

## 00105 Clonal spread of vancomycin-resistant *Enterococcus faecium* ST80, ST117 and ST203 across Belgian hospitals

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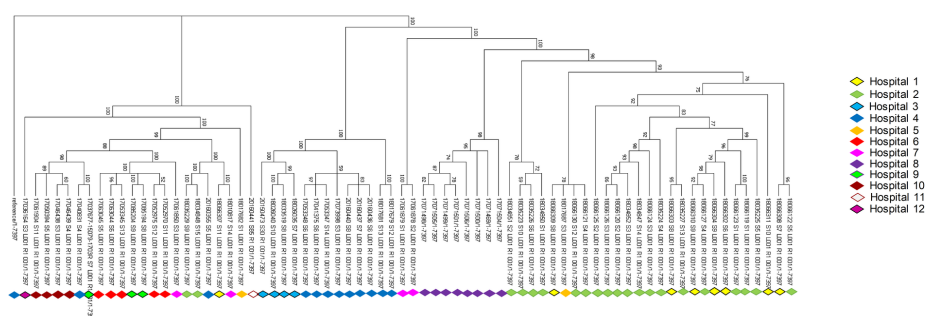
**Background:** Since 2014, the Belgian National Reference Centre (NRC) receives an increasing number of vancomycin resistant *E. faecium* (VREfm) strains from infected or colonized patients. Many hospitals reported on outbreaks with VREfm (n=4 in 2012 to ≥20 in 2015-2017). Our aim was to study the molecular epidemiology of VREfm across Belgian hospitals based on whole genome sequencing (WGS)

**Materials/methods:** VREfm were submitted on a voluntary basis to the NRC. Species identification was confirmed by MaldiToF (Bruker). Antibiotic susceptibility was determined according to CLSI before and to EUCAST since 2013. WGS was performed on a selection of 338 VREfm using Nextera XT (2 x250bp), MiSeq (Illumina Inc.), and followed by comparative genome analysis using Mauve and CLC Genomics Workbench v9.5.3 (clcbio, Denmark). Core genome phylogenetic analysis was performed using ParSNP followed by gene by gene analysis using Chewbbacca to identify the core genome MLST allelic differences.

**Results:** The majority of the sequenced strains belong to ST80 *vanA* (n= 80, 12 hospitals), ST117 *vanA* (n= 48, 17 hospitals), ST117 *vanB* (n= 78, 27 hospitals), and ST203 *vanA* (n= 45, 10 hospitals). Of these, 121 were isolated from an infection, 130 were screening isolates. WGS analysis revealed a polyclonal structure of VREfm outbreaks: 4 major ST80 clusters with several subclusters and 6 ST117 *vanA* clusters, were identified. A VREfm ST117 *vanB* cluster was found in 6 hospitals within the same region; a second cluster was detected in 6 hospitals in Brussels Capital region. Concentrating on ST80 *vanA*, clonal spread was found in 3 hospitals within the same area (27 genetically closely related isolates, separated by 29 core genome SNPs). The first strains were isolated in H2, followed by H1. H5 submitted 6 VREfm; 2/6 ST80 *vanA*. The postal code of 1 of them fell within the area of H1 and H2 and within the clade (Fig).

**Conclusions:** Based on the core genome data VREfm ST80, ST117 and ST203 can be divided into distinct clusters. Clonal spread of VREfm ST80 *vanA* and ST117 *vanB* within several hospitals is shown. Typing of VREfm is critical to prevent further spread of dominant clones.

Tree Belgian ST80 *vanA* positive *E. faecium* strains (WGS-based)



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