

RAPID COMMUNICATION

Outbreak of vancomycin-resistant *Enterococcus faecium* clone ST796, Switzerland, December 2017 to April 2018

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Citation style for this article:

Wassilew Nasstasja, Seth-Smith Helena MB, Rolli Eveline, Fietze Yvonne, Casanova Carlo, Führer Urs, Egli Adrian, Marschall Jonas, Buetti Niccolò. Outbreak of vancomycin-resistant *Enterococcus faecium* clone ST796, Switzerland, December 2017 to April 2018. *Euro Surveill.* 2018;23(29):pii=1800351. <https://doi.org/10.2807/1560-7917.ES.2018.23.29.1800351>

Article submitted on 02 Jul 2018 / accepted on 19 Jul 2018 / published on 19 Jul 2018

Projektrapport, 23.8.2018

VRE-Outbreak Bern 30.12.2017 – 30.4.2018

- Beginn: 2 BSI mit VRE Hämato-Onkologie 30.12.2017
- Outbreak Abklärung:
 - MALDI-TOF= >E. faecium =>
 - Rapid PCR vanA und vanB
 - Whole Genome Sequencing (WGS, USB)

Resultate Screening

- 3'096 Abstriche von Kontaktpatienten
- 89 kolonisiert
- 77/89 (86.5%) => MLST Type ST 796

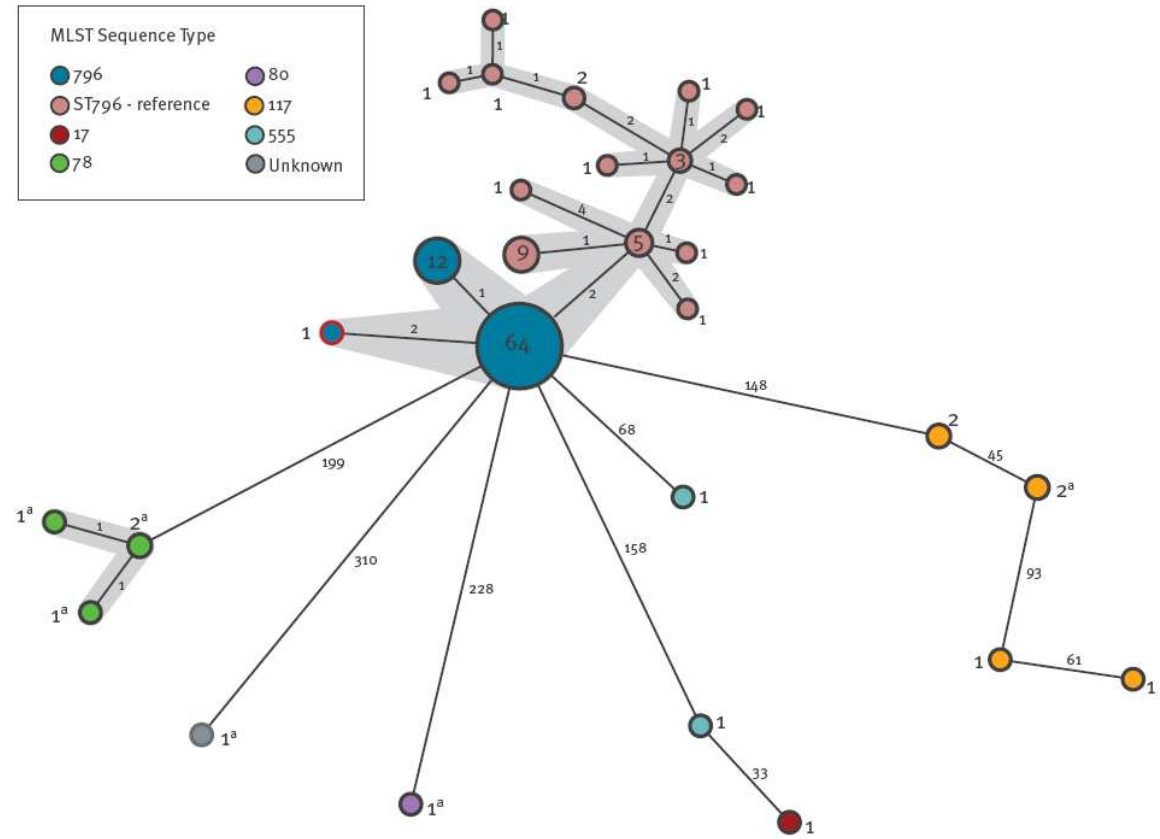
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FIGURE 2

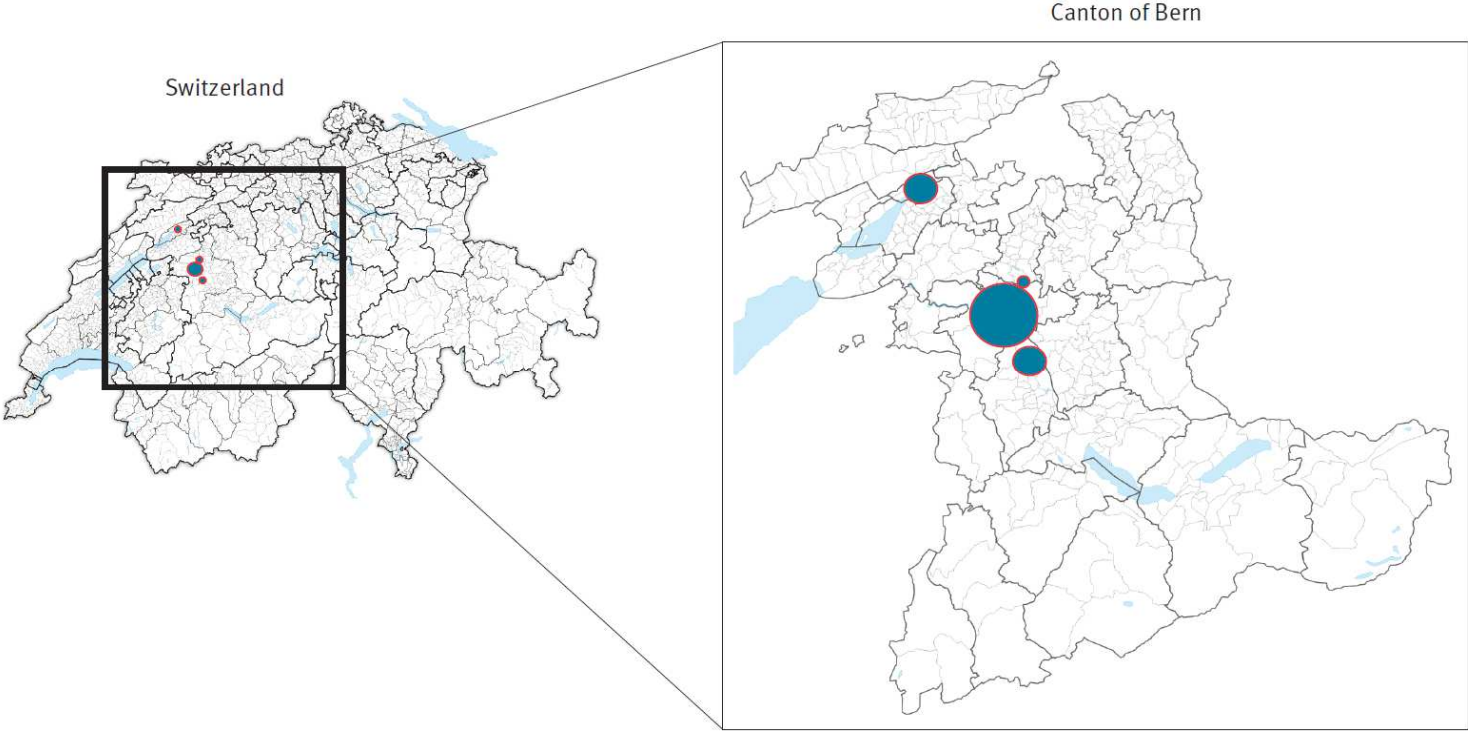
Core genome multilocus sequencing typing multiple spanning tree of *Enterococcus faecium* isolates, the Canton of Bern outbreak, Switzerland and isolates detected in Australia, 30 December 2017–30 April 2018



The core genome multi locus sequencing typing (cgMLST) analysis is based on 1423 loci [14] and was performed in Ridom SeqSphere v4.1.6.

Number of isolates belonging to each cluster is shown in the circles and the number of allele differences between clusters is presented on the connecting lines. Outbreak strains are shown in dark blue*, with the clonal complex highlighted in grey. Reference ST796 strains from Australia are shown in pink.

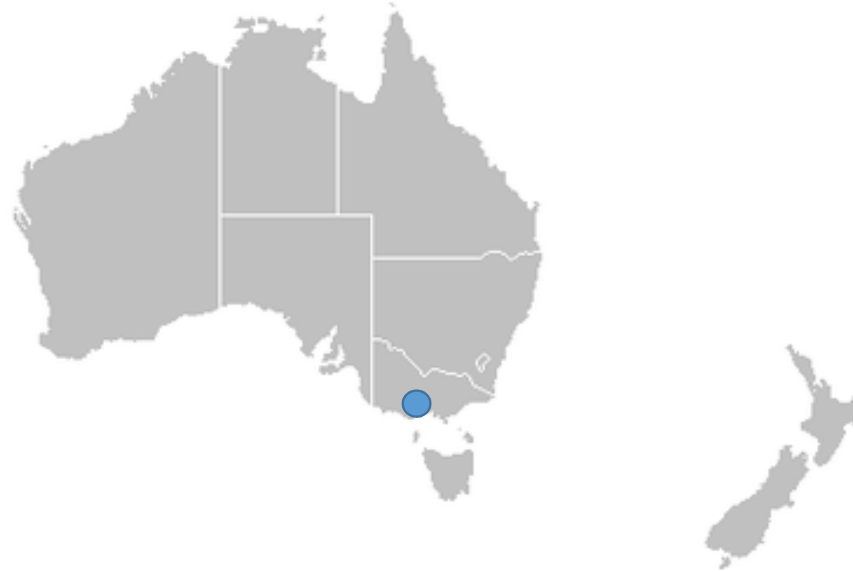
Ausbreitung CH



- 3/6 Spitaler Inselgruppe
- Biel

Ausbreitung in Australien und New Zealand

2011



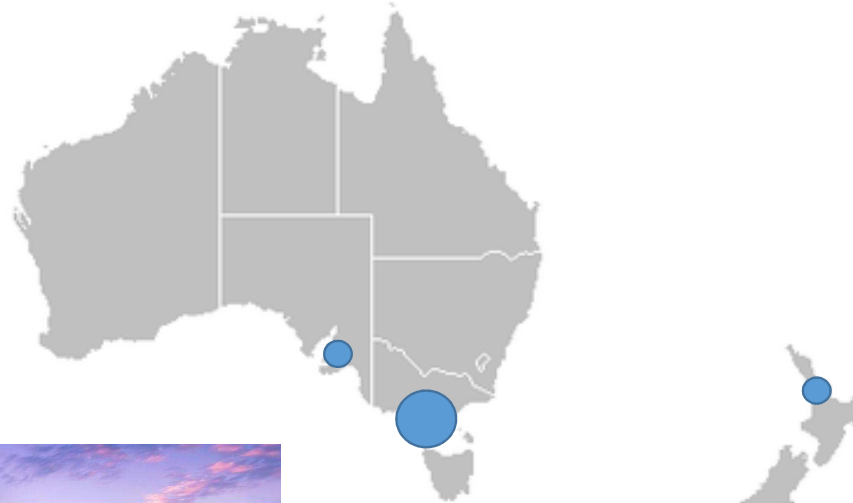
Ausbreitung in Australien und New Zealand

2012



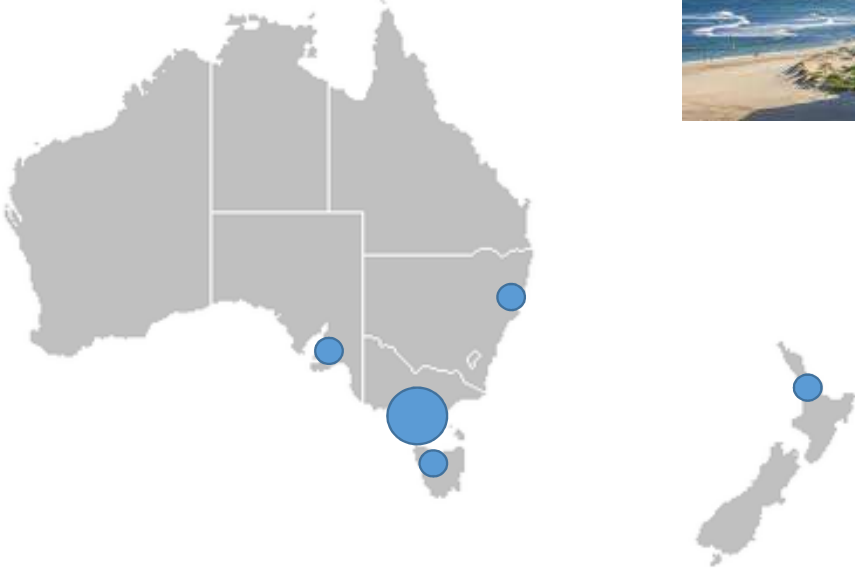
Ausbreitung in Australien und New Zealand

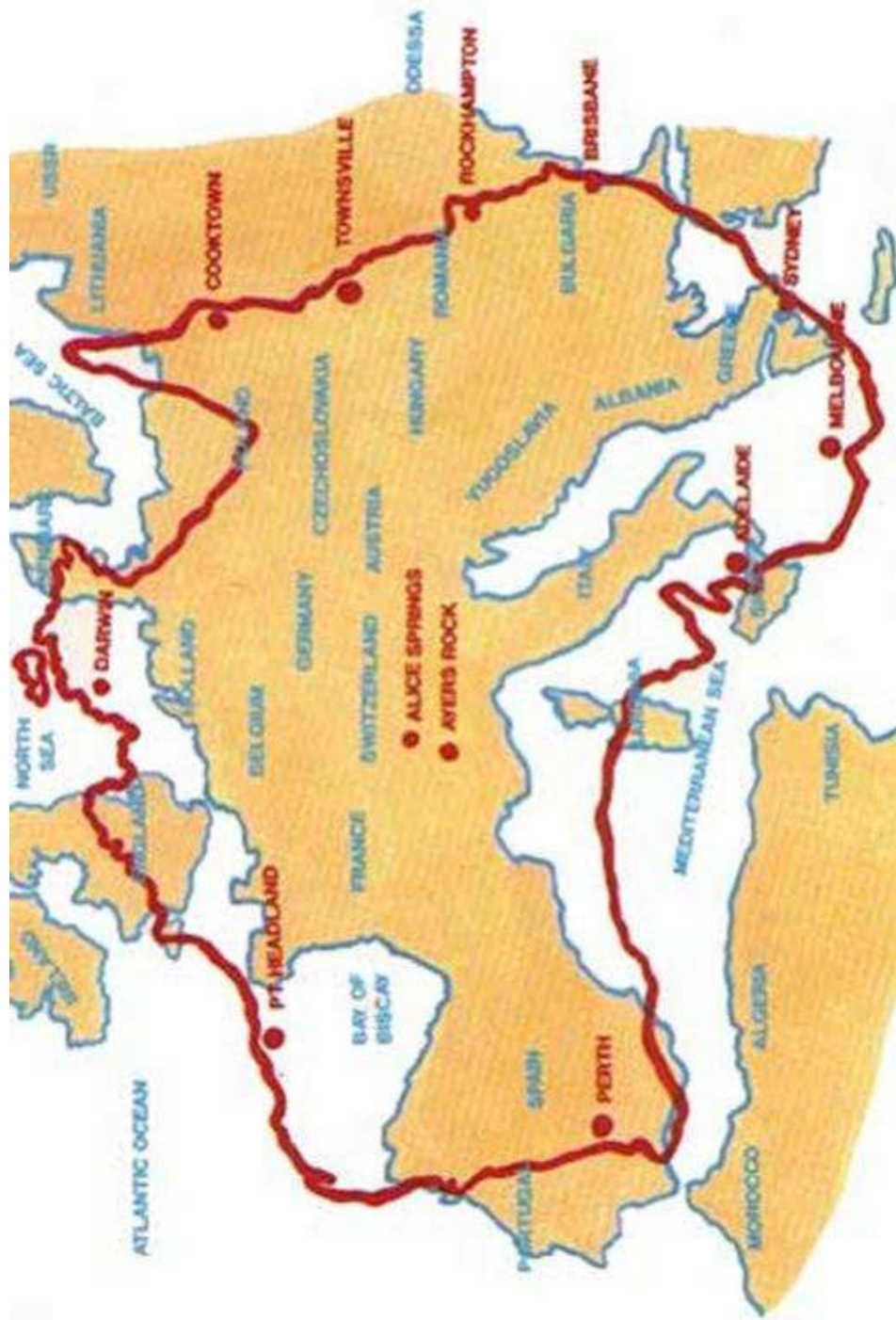
2013/ 2014



Ausbreitung in Australien und New Zealand

2015





Klinische Relevanz

- 6/89 Klinische, nicht Screening-Proben, davon 5 ST 796
- Invasive Infektionen 7/77 ST 796 (9.1%)
 - 5 BSI (6.5%)
 - 1 abdomineller Abszess
 - 1 tiefe Wundinfektion

BSI 30-Tagesmortalität in Australien

Table 4: *E. faecium*: By Place of Onset, Thirty Day All-cause Mortality and Vancomycin Susceptibility

Species	Community-Onset		Hospital-Onset		Total	
	N	Mortality (%)	N	Mortality (%)	N	Mortality (%)
Vancomycin non-susceptible <i>E. faecium</i>	39	9 (23.1)	142	43 (30.3)	181	52 (28.7)
Vancomycin susceptible <i>E. faecium</i>	56	11 (19.6)	142	40 (28.2)	199	51 (25.6)
All <i>E. faecium</i>	95	20 (21.1)	284	83 (29.1)	379	103 (27.2)

The Australian group on Antimicrobial Resistance (AGAR). Australian Enterococcal Sepsis Outcome Program (AESOP) 2016. Australia: AGAR; 2016.

Phänotypische Resistenzbestimmung (Bern)

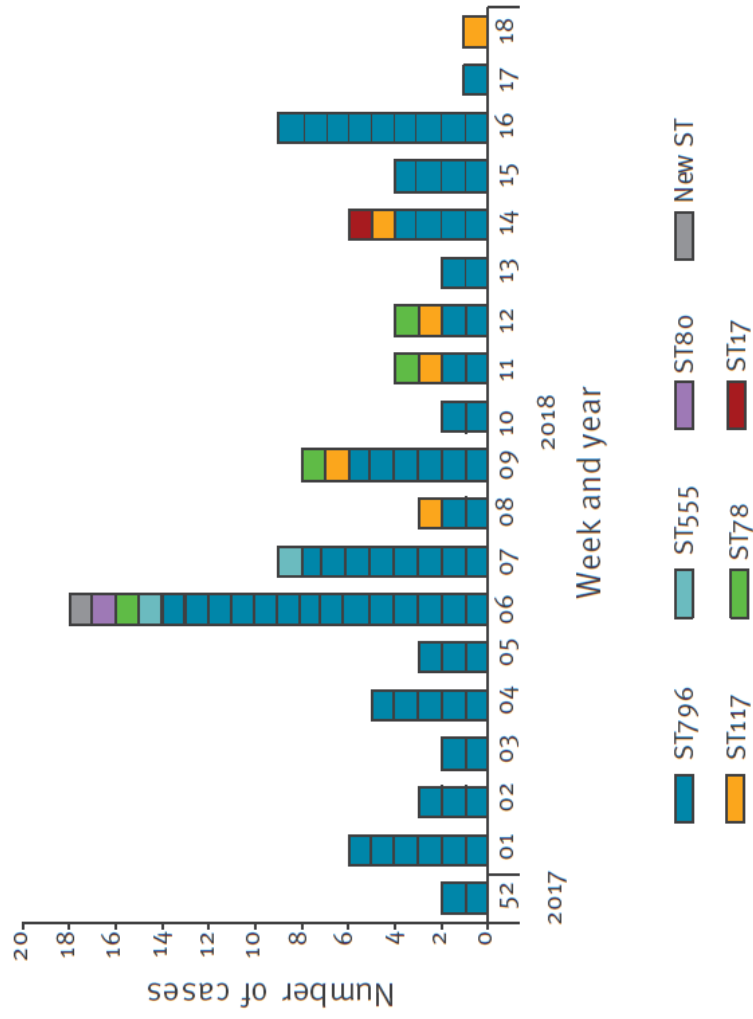
- 77/68 Antibiogramm
- 68/68 Resistent Ampicillin, Levofloxacin, high-level Gentamycin
- Vancomycin:
 - R (MIC > 16 mg/l): 46/68
 - I (MIC 8-16 mg/l): 21/68
 - S (MIC 4mg/l: 1/68
- Teicoplanin: S 68/68

Präventionsmassnahmen Inselgruppe

- Evaluation von Kontaktpatienten
 - Screening Tag 7,14,21
 - Präemptive Kontaktisolation
- Kolonisierte Patienten
 - Kohortierung
 - Kontaktisolation
- Personalkohortierung
- Passagerer Aufnahmestop in betroffenen Abteilungen
- Umgebungsdesinfektion intensiviert
- Händehygiene compliance intensiviert

FIGURE 3

Epidemic curve of vancomycin-resistant enterococci (VRE) cases by sequence type, Canton of Bern outbreak, Switzerland, December 2017–April 2018 (n = 89)



What now?

- 5/2018: Umfrage VRE CH:
 - 2015: 96 Fälle, Inz 0.26 Fälle/d
 - 1-3/18: 146 Fälle, Inz 1.58 Fälle/d
- 19.7.2018: Task force Swissnoso mit BAG und Kantonsärzten
- Empfehlungen zu Screening und Isolationsmassnahmen



Cost, lack of single rooms and isolation fatigue make VRE control for those hospitals with endemic colonization a major challenge [21, 29]. Where VRE is not endemic, swift recognition and enhanced infection control may still be effective [17, 30]. Our data suggest that if we wish to control VRE colonization and infection in hospitals that are not yet endemic then more attention must be paid to movements of patients and possibly staff who have had contact with VRE-endemic hospitals.

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