Epidemiological and molecular characterization of the hospital-associated outbreak with vancomycin-resistant enterococci circulated in the Copenhagen area during 2013-2014 for a single hospital

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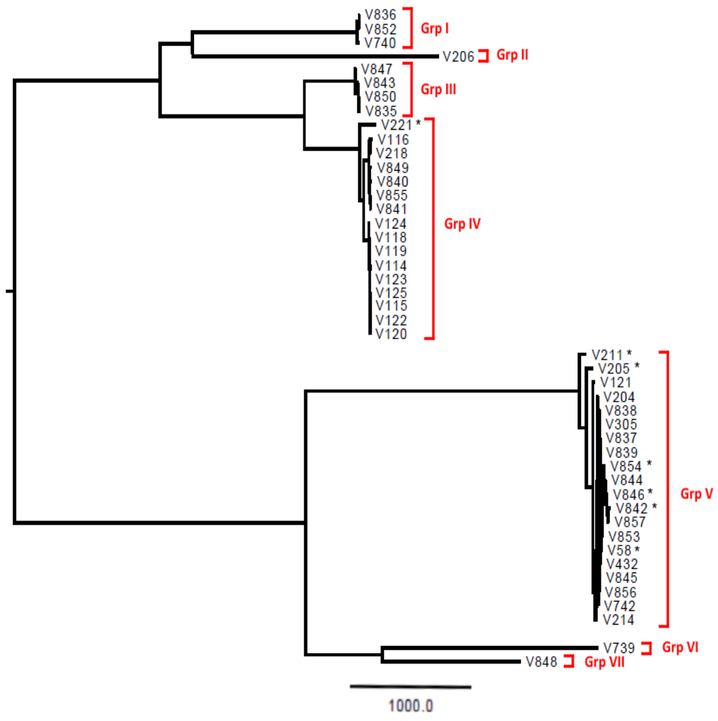
Introduction: Vancomycin-resistant *Enterococcus faecium* (VRE) is a nosocomial pathogen, frequently associated with multidrug resistance. Typing methods used for outbreak investigation is an essential tool in determining bacterial relatedness.

Objectives: Hospital-associated outbreak with vancomycin-resistant *Enterococcus faecium* has been previously reported in the Copenhagen area. We would like to describe the situation with the VRE in a single hospital during the last 3½ years and present the results of 2 different molecular methods, which were used to define the similarity between the isolates.

Methods: Species identification was done by MALDI-TOF. Susceptibility testing for vancomycin was performed using Etest (BioMerieux) and interpreted according to the recommendation by EUCAST and confirmed by VanA gene PCR at the Reference laboratory.

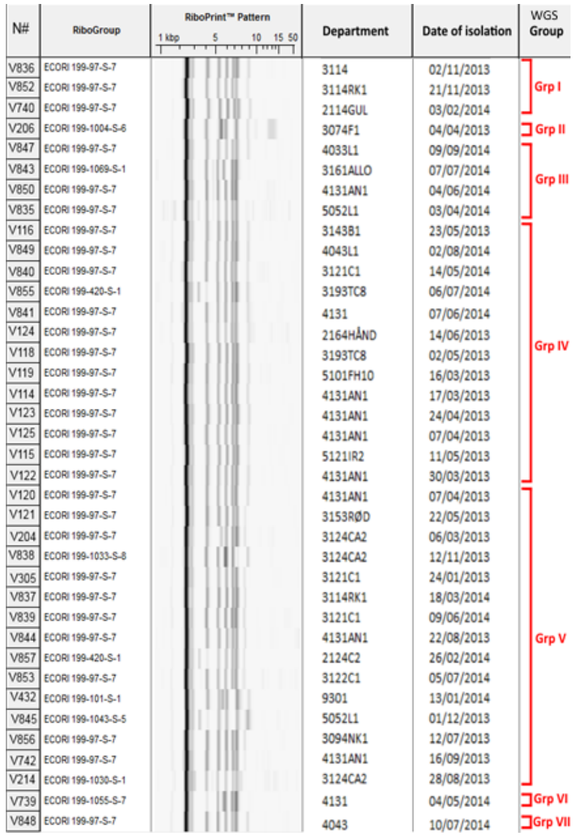
Figure 1. Distribution of the vancomycin-resistant *E.faecium* based on the results for whole-genome sequencing.



*Pattern for ribotypning is not available.

Selected isolates were sequenced on the Illumina MiSeq platform. 2 x 150 bp paired-end-reads were produced. Reads were mapped with Stampy to a reference genome (AUS004_NC-017022).

Figure 2. Results for ribotyping combined with epidemiological data for *E.faecium* isolates.



Ribotypning was performed on the selected isolates using the Riboprinter® microbial characterization system (DuPont Qualion) with the restriction enzyme EcoRI.

The analysis was performed according to manufacture precept and the analysis of the generated data was performed using the Riboprinter software.

The diversity of the samples were represented by cerebrospinal fluid (N=1); blood culture (N=4), urine culture (N=9); fluid from abdominal drain (N=4); tips of central venous catheter (N=5); swabs of various sample sides (N=4), as well as eleven other single isolates.

Dissemination of the isolates based on WGS and ribotypning is presented in the Figure 1 and 2. The results of WGS showed presence of 2 large (Group IV and Group V) and two small clones (Group I and III), as well as some sporadic isolates (Group II, Group VI, Group VII). In opposite, almost all isolates belong to a single type 97-S-7 due to the results of ribotypning. We did not found any consistence between these two methods.

Conclusions: Based on the WGS results there are two main VRE clonal types, causing the VRE outbreak. The results of ribotypning shows dissemination of one large VRE clonal type at Rigshospitalet in the period of investigation. Comparing the two molecular biology methods shows that WGS divides the VRE isolates in more clonal groups than ribotyping, which made it more discriminative.

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