Outbreak of vancomycin-resistant Enterococcus faecium starting among patients admitted to a Surgical Unit in a Swedish county

Maria Gideskog (maria.gideskog@regionostergotland.se)
Department of Communicable Disease and Infection Control, and Department of Biomedical and Clinical Sciences, Linköping University

Jenny Welander
Department of Clinical Microbiology, and Department of Biomedical and Clinical Sciences, Linköping University

Anita Hällgren
Department of Infectious Diseases in Östergötland, and Department of Biomedical and Clinical Sciences, Linköping University

Research Article

Keywords: VRE, outbreak, Surgical Unit, infection control, antibiotic stewardship

Posted Date: February 9th, 2022

DOI: https://doi.org/10.21203/rs.3.rs-1306542/v1

Abstract

Background

Vancomycin-resistant Enterococcus faecium (VRE) is a nosocomial pathogen causing infection mainly in patients with critical illnesses in intensive care units, severe underlying disease or weakened immune system. Intensive pre-treatment with antibiotics and use of urinary catheters also constitute a risk. Due to its hardy nature, the bacterium can survive for long periods in a hospital environment. The aim of this study was to describe the investigation of a sudden increase in VRE cases admitted to the Surgical Unit at Vrinnevi Hospital in Norrköping, Sweden, and the control measures taken.

Methods

Faeces cultures from patients admitted to the Surgical Unit were obtained, and environmental cultures were collected from different locations in patient rooms and medical devices. In addition, screening samples were obtained from units with high-risk patients in the Östergötland County. Isolates identified as E. faecium were subjected to antibiotic susceptibility testing. Vancomycin-resistant isolates PCR-positive for the vanA/vanB gene were further analysed with whole genome sequencing (WGS).

Results

A total of 35 VRE isolates were found (22 from patients and 13 from the environment). The WGS identified three outbreak clusters, sequence type (ST) 203, ST 1839, ST 80 and one unique clone (ST 612). The ST 203 clone predominated among VRE cases admitted to the Surgical Unit.

Conclusions

With prompt infection control measures, the VRE outbreak was over after approximately four months. To prevent further outbreaks of VRE, active screening, antibiotic stewardship, improved cleaning and hand hygiene, and restriction of multiple-bed rooms are essential.

Background

Enterococci are Gram-positive bacteria that normally colonize the gastrointestinal tract of human beings. The two predominant enterococcal species are *Enterococcus faecalis* and *Enterococcus faecium*, which have clinically relevant differences in their susceptibility to antibiotics. In contrast to *E. faecalis*, a high proportion of *E. faecium* are resistant to beta-lactams. Treatment of infections caused by this bacterium usually requires a glycopeptide (1).

Vancomycin-resistant *E. faecium* (VRE) has emerged as an important nosocomial pathogen. The broad-spectrum glycopeptidic antibiotic vancomycin inhibits bacterial cell wall synthesis, and is one of the only few antibiotics effective against several antibiotic-resistant bacteria such as VRE. The most common genes encoding glycopeptide-resistance are *vanA* and to a lesser extent *vanB*. *VanA* results in

higher minimum inhibitory concentrations (MICs) for vancomycin and teicoplanin, whereas *vanB* strains remain susceptible to teicoplanin (2, 3).

Colonization of the gastrointestinal tract regularly precedes invasive infection. Asymptomatic colonization of the gastrointestinal tract is more common than clinically recognized infection. Infections caused by VRE include infective endocarditis, catheter-associated bloodstream infections, urinary tract infections and bacteraemia. Patients at risk for infection include those with critical illnesses in intensive care units, severe underlying disease or weakened immune system. The use of urinary catheters, antibiotics and exposure to another patient with VRE also constitute a risk. Healthy individuals are usually not at risk of becoming infected with VRE (4, 5).

Transmission of VRE between patients may occur by direct contact (e.g. unwashed hands) or indirectly by touching contaminated surfaces. For an individual to become colonized with VRE, other than transiently on the skin, the bacteria must enter the body through the mouth, i.e. faecal-oral transmission. VRE are hardy organisms with the ability to survive for long periods in adverse environmental conditions such as high temperature and drying (6). Thus, practicing good hand hygiene and adequate cleaning in hospital environments are essential to reduce reservoirs of VRE.

The prevalence of VRE in Sweden remained low until 2007, when a large outbreak involving three hospitals in separate counties occurred (7). Since then, VRE outbreaks have been reported in several counties in Sweden. However, only sporadic cases of VRE have been identified in the Östergötland County, and the health care never experienced an outbreak. The aim of this study was to investigate a sudden increase in VRE cases among patients admitted to a Surgical Unit at Vrinnevi Hospital, Norrköping, Sweden, and to describe the measures taken to control the outbreak.

Methods

Settings

There are three hospitals in the Östergötland County: one tertiary care hospital (Linköping University Hospital) and two secondary care hospitals (Vrinnevi Hospital in Norrköping and Motala Hospital). The Surgical Unit at Vrinnevi Hospital in Norrköping treats patients with diseases and injuries that require surgery or care. The unit consists of two wards, ward 11 with focus on colorectal and acute general surgery, and ward 12 with focus on upper abdominal surgery and urology. Each ward offers a total of 28 beds divided into 14 rooms, six multiple-bed rooms (four four-bed rooms and two two-bed rooms) and eight single-bed rooms. Health care workers and storage of medical supplies are shared between the two wards.

Epidemiological investigation

In April 2021, a VRE-positive patient (index) was re-admitted and placed in a single-bed room (room 14) in ward 12 at the Surgical Unit at Vrinnevi Hospital in Norrköping (Figure 1). The patient suffered from

severe underlying diseases, had received multiple antibiotic treatment, and had recently undergone a nephrostomy procedure, i.e. an artificial opening created between the kidney and the skin allowing for the urinary diversion directly from the upper part of the urinary system. The patient had been admitted to the ward on several previous occasions with placement in different single- and four-bed rooms. A few months earlier, the patient was involved in a VRE-transmission event including another patient. The transmitted *E. faecium* strain carried the *vanA* gene and showed resistance to ampicillin, imipenem, piperacillin/tazobactam and vancomycin.

Subsequent screening for VRE by collecting rectal swabs was initiated for all patients admitted to ward 11 and 12 at a weekly basis and when discharged. The screening was later extended to also include a cultivation sample from patients admitted to any of the three hospitals in the Östergötland County who had previously been admitted to the Surgical Unit at Vrinnevi Hospital in Norrköping. Also, screening samples were collected from a number of chosen units in the Östergötland County with high-risk patients. Cases were defined as patients colonized or infected with VRE, with the same antibiogram and *van* gene as the index patient. An additional inclusion criterion was that there had to be a connection in time and space with the index patient or another VRE-positive patient involved in the outbreak.

Environmental sampling

To control the environmental contamination and cleaning efficacy after one discharge cleaning, and to evaluate the implemented cleaning routine with three approved quality controlled discharge cleanings, environmental samples were collected in ward 12 during the ongoing outbreak. Sampling were obtained from possible contaminated sites, including bed mattresses, -rails and -lamps, chairs, tables, shelves, window boards, door knobs, call buttons and -wall panels, toilet seats, -handles, and -paper roll holders, wash basins, shower heads and -stools, and medical devices in seven rooms previously occupied by VRE cases, one wash room, and one shared bathroom in the corridor. In addition, environmental samples were collected in one single-bed room at the Emergency Unit at Vrinnevi Hospital in Norrköping to which one of the VRE cases in ward 12 had been relocated. Also, environmental sampling was obtained from two examination rooms at the Urological Unit at Vrinnevi Hospital in Norrköping.

Bacterial cultures

Environmental samples were collected with ESwabs (Copan Diagnostics Inc. Murrieta, CA, USA) and inoculated into VRE-broth supplemented with vancomycin (0.75 mg/L, Sigma-Aldrich, USA) and aztreonam (10 mg/L, MP Biomedicals, France) overnight, and thereafter onto VRE Chromagar plates supplemented with chloramphenicol and dipotassium telluride (CHROMagar, France). The plates were incubated at 35 °C for approximately 48 h. Bacteria were identified to the species level with a MALDI Biotyper 3.0 (Bruker Corporation, Karlsruhe, Germany). The antibiotic susceptibility to ampicillin, imipenem, piperacillin/tazobactam, linezolid and vancomycin was tested according to the recommendations of EUCAST (www.eucast.org).

PCR

Carriage of the *vanA* or *vanB* gene was verified with GeneXpert, using the Xpert *vanA*/ *vanB* kit (Cepheid, Sunnyvale, CA, USA), according to the manufacturer´s instructions. Cepheid GeneXpert is an entirely integrated and automated analytic system where sample preparation, extraction, amplification and detection with real-time polymerase chain reaction (PCR) are conducted in individual reagent cassettes. Every cassette contains a sample processing control (SPC) and a probe check control (PCC). The SPC contains spores of *Bacillus globigii* and controls the deoxyribonucleic acid (DNA) lysis, sufficient sample preparation and that the PCR-reaction has not been inhibited. The PCC controls the efficiency of the reagent cassette by measuring a fluorescent signal and calculate algorithms before starting the PCR reaction.

WGS

All VRE isolates from patients and the environment were subjected to whole genome sequencing (WGS). DNA was prepared from 10µL of each isolate, using EZ1 DNA Tissue Kit (Qiagen, Germantown, MD, USA), with an included pre-heating step at 95 °C and shaking at 350 rpm. Twenty ng of DNA was used for library preparation, using QIAseq FX DNA Library Kit (Qiagen, Germantown, MD, USA) with 8 min of fragmentation time. DNA libraries were sequenced on the MiSeq platform (Illumina, San Diego, CA, USA) with 2 x 300 bp paired-end reads, and the samples obtained an average sequencing depth of 214x.

Data analysis was performed in CLC Genomics Workbench v. 10.1.1 with the Microbial Genomics Module v. 2.5.1 (Qiagen, Germantown, MD, USA). Multilocus sequence typing (MLST) analysis was performed using the PubMLST (pubmlst.org) (8) scheme for *Enterococcus faecium* (9). Read mapping and variant calling was performed against the *E. faecium* reference genome with NCBI accession number NC_021994, with the following thresholds to call a variant: depth of coverage ≥ 20, frequency ≥ 90% and Phred score ≥ 20. A quality filter was then applied that retained variants with a sequencing depth of ≥ 20x in all samples and a distance ≥ 10 bp to the next variant, and the resulting variants were used to create an SNP (single nucleotide polymorphism) tree and calculate genetic distances between samples. Previous studies suggest that isolates of *E. faecium* with a distance of ≤16 SNPs are likely to belong to the same clone (10).

Results

Outbreak cases

Approximately 800 patients were screened for VRE during the screening period lasting from the end of April until the end of August 2021. Within a week from re-admittance of the index patient in ward 12, two more VRE cases were reported. These patients were placed in two different four-bed rooms with shared bathroom in ward 12, of which one (room 9) had previously been occupied with the index patient at the exact same bed space. The patient who was involved in an earlier VRE-transmission event with the index patient had also stayed in this four-bed room. Nine more cases were reported in ward 12 up until the end of May (Figure 1). Additional VRE cases were reported in the Geriatric Unit (*n* = 2), the Emergency Unit (*n* = 2), ward 11 at the Surgical Unit (*n* = 1), the Cardiology Unit (*n* = 1) and the Infectious Diseases Unit (*n* = 1)

at Vrinnevi Hospital, and one case in a senior centre in Norrköping. Also, yet another case was admitted to the Haematology Unit at Linköping University Hospital. Like the index patient, all VRE cases carried the *vanA* gene and were resistant to ampicillin, imipenem, piperacillin/tazobactam and vancomycin. The majority had previously received multiple antibiotic treatments, and a large proportion of the cases identified in ward 12 had undergone a cystoscopy and/or transrectal ultrasound.

Environmental sampling results

A total of 417 environmental samples were collected, of which 346 (83%) in ward 12 at the Surgical Unit (104 samples collected after three discharge cleanings), 28 (7%) in the Emergency Unit, and 43 (10%) in the Urological Unit at Vrinnevi Hospital in Norrköping. Of these, 13 (3%) showed growth of VRE carrying the *vanA* gene and were resistant to ampicillin, imipenem, piperacillin/tazobactam and vancomycin. To the culture-positive locations belonged one bed mattress, the window board, the toilet seat, -handles, and -paper roll holder in one of the four-bed rooms (room 9) in ward 12; the toilet paper roll holder, shower stool, chair and one medical device in one of the single-bed rooms in ward 12 (room 14 where the index patient was recently placed); the bed rails in another single-bed room in ward 12 (room 8); the call button, the alarm wall panel and wash basin in the single-bed room at the Emergency Unit where one of the VRE cases from ward 12 had stayed. Only one environmental sample (1%) showed growth of VRE after three approved quality controlled discharge cleanings in ward 12 (Figure 1).

WGS results

Three outbreak clusters and one unique clone were recognized with MLST and whole genome-wide phylogenetic analysis (Figure 2). The larger cluster consisted of 25 isolates (71%) with a difference of 0-7 SNPs, and belonged to the ST 203 clone. Included in this cluster were 12 VRE cases reported in ward 12 and all 13 VRE-positive environmental samples. In the second cluster, seven isolates (20%) with a difference of 0-5 SNPs and that belonged to ST 1839 were included. Among these isolates were two VRE cases reported in the Geriatric Unit and the Emergency Unit, respectively; one case reported in ward 12, the Cardiology Unit, and a senior centre in Norrköping, respectively. The third cluster consisted of two isolates (6%) belonging to ST 80 with a difference of 1 SNP among them. One of the patients in this cluster had recently returned from abroad and were cared for at the Emergency Unit, while the other patient was admitted to ward 11 at the Surgical Unit at Vrinnevi Hospital, Norrköping. The unique clone (ST 612) belonged to a patient admitted to the Haematology Unit at Linköping University Hospital (3%).

Control measures

In order to quickly and effectively minimize the extent of the VRE outbreak, a group with representatives from the Surgical Unit, Chief Physician and the Hospital Management at Vrinnevi Hospital in Norrköping, the Department of Communicable Disease and Infection Control, the Department of Infectious Diseases, the Department of Clinical Microbiology, the Communication Unit, and the Cleaning organization of the Östergötland County was established and had weekly meetings to discuss the current situation and operatively handle the outbreak. Control measures were immediately taken, which included improved

compliance to basic hygiene and cleaning routines, replacing all furniture and equipment that were worn or impossible to disinfect, cleaning encumbered shelves, removing tape from different medical devises and equipment, disposal of long curtains in windows and cubicle curtains that had not been properly changed between patients. Patient admittance stop and contact isolation was implemented in ward 12, and all multiple-bed rooms were used as single-bed rooms.

Initially, discharge cleaning with virkon (1%) and alcohol-based disinfectant with tenside of rooms to which a confirmed VRE-positive patient had been admitted was performed once. However, since environmental cultures remained positive, triggering new episodes of VRE transmission, the discharge cleaning was intensified to three times followed by a visual hygiene observation and an approved quality control in terms of adenosine triphosphate (ATP) measurement detecting actively growing microorganisms. Twenty locations in each patient room, including the bathroom, were subjects for ATP measurement, i.e. a total of 60 locations were measured in each discharge cleaned patient room. All additional patient rooms in the unit (non-VRE) were discharge cleaned once with a following approved quality control. Even the daily cleaning in the Surgical Unit was quality controlled and disinfection of general surfaces was extended. For a limited period, the Cleaning organization of the Östergötland County took over the cleaning of patient rooms from the health care workers who normally performed the cleaning. The cleaning routine with three approved quality controlled discharge cleanings was later implemented in the Geriatric Unit after observing an increasing number of VRE cases with connection to this unit. The routine was also implemented in other hospital units in the Östergötland County with VRE-positive patients.

From September 2018 to May 2019, an antibiotic audit and feedback program regarding patients with infections related to abdominal surgery had been implemented. The result was a decrease in the use of carbapenems and cephalosporins, and an increase in the use of piperacillin/tazobactam. When the VRE outbreak was identified, prescriptions for the three months preceding the outbreak were analysed. The result was that the prescription pattern obtained by the previous project had not changed as piperacillin/tazobactam was prescribed in >50% of cases. However, no similar audit and feedback program regarding patients with infections related to urological surgery had ever been done. An analysis of prescriptions for the three months preceding the outbreak showed that cephalosporins and ciprofloxacin were dominating the prescription pattern. In a meeting with the prescribing urological surgeons, recommendations regarding antibiotic use aiming to reduce the impact of the patient colonisation resistance (i.e. gut flora) with respect to the ongoing outbreak were discussed and implemented.

Discussion

In the present study, an outbreak of VRE starting at the Surgical Unit at Vrinnevi Hospital in Norrköping, Sweden was described. Active screening, which has been shown to reduce VRE transmission (11), was initiated. A total of 22 patients were involved in the outbreak, and four different clones of VRE were identified, ST 203 (*n* = 12), ST 1839 (*n* = 7), ST 80 (*n* = 2) and ST 612 (*n* = 1) (Figure 2). The ST 203 clone

caused the largest cluster and predominated among patients in ward 12 at the Surgical Unit, and most likely originated from the index patient. The ST 1839 clone was mainly found among patients admitted to, or who had previously been admitted to, the Geriatric Unit at Vrinnevi Hospital, whereas no obvious connection was observed among the other clones. The different clusters were unrelated to each other, and the existence and transmission of the ST 1839, ST 80 and ST 612 clones were possibly revealed as a result of the extended VRE screening and had otherwise remained unidentified.

Antibiotic exposure, especially to substances with a high likelihood of disturbing the gut flora, has been identified as a risk factor for both acquisition and transmission of VRE, and consequently antibiotic stewardship is of importance both to prevent and confine an outbreak of VRE (12-14). The present outbreak, although the main efforts focused on hygiene measures, shed light on the fact that antibiotic prescribing related to urological surgery needed improvement, and measures were taken accordingly.

The majority (77%) of the cases reported in ward 12 (*n* = 13) had been placed in one of the four-bed rooms (room 9) at some time during admittance. The index patient stayed in this room on several different occasions both before and when diagnosed with VRE in December 2020, and was placed at the same bed space each time. One of the two VRE cases reported in April 2021, and another case reported in May, had been placed at the exact same bed space as the index patient. Remaining cases admitted to this room had been placed at some of the other three available bed spaces (Figure 1). All environmental samples collected during the outbreak belonged to the ST 203 cluster (Figure 2). Of the 10 VRE-positive environmental samples collected in ward 12, nine samples were found either in the single-bed room (40%) where the index patient had recently stayed (room 14), or in the above mentioned four-bed room (50%). Most findings were associated with the bathroom (Figure 1). Colonization pressure, generally defined as the proportion of VRE-positive patients in a unit during a specific period, is significantly associated with VRE acquisition. Studies have shown an increase in VRE colonization during hospital stay and that patients sharing room and toilet with a VRE carrier had a high acquisition rate (4, 15). This is consistent with our findings, which indicate a high proportion of VRE cases and VRE-positive environmental samples in ward 12, and especially in the four-bed room.

Hygiene observations performed by the Department of Communicable Disease and Infection Control revealed several scarcities in the hospital environment at the Surgical Unit, which were immediately attended to. For example, the cubicle curtains used as separation barriers between bed spaces in the multiple-bed rooms had not been properly handled. According to the recommendations established by the Department of Communicable Disease and Infection Control, separation barriers should not be made of fabric but have a hard and flat surface able to manage disinfection. If used, cubicle curtains should always be changed between patients. Cubicle curtains are widely used in hospitals and other health care facilities. They are frequently handled by patients, visitors and health care workers, and easily become contaminated. Studies have shown that cubicle curtains become progressively contaminated with pathogenic bacteria and may be involved in transmission among patients (16, 17).

Improved cleaning and disinfection in hospital environments decreases contamination of surfaces and VRE acquisition among patients. It has been shown that a high proportion of rooms with VRE-positive patients had positive environmental cultures even after discharge cleaning (4, 18). Thus, repeated cleaning may be more effective (19). The implemented cleaning routine in the Surgical Unit was shown to be successful. The number of VRE cases and VRE-positive environmental samples were drastically reduced after three approved quality controlled discharge cleanings per room after a VRE-positive patient. One of the big challenges in this outbreak was the confusion regarding whether the health care workers at the unit or the Cleaning organization of the Östergötland County was responsible for cleaning certain environmental surfaces and medical devices. In addition, a lack in knowledge on how to perform disinfection in terms of frequency and method was observed among the executors. This may have resulted in environmental surfaces not being properly disinfected, thus constitute a risk for VRE transmission. The concern of assigning responsibility for cleaning, which methods should be used, and how often it should be performed has been reported in other studies (18, 20, 21). Recently, automated no-touch technologies have been used to enhance the effectiveness of disinfection of VRE and other pathogens. Disinfection with hydrogen peroxide vapour can have important advantages. Hydrogen peroxide is a broad-spectrum disinfectant considered active against the majority of pathogens implicated in nosocomial infections (22). Studies have shown that using hydrogen peroxide vapour may reduce the risk of VRE acquisition with 80-100% (23-25). Ultraviolet light is another technology that have proven effective against VRE (26). These methods may with advantage be used as a supplement to routine discharge cleaning of rooms in hospital settings.

Conclusion

An outbreak of VRE, including four different clones and involving 22 patients, starting in a Surgical Unit was confirmed with WGS. The control measures taken were successful, and when no further VRE cases had been reported in nearly two months the outbreak was declared over. To prevent emergence of further outbreaks, VRE screening among high-risk patients in the Östergötland County was extended, efforts in antibiotic stewardship were increased, the routine with three approved quality controlled discharge cleanings was maintained, and the use of multiple-bed rooms was restricted.

Abbreviations

VRE: Vancomycin-resistant *Enterococcus faecium*

MIC: Minimum inhibitory concentration

PCR: Real-time polymerase chain reaction

SPC: Sample processing control

PCC: Probe check control

DNA: Deoxyribonucleic acid

WGS: Whole genome sequencing

MLST: Multilocus sequence typing

ST: Sequence type

SNP: Single nucleotide polymorphism

ATP: Adenosine triphosphate

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and materials

All data generated or analysed during this study are included in this published article.

Competing interests

The authors declare that they have no competing interests.

Funding

No funding source

Authors' contributions

MG was the lead investigator of this study, performed the environmental sampling and was the major contributor to writing the manuscript. JW supervised the PCR and WGS analysis, analysed and visualized the study data, and contributed to writing the manuscript. AH contributed to writing the manuscript. All authors read and approved the final manuscript.

Acknowledgements

Not applicable

References

1. Vehreschild M, Haverkamp M, Biehl LM, Lemmen S, Fatkenheuer G. Vancomycin-resistant enterococci (VRE): a reason to isolate? Infection. 2019;47(1):7-11.

2. Asgin N, Otlu B. Antibiotic Resistance and Molecular Epidemiology of Vancomycin-Resistant Enterococci in a Tertiary Care Hospital in Turkey. Infect Drug Resist. 2020;13:191-8.

3. Miller WR, Murray BE, Rice LB, Arias CA. Resistance in Vancomycin-Resistant Enterococci. Infect Dis Clin North Am. 2020;34(4):751-71.

4. Reyes K, Bardossy AC, Zervos M. Vancomycin-Resistant Enterococci: Epidemiology, Infection Prevention, and Control. Infect Dis Clin North Am. 2016;30(4):953-65.

5. Levitus M, Rewane A, Perera TB. Vancomycin-Resistant Enterococci. StatPearls. Treasure Island (FL)2021.

6. Fiore E, Van Tyne D, Gilmore MS. Pathogenicity of Enterococci. Microbiol Spectr. 2019;7(4).

7. Soderblom T, Aspevall O, Erntell M, Hedin G, Heimer D, Hokeberg I, et al. Alarming spread of vancomycin resistant enterococci in Sweden since 2007. Euro Surveill. 2010;15(29).

8. Jolley KA, Bray JE, Maiden MCJ. Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome Open Res. 2018;3:124.

9. Homan WL, Tribe D, Poznanski S, Li M, Hogg G, Spalburg E, et al. Multilocus sequence typing scheme for Enterococcus faecium. J Clin Microbiol. 2002;40(6):1963-71.

10. Schurch AC, Arredondo-Alonso S, Willems RJL, Goering RV. Whole genome sequencing options for bacterial strain typing and epidemiologic analysis based on single nucleotide polymorphism versus gene-by-gene-based approaches. Clin Microbiol Infect. 2018;24(4):350-4.

11. Cheah ALY, Cheng AC, Spelman D, Nation RL, Kong DCM, McBryde ES. Mathematical modelling of vancomycin-resistant enterococci transmission during passive surveillance and active surveillance with contact isolation highlights the need to identify and address the source of acquisition. BMC Infect Dis. 2018;18(1):511.

12. Donskey CJ, Chowdhry TK, Hecker MT, Hoyen CK, Hanrahan JA, Hujer AM, et al. Effect of antibiotic therapy on the density of vancomycin-resistant enterococci in the stool of colonized patients. N Engl J Med. 2000;343(26):1925-32.

13. Webb BJ, Majers J, Healy R, Jones PB, Butler AM, Snow G, et al. Antimicrobial Stewardship in a Hematological Malignancy Unit: Carbapenem Reduction and Decreased Vancomycin-Resistant Enterococcus Infection. Clin Infect Dis. 2020;71(4):960-7.

14. Hughes A, Sullivan SG, Marshall C. Factors associated with vanA VRE acquisition in Cardiothoracic Surgery patients during an acute outbreak. Infect Dis Health. 2021.

15. Ajao AO, Harris AD, Roghmann MC, Johnson JK, Zhan M, McGregor JC, et al. Systematic review of measurement and adjustment for colonization pressure in studies of methicillin-resistant Staphylococcus aureus, vancomycin-resistant enterococci, and clostridium difficile acquisition. Infect Control Hosp Epidemiol. 2011;32(5):481-9.

16. Larocque M, Carver S, Bertrand A, McGeer A, McLeod S, Borgundvaag B. Acquisition of bacteria on health care workers' hands after contact with patient privacy curtains. Am J Infect Control. 2016;44(11):1385-6.

17. Shek K, Patidar R, Kohja Z, Liu S, Gawaziuk JP, Gawthrop M, et al. Rate of contamination of hospital privacy curtains in a burns/plastic ward: A longitudinal study. Am J Infect Control. 2018;46(9):1019-21.

18. Goodman ER, Platt R, Bass R, Onderdonk AB, Yokoe DS, Huang SS. Impact of an environmental cleaning intervention on the presence of methicillin-resistant Staphylococcus aureus and vancomycin-resistant enterococci on surfaces in intensive care unit rooms. Infect Control Hosp Epidemiol. 2008;29(7):593-9.

19. Byers KE, Durbin LJ, Simonton BM, Anglim AM, Adal KA, Farr BM. Disinfection of hospital rooms contaminated with vancomycin-resistant Enterococcus faecium. Infect Control Hosp Epidemiol. 1998;19(4):261-4.

20. Mitchell BG, White N, Farrington A, Allen M, Page K, Gardner A, et al. Changes in knowledge and attitudes of hospital environmental services staff: The Researching Effective Approaches to Cleaning in Hospitals (REACH) study. Am J Infect Control. 2018;46(9):980-5.

21. Dancer SJ, Kramer A. Four steps to clean hospitals: LOOK, PLAN, CLEAN and DRY. J Hosp Infect. 2019;103(1):e1-e8.

22. Falagas ME, Thomaidis PC, Kotsantis IK, Sgouros K, Samonis G, Karageorgopoulos DE. Airborne hydrogen peroxide for disinfection of the hospital environment and infection control: a systematic review. J Hosp Infect. 2011;78(3):171-7.

23. Passaretti CL, Otter JA, Reich NG, Myers J, Shepard J, Ross T, et al. An evaluation of environmental decontamination with hydrogen peroxide vapor for reducing the risk of patient acquisition of multidrug-resistant organisms. Clin Infect Dis. 2013;56(1):27-35.

24. Frakking FNJ, Bril WS, Sinnige JC, Klooster JEV, de Jong BAW, van Hannen EJ, et al. Recommendations for the successful control of a large outbreak of vancomycin-resistant Enterococcus faecium in a non-endemic hospital setting. J Hosp Infect. 2018;100(4):e216-e25.

25. McKew G, Phan T, Cai T, Taggart S, Cheong E, Gottlieb T. Efficacy of aerosolized hydrogen peroxide (Deprox) cleaning compared to physical cleaning in a Burns Unit. Infect Dis Health. 2021;26(3):161-5.

26. Yang JH, Wu UI, Tai HM, Sheng WH. Effectiveness of an ultraviolet-C disinfection system for reduction of healthcare-associated pathogens. J Microbiol Immunol Infect. 2019;52(3):487-93.

Figures

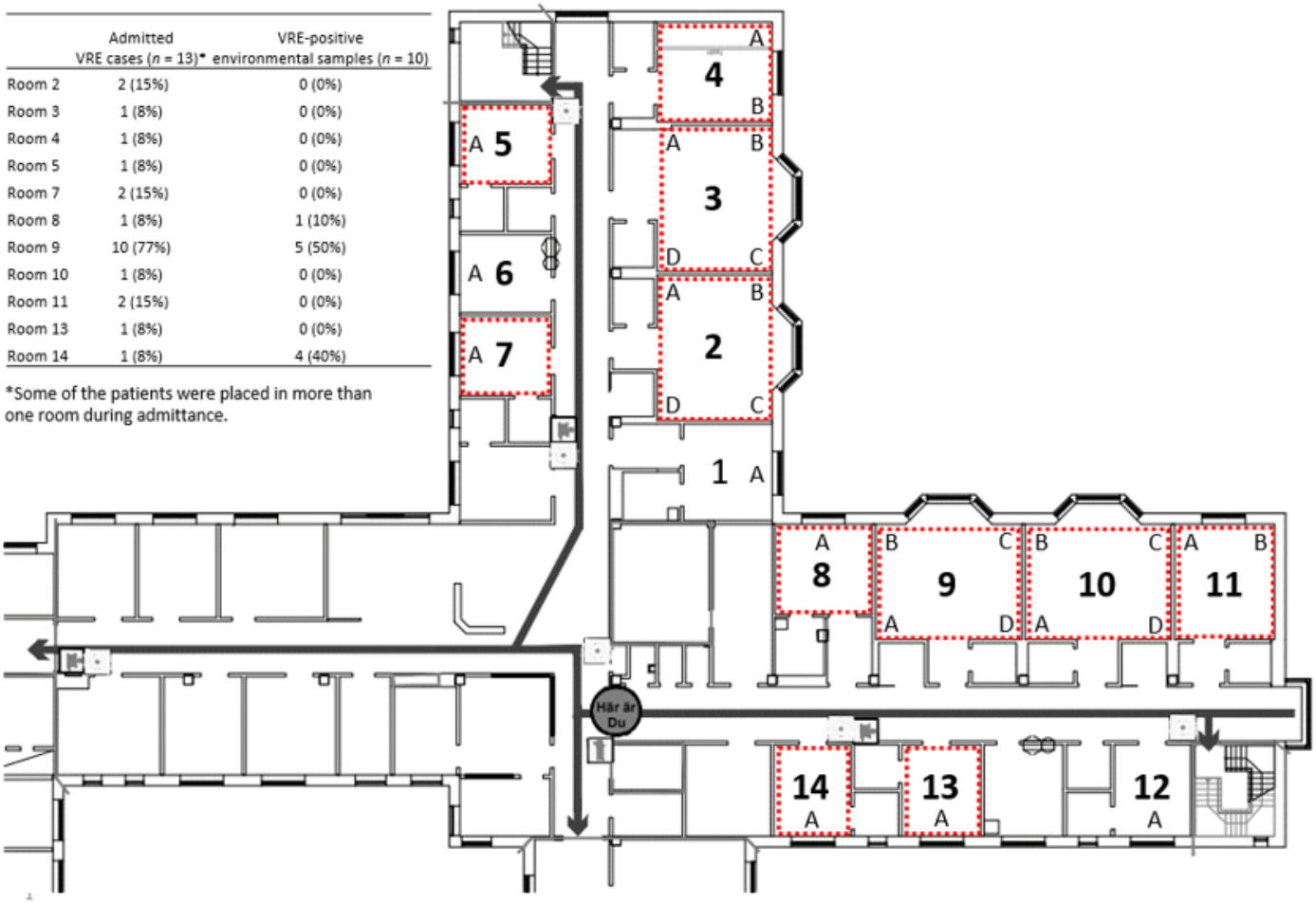

Figure 1

Drawing of ward 12 at the Surgical Unit where the clustering of vancomycin-resistant *Enterococcus faecium* (VRE) took place. Letters (A-D) indicating the number of available bed spaces per room. Rooms where patients culture-positive for the bacterium had been placed are marked with a dotted red square. The number of admitted VRE cases and VRE-positive environmental samples per room are shown in the inserted table.

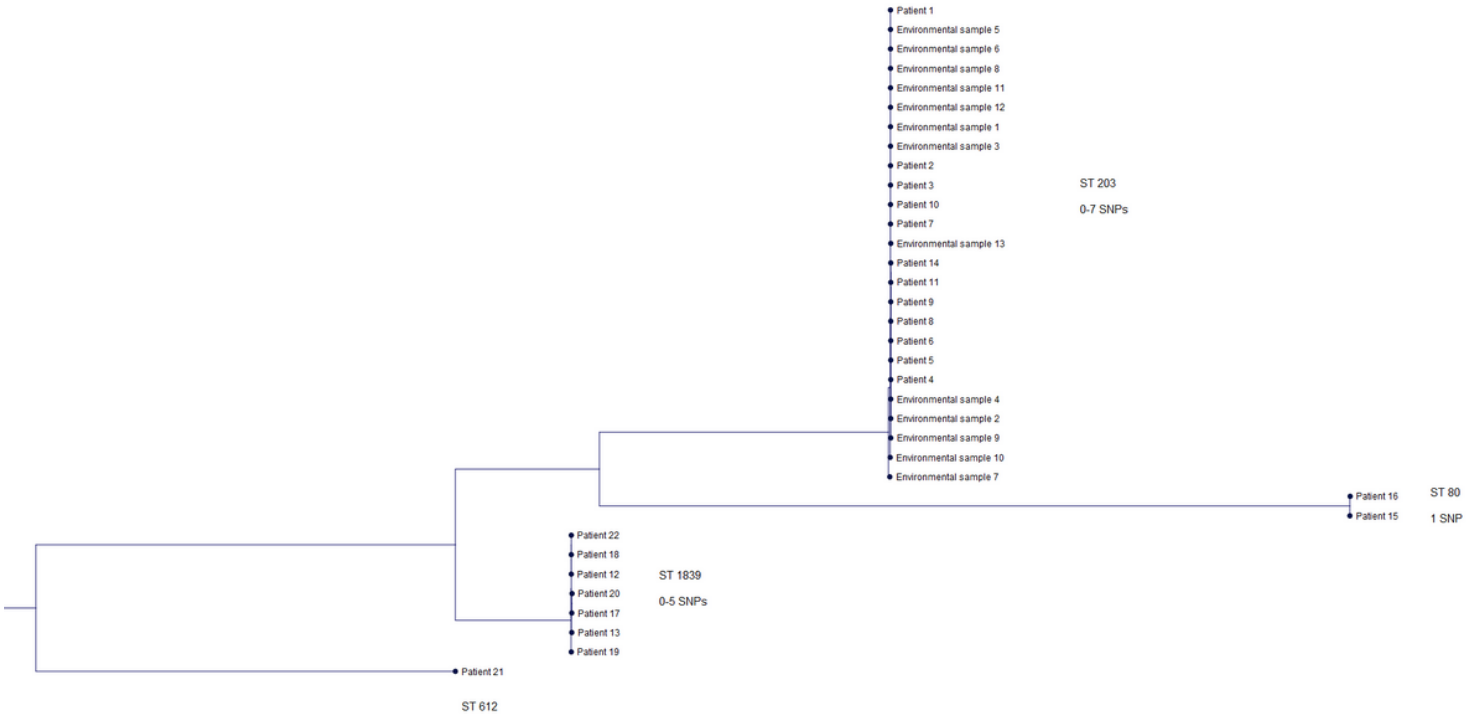

Figure 2

Phylogenetic tree based on single nucleotide polymorphism (SNP) analysis of whole genome sequencing (WGS) data from 35 vancomycin-resistant *Enterococcus faecium* (VRE) isolates. Four outbreak clones were identified: ST 203 (isolates differing by 0-7 SNPs), ST 1839 (isolates differing by 0-5 SNPs), ST 80 (isolates differing by 1 SNP) and ST 612 (unique clone).