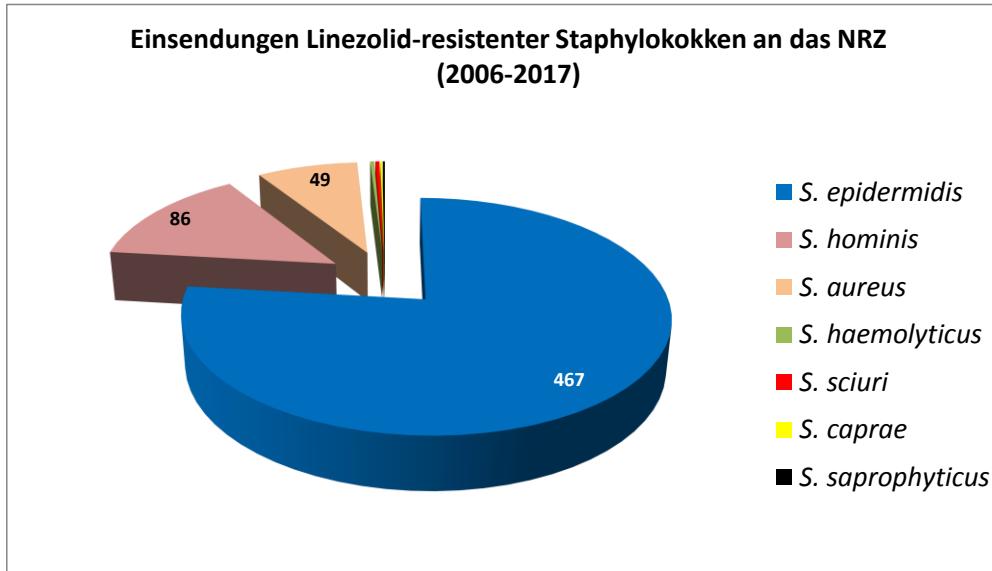
Analyse der *cfr*-Plasmide, Übertragbarkeit

Linezolid-abhängiges Wachstum

(NGS-Daten zur Typisierung)



## Daten aus dem NRZ





# Charakterisierung von Linezolid-resistenten *S. epidermidis* (LRSE) aus deutschen Krankenhäusern

(Bender *et al.*, J Antimicrob Chemother. 2015)

No. of isolates	Hospital	ST	PFGE type	MIC of linezolid (mg/L)	cfr
8	A	2	IV	16–256	–
2	A	2	IV	>256	+
1	C	2	IV	8	+
1	G	2	V	>256	+
1	B	5	II	8	–
3	F	5	II	16–32	–
1	C	22	I	16	+
14	D	22	I	>256	–
2	E	22	I	>256	–
1	E	22	I	>256	–
1	H	22	I	>256	–
1	C	23	III	8	+

- multiresistant
- LZD MHK 8 - >256 mg/L
- vier Genotypen (I – IV) nach *Sma*I-Makrorestriktion/ PFGE
- vier Sequenztypen (CC5 häufig unter nosokomialen *S. epidermidis*)
- sechs *cfr*-positive Stämme



KH	MIC LZD (µg/ml)	cfr	23SrRNA V region	rpLC gene / Protein L3				rpID gene / Protein L4			
A	16	-	G2576T	-				-			
A	32	-	G2576T	-				-			
A	>256	+	G2576T	-				138 His Insertion			
A	>256	+	G2576T	-				138 His Insertion			
A	64	-	G2576T	-				138 His Insertion			
A	>256	-	G2576T	-				138 His Insertion			
A	32	-	G2576T	-				138 His Insertion			
A	48	-	G2576T	-				138 His Insertion			
A	96	-	G2576T	-				138 His Insertion			
A	32	-	-	His146Gln	Val154Leu	Ala157Arg	-	-			
C	8	-	-	-	-	Ala157Arg	-	-			
C	16	+	-	-	-	-	-	-			
C	6	+	-	-	-	-	-	Glu128Ala	Gln174Arg	Arg182Gln	-
D	8	+	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
D	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
E	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln*	-
E	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
E	>256	-	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-
F	>256	-	-	His146Gln	Val154Leu	Ala157Arg	-	Glu128Ala	Gln174Arg	Arg182Gln*	-
F	32	-	-	His146Gln	Val154Leu	Ala157Arg	-	Glu128Ala	Gln174Arg	Arg182Gln*	-
F	32	-	-	His146Gln	Val154Leu	Ala157Arg	-	Glu128Ala	Gln174Arg	Arg182Gln*	-
G	16	-	G2576T	-	-	-	-	-	-	-	-
H	>256	+	T2502A/C2532T	Gly152Asp	-	-	Asp159Tyr	Glu128Ala	Gln174Arg	Arg182Gln	-

\*138 His Insertion

- Bekannte und neue Mutationen:

23SrRNA: G2576T am häufigsten in klinischen Isolaten beschrieben, assoziiert mit erhöhten MHKs; alle anderen Mutationen neu

alle nicht synonymen Mutationen in rpLC bereits beschrieben

neue Mutationen in rpID, nicht in der Nähe des PTC

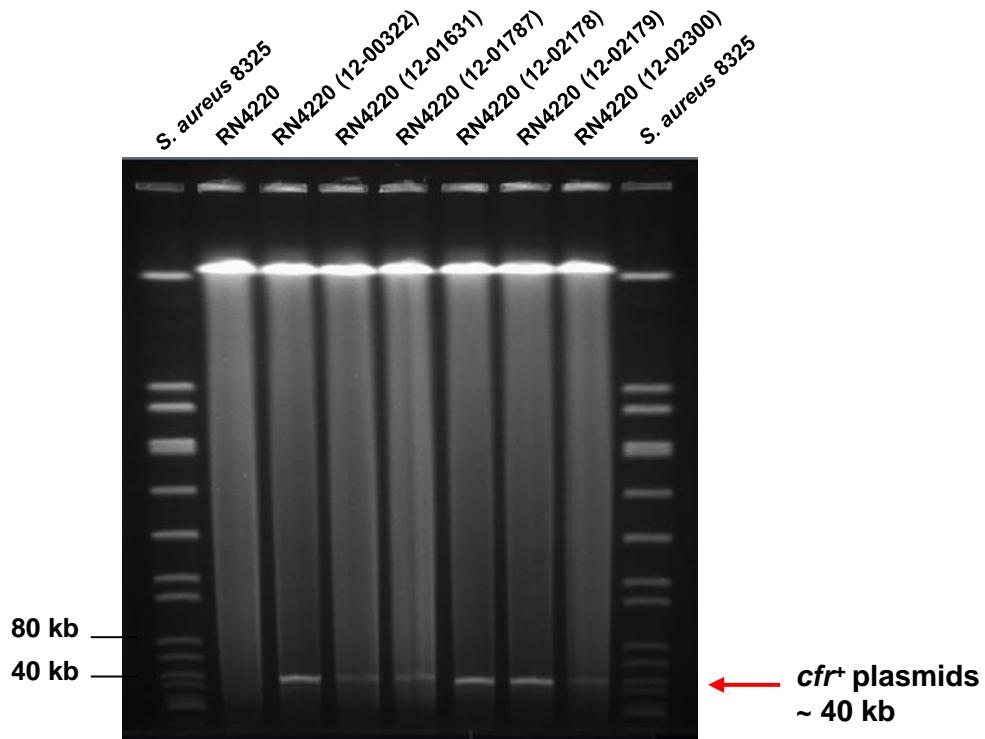
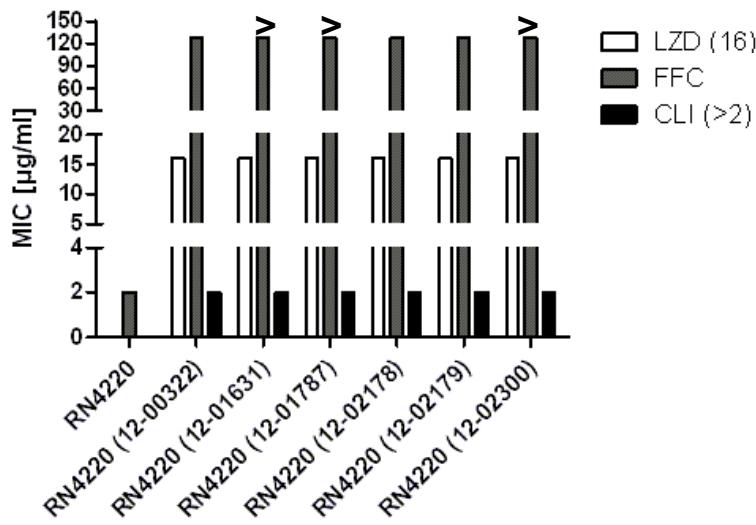
synonyme Mutationen in rpLV/LL22

- keine Korrelation zwischen MHK und den Resistenzmutationen/cfr



# Charakterisierung von LRSE aus deutschen Krankenhäusern

- Analyse der *cfr*-Plasmide



➤ Transfer der Plasmide in *S. aureus*  
RN4220

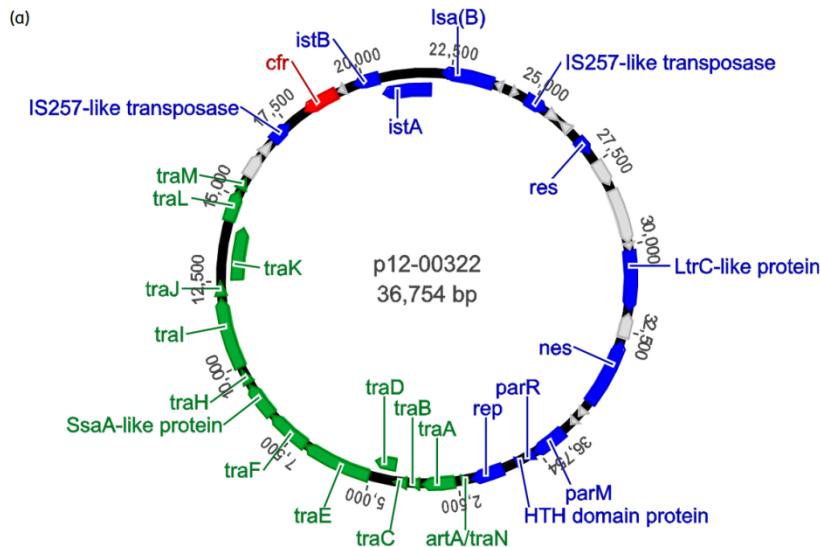
➤ S1 Nuclease-PFGE (+ Southern Blot  
hybridisiert mit einer *cfr*-Sonde)



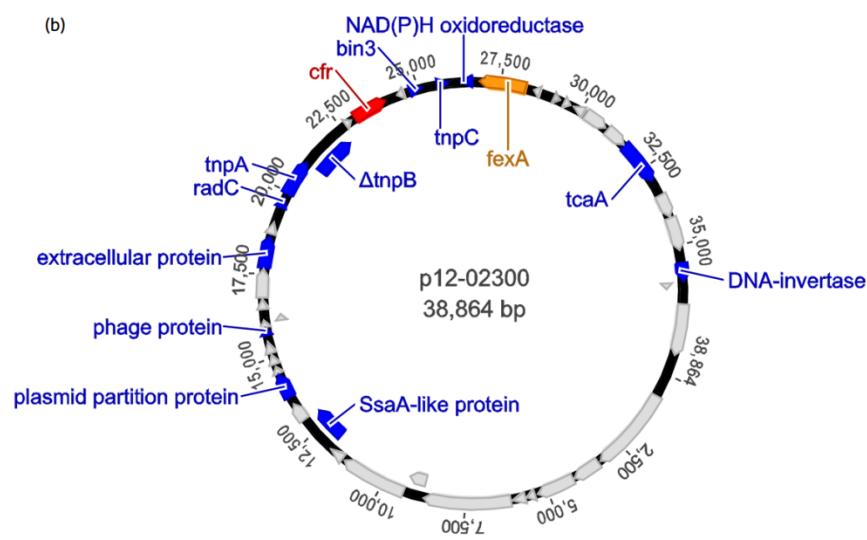
# Charakterisierung von LRSE aus deutschen Krankenhäusern

- cfr-Plasmide: bekannte und neue Strukturen

**Kategorie C1**  
(pSK41/pGO1-Familie)



**Kategorie C2**  
(pSCFS3-ähnlich)



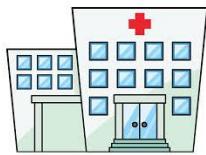
LRSE ST2, ST22, ST23 aus einem  
Krankenhaus

- klonale Verbreitung LZD-resistenter Stämme und/ oder *cfr*-tragender Plasmide

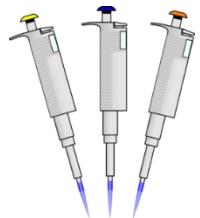


# Häufung von LRSE auf einer deutschen Intensivstation

(Weßels et al., J Antimicrob Chemother. 2018)



- Krankenhaus der Sekundärversorgung in NRW mit 465 Betten
- interdisziplinäre ICU mit 21 Betten
- in 15 Monaten Nachweis von LRSE bei 14 Patienten aus verschiedenen klinischen Materialien



- Resistenzbestätigung
- molekulare Typisierung
- Analyse der *cfr*-Plasmide und Resistenzmutationen



- Verschiedene Maßnahmen zur Infektionskontrolle/ Interventionen (Reduktion des Einsatzes von LZD, Information und Schulung des Personals, Umgebungsscreening, Isolationsmaßnahmen bei LRSE-positiven Patienten, u.a.)
- Review der Krankenakten und des Antibiotika-Verbrauchs des Krankenhauses und der ICU



# Häufung von LRSE auf einer deutschen Intensivstation

- Charakteristika LRSE-positiver Patienten

Patient	Sex	Age (years)	Ward	Culture site	Date of culture	Infection due to LRSE <sup>a</sup>	Infection <sup>a</sup>	MRSA (culture site)	Underlying disease and/or condition	Linezolid consumption (DDDs) <sup>b</sup>	VRE (culture site)	LZD-R VRE (culture site)
1	male	57	ICU	blood	22/11/2013			negative	haemorrhage after ERCP	15		
2 <sup>c</sup>	male	71	ICU	central line tip blood central line tip urine	02/01/2014 07/03/2014 18/03/2014	BSI with Enterococcus faecium		negative	fracture of trochanter major	48	positive (urine)	
3	male	87	ICU	urine	12/12/2013			negative	cardiac decompensation, pneumonia	56		
4	female	66	ICU	central line tip	15/05/2014	BSI due to UTI and BSI with MRSA	positive (blood, tracheal secretion)	ileus		55		
5	male	61	ICU	blood	16/05/2014	BSI with MRSA	positive (blood)	myocardial infarction, CPR		26	positive (wound)	
6	male	72	ICU	wound	21/07/2014			negative	ulcus duodeni haemorrhage	17	positive (secretion drainage)	
7	male	64	ICU	secretion drainage	22/07/2014	pneumonia with MRSA	positive (punctate)	pancreatic cancer		13		
8	female	78	SU	blood	26/07/2014		positive (bronchial secretion)	pneumonia		14		
9	female	76	ICU	secretion drainage	01/08/2014			negative	peritonitis	32		
10	male	90	ICU	blood	04/08/2014			negative	colon cancer	15		
11	male	77	ICU	blood	07/09/2014	BSI	pneumonia	positive (wound)	renal failure	23		
12	male	76	ICU	axilla	19/09/2014			negative	media infarction	0		
13	female	79	ICU	decubitus	18/09/2014	UTI	negative	incarcerated incisional hernia		65		positive (wound)
14	male	77	ICU	blood	08/01/2015		positive (screening)	pneumonia		14		

ERCP, endoscopic retrograde cholangiopancreatography; CPR, cardiopulmonary resuscitation; SU, surgical unit; BSI, bloodstream infection; UTI, urinary tract infection; LZD-R, linezolid resistant.

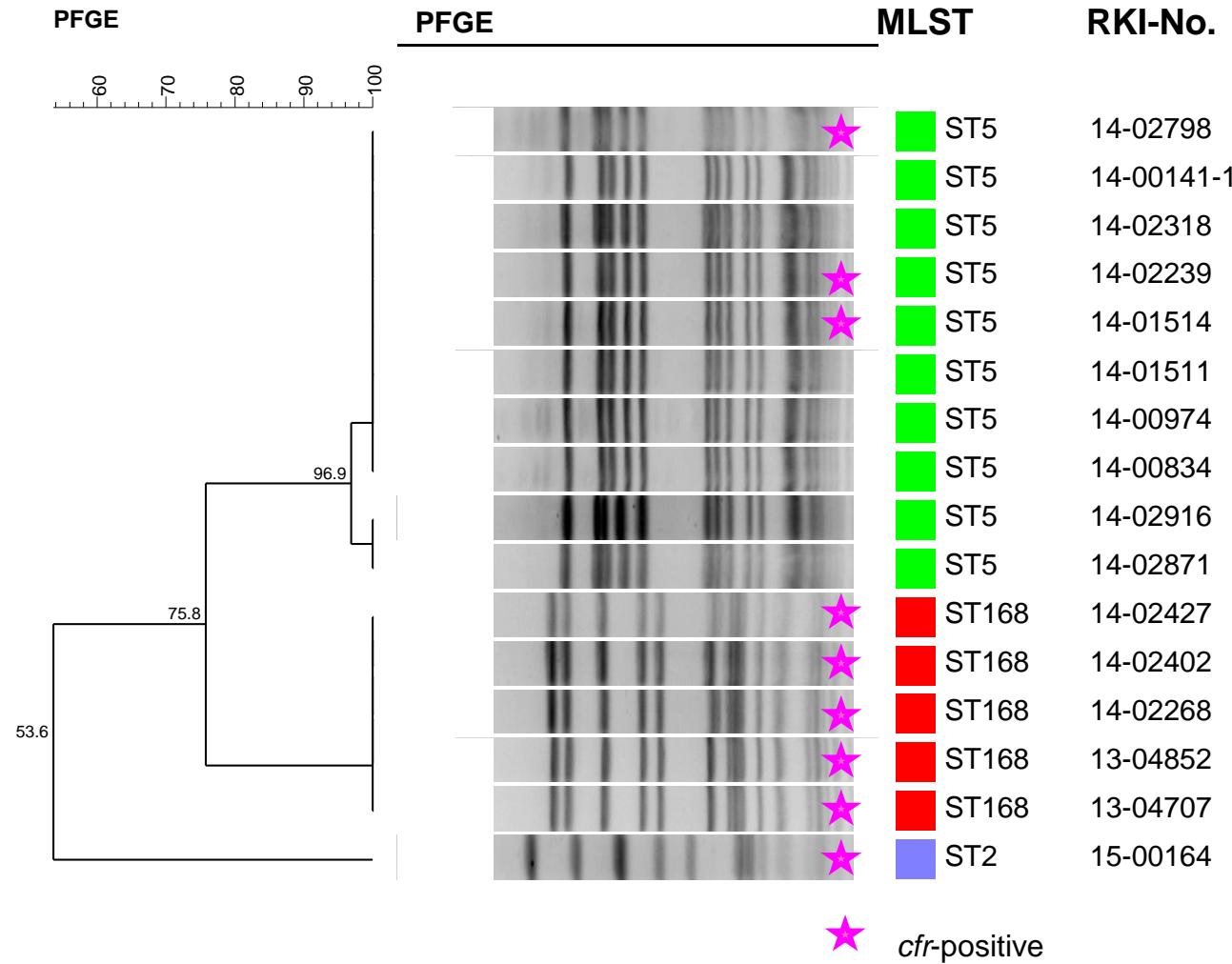
<sup>a</sup>Infection: cases were defined as described elsewhere.<sup>22</sup>

<sup>b</sup>Linezolid consumption of the respective patient before the first LRSE was cultured. Linezolid doses of 600 mg/day were considered 1 DDD.

<sup>c</sup>For Patient 2, three LRSE isolates were sent to the NRC for further analysis.

## Häufung von LRSE auf einer deutschen Intensivstation

- #### ▪ Ergebnisse der molekularen Typisierung





# Häufung von LRSE auf einer deutschen Intensivstation

patient	Oct 13	Nov 13	Dec 13	Jan 14	Feb 14	Mar 14	Apr 14	May 14	Jun 14	Jul 14	Aug 14	Sep 14	Oct 14	Nov 14	Dec 14	Jan 15	strain characteristics*
1			29.10.2013 - 05.01.2014														cfr-positive ST168
	D 08.11.2013	B* 22.11.2013	LZD														
2			03.11.2013 - 14.03.2014		C* 02.01.2014	B* 07.03.2014											cfr-negative ST5
			LZD		C* 18.03.2014	LZD											
3			14.10.2013 - 02.01.2014		U* 12.12.2013	LZD											cfr-positive ST168
							24.02. - 24.06.2014										
4							C* 15.05.2014	LZD									cfr-negative ST5
							B (LZD-S) 18.04.2014	B* 16.05.2014	09.05. - 18.06.2014	LZD							
5									26.06. - 16.08.2014								cfr-positive ST5
									V* 21.07.2014								
6									B 30.07.2014	LZD							cfr-positive ST5
											11.06. - 03.07. + 14.07.-05.08.2014						
7									D* 22.07.2014	LZD							cfr-positive ST168
8									05.07. - 14.07.2014								cfr-negative ST5
									B* 26.07.2014	LZD							
9										27.06. - 10.11.2014							cfr-positive ST168
									D* 01.08.2014	LZD							
10										11.07. - 17.08.2014							cfr-positive ST168
									B* 04.08.2014	LZD							
11										28.08. - 20.08.2014							cfr-positive ST5
										B* 07.09.2014	LZD						
12										28.08. - 12.11.2014							cfr-negative ST5
										S* 19.09.2014	LZD						
13										27.06.2014 - 06.01.2015							cfr-positive ST5
										DS* 18.09.2014	LZD						
14															29.12.2014 - 20.01.2015		cfr-positive ST2
															B* 08.01.2015	LZD	

= ICU stay  
= LZD usage

★ cfr-positive



# Häufung von LRSE auf einer deutschen Intensivstation

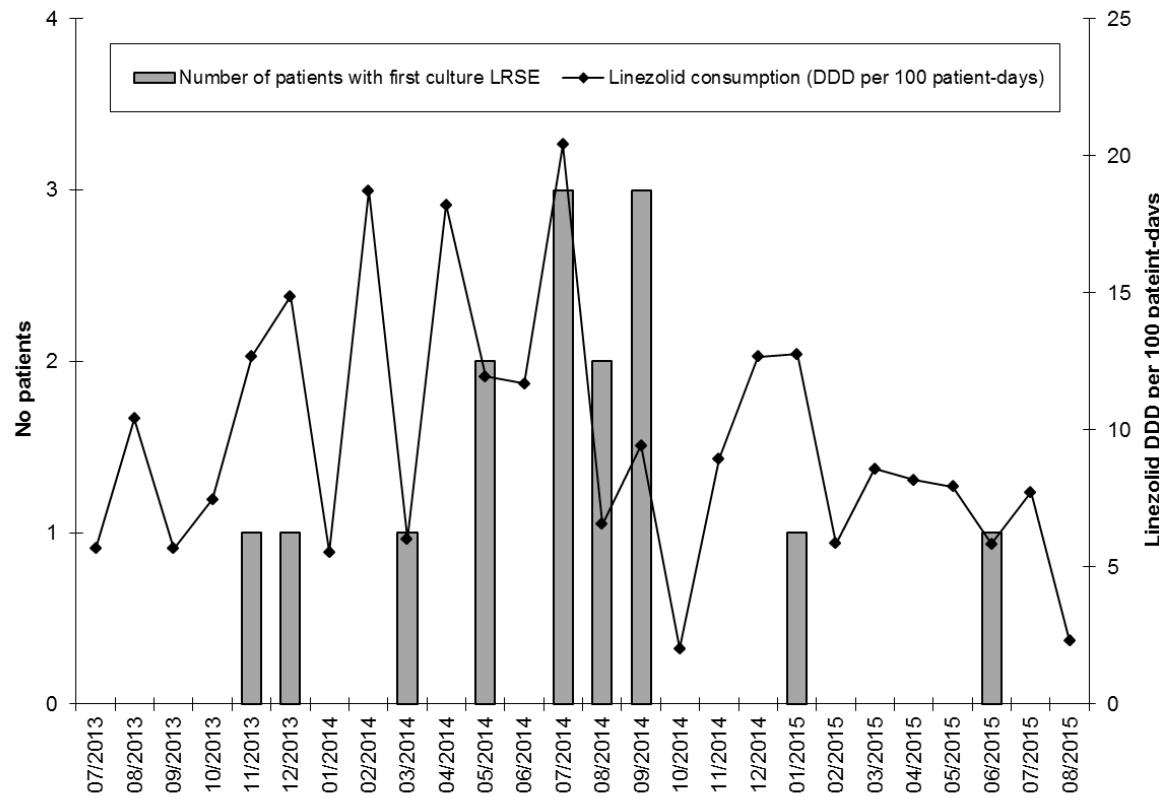
RKI-No.	MLST	MIC LZD mg/L	<i>cfr</i>	mutations in ribosomal genes / proteins							
				23SrRNA*	<i>rplC</i> (L3)			<i>rplD</i> (L4)			<i>rplV</i> (L22)
13-04707	ST168	16	+	C2190T		Gly152Asp			-		-
13-04852	ST168	>256	+	C2190T		Gly152Asp			-		-
14-02268	ST168	>256	+	C2190T		Gly152Asp			-		-
14-02402	ST168	>256	+	C2190T		Gly152Asp			-		-
14-02427	ST168	n.d.	+	C2190T		Gly152Asp			-		-
14-00141-1	ST5	>256	-	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-00834	ST5	>256	-	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-00974	ST5	>256	-	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-01511	ST5	>256	-	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-01514	ST5	>256	+	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-02239	ST5	>256	+	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-02318	ST5	>256	-	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-02798	ST5	>256	+	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-02871	ST5	>256	-	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
14-02916	ST5	>256	+	C2190T	His146Gln		Val154Leu	Ala157Arg	71-Gly-72	Ser81Arg	Asn158Ser
15-00164	ST2	8	+	C2190T		-			-		-

\*the nucleotide positions of the mutations are listed according to *E. coli*/ numbering

- bekannte ribosomale Mutationen (neu Ser81Arg in L4)
- fast identische 39kb große *cfr*-Plasmide aus ST2, ST5, ST168; große Ähnlichkeit mit p12-02300 (C2)

# Häufung von LRSE auf einer deutschen Intensivstation

- Linezolid-Verbrauch auf der ICU



- 13/ 14 Patienten erhielten Linezolid (empirisch, VRE- bzw. MRSA-Infektionen)
- Anstieg von 5,55 DDDs/100 Patiententage (Januar 2014) auf 20,41 DDDs/100 Patiententage (Juli 2014)



# Häufung von LRSE auf einer deutschen Intensivstation

- Antibiotikaverbrauchsdaten ICU/ Krankenhaus

**Table S2.** Antibiotic consumption (DDD per 100 patient-days) of the effected hospital and ICU in comparison to reference values for Germany. Reference data from SARI<sup>a</sup> were used for time spans. AVS<sup>b,c</sup> reference values were used for annual benchmarks. (SARI surveillance of antibiotic use and bacterial resistance in ICUs, AVS Antibiotika-Verbrauchs-Surveillance)

	linezolid			vancomycin			glycopeptides	carbapenems	combination of penicillins and inhibitors
	2009-2013	2013	2014	2009-2013	2013	2014	2014	2014	2014
hospital	0.76 (0.6;1.1) median (min;max)		1.2	1.02 (0.81;1.48) median (min;max)		1.1	1.2	4	26.9
reference value for German hospitals			0.51 mean, AVS <sup>b</sup>			0.69 mean, AVS <sup>b</sup>	0.6 (0.4-0.8) median (IQR), AVS <sup>c</sup>	2.1 (1.4-3.0) median (IQR), AVS <sup>c</sup>	15.1 (11.1-19.4) median (IQR), AVS <sup>c</sup>
ICU	5.72 (3.4;8.5) median (min;max)	8.5	11.1	3.36 (2.92;6.99) median (min;max)	6.99	5.4	5.9	26	29.6
reference value for German ICUs	3.27 median, SARI <sup>a</sup>	2.78 mean, AVS <sup>b</sup>		2.28 median, SARI <sup>a</sup>	1.94 mean, AVS <sup>b</sup>	2.1 (1.1-3.6) median (IQR), AVS <sup>c</sup>	15.5 (10.7-20.5) median (IQR), AVS <sup>c</sup>	27.9 (22.7-35.2) median (IQR), AVS <sup>c</sup>	

a: SARI: Surveillance of antibiotic use and bacterial resistance in German intensive care units 2012-2016; <http://www.sari-antibiotika.de>

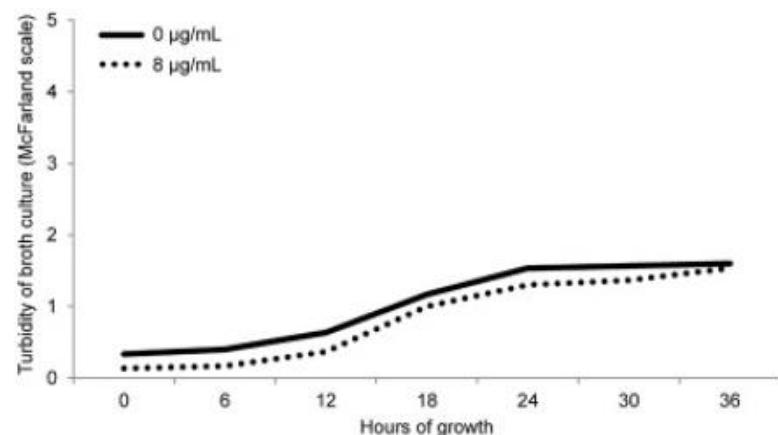
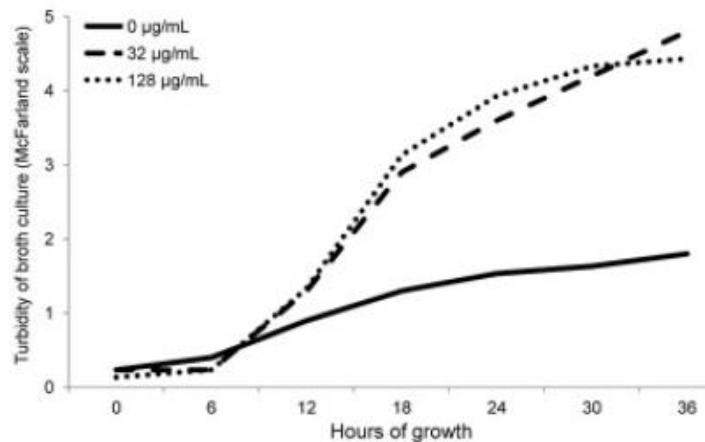
b: Robert Koch-Institut: AVS, Antibiotika Verbrauchs Surveillance 2015: <http://avs.rki.de>, data status: 07.11.2017

c: Marcel Feig, Michael Behnke, Luis Alberto Pena Diaz et al, Antibiotic consumption in German acute care hospitals: first data of a new web-based national surveillance system, 27th ECCMID Vienna, Austria, 22.-25. April 2017, Session: EV023 Pharmacoepidemiology, improved prescribing and antibiotic stewardship.

- der Antibiotikaverbrauch der ICU und des Krankenhauses überschritt verschiedene Referenzlevel
- Antibiotic Stewardship für adäquaten Antibiotikaeinsatz notwendig

## Linezolid-abhängiges Wachstum klinischer LRSE

- LRSE werden in griechischen Krankenhäusern vermehrt nachgewiesen (2011-2013)
- vor allem LRSE ST22; diese zeigen zum größtenteils ein Linezolid-abhängiges Wachstum (Pournaras *et al.* EID 2013, Karavasilis *et al.*, J Antimicrob Chemother. 2015)



Growth curve of a representative LZD-dependent and a LZD-non-dependent isolate.

- in Anwesenheit von Linezolid ist die katalytische Aktivität der Peptidyltransferase von Ribosomen Linezolid-abhängiger LRSE höher (Kokkori *et al.* AAC 2014)



# Linezolid-abhängiges Wachstum klinischer LRSE

(Layer *et al.*, J Antimicrob Chemother. 2018)

Index no./ hospital	Culture site	Infection	MLST <sup>a</sup>	Linezolid						
				cfr gene	MIC (mg/L)	treatment	23S rRNA	Protein L3	Protein L4	Protein L22
12-00322/C	blood	sepsis	ST22	+	16	NA	C2161T	Leu101Val Ala157Arg	WT	WT
12-01569/D	urine	UTI	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	Glu128Ala Gln174Arg Arg182Gln	WT
12-02439/D	blood	sepsis	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	Glu128Ala Gln174Arg Arg182Gln	WT
12-03718/D	NA	NA	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	Glu128Ala Gln174Arg Arg182Gln	WT
12-03723/D	blood	sepsis	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	Glu128Ala Gln174Arg Arg182Gln	WT
13-00905/E	blood	NA	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	Glu128Ala Gln174Arg Arg182Gln Ins1His138	WT
13-01045/E	NA	NA	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	Glu128Ala Gln174Arg Arg182Gln	WT
13-01084/H	NA	sepsis	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	Glu128Ala Gln174Arg Arg182Gln	WT
14-03576/Y	blood	NA	ST2	-	>256	NA	C2190T C2561T G2603T	-	Ser61Arg Asn158Ser	WT
14-03623/Y	NA	decubitus	ST2	+	12	+	C2190T	-	-	WT
14-01514/Y	blood	endocarditis	ST5	+	>256	+	C2190T	His146Gln Val154Leu Ala157Arg	Ser61Arg Asn158Ser	WT
14-00183/Y	NA	NA	ST23	-	8	+	C2190T	-	Ser61Arg Asn158Ser	WT
14-02427/Y	blood	NA	ST168	+	>256	+	C2190T	Gly152Asp	-	WT
13-04707/Y	blood	sepsis	ST168	+	>256	+	C2190T	Gly152Asp	-	WT

NA, data not available; UTI, urinary tract infection.

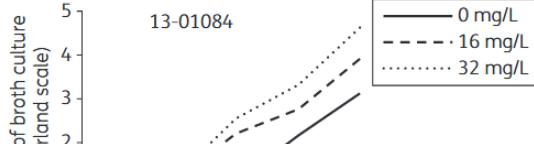
<sup>a</sup>ST2, ST5, ST22 and ST168 belong to CC5.

- 14 klinische LRSE (2012-2014) aus fünf verschiedenen Krankenhäusern
- unterschiedliche klonale Linien
- Wachstumskurven (16 und 32 mg/L LZD)

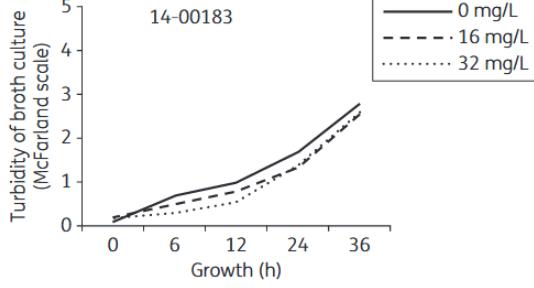
# Linezolid-abhängiges Wachstum klinischer LRSE

(Layer et al., J Antimicrob Chemother. 2018)

(a)



(b)



Growth curve of a representative (a) LZD-dependent and a (b) LZD-non-dependent isolate

Index no./ hospital	Culture site	Infection	MLST <sup>a</sup>	cfr gene	Linezolid						Linezolid dependence
					MIC (mg/L)	treatment	23S rRNA	Protein L3	Protein L4	Protein L22	
12-00322/C	blood	sepsis	ST22	+	16	NA	C2161T	Leu101Val Ala157Arg	WT	WT	no
12-01569/D	urine	UTI	ST22	-	>256	NA	C2161T T2502A C2532T	Glu128Ala Gly152Asp Asp159Tyr	WT	WT	yes
12-02439/D	blood	sepsis	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	WT	WT	yes
12-03718/D	NA	NA	ST22	-	>256	NA	C2161T T2502A C2532T	Glu128Ala Gly152Asp Asp159Tyr	WT	WT	yes
12-03723/D	blood	sepsis	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Glu128Ala Gly152Asp	WT	WT	yes
13-00905/E	blood	NA	ST22	-	>256	NA	C2161T T2502A C2532T	Glu128Ala Gly152Asp Asp159Tyr	WT	WT	yes
13-01045/E	NA	NA	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	WT	WT	yes
13-01084/H	NA	sepsis	ST22	-	>256	NA	C2161T T2502A C2532T	Leu101Val Gly152Asp Asp159Tyr	WT	WT	yes
14-03576/Y	blood	NA	ST2	-	>256	NA	C2190T C2561T G2603T	— Ser61Arg Asn158Ser	WT	WT	yes
14-03623/Y	NA	decubitus	ST2	+	12	+	C2190T	—	WT	WT	no
14-01514/Y	blood	endocarditis	ST5	+	>256	+	C2190T	His146Gln Val154Leu Ala157Arg	WT	WT	yes
14-00183/Y	NA	NA	ST23	-	8	+	C2190T	— Ser61Arg Asn158Ser	WT	WT	no
14-02427/Y	blood	NA	ST168	+	>256	+	C2190T	Gly152Asp	WT	WT	yes
13-04707/Y	blood	sepsis	ST168	+	>256	+	C2190T	Gly152Asp	WT	WT	no

NA, data not available; UTI, urinary tract infection.

<sup>a</sup>ST2, ST5, ST22 and ST168 belong to CC5.

- 10 Isolate zeigen Linezolid-abhängiges Wachstum



## Zusammenfassung

- das NRZ erhält verstärkt Linezolid-resistente *S. epidermidis* (LRSE)
- ca. 30% der LRSE sind *cfr*-positiv
- LRSE tragen verschiedene ribosomale Mutationen, die ebenfalls eine Resistenz gegen Linezolid bedingen können
- *cfr* befindet sich auf bekannten aber auch neuen Plasmiden, diese sind zum Teil übertragbar
- LRSE im Rahmen von Häufungen:
  - klonale Verbreitung bestimmter Stämme
  - Übertragung *cfr*-assoziiierter Plasmide wahrscheinlich
- LRSE aus deutschen Krankenhäusern weisen zum Teil ein Linezolid-abhängiges Wachstum auf
- Selektion und Ausbreitung Linezolid-resistenter Stämme wird durch den verstärkten Einsatz von Linezolid begünstigt

# Danke!

- allen einsenden Laboren für die interessanten Stämme
- nationalen und internationalen Kooperationspartnern
- Mitarbeitern des NRZ und Fachgebietes



Quelle: RKI / Fokus-Fotostudio Wernigerode

"COULD BE AN OUTBREAK!"

