

**P0675**

**Paper Poster Session  
The MDR enterococcus**

**First 2 cases of vancomycin variable *Enterococcus faecium* in Belgium**

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**Background:** Enterococci, particularly vancomycin-resistant *Enterococcus faecium* (VRE), are important nosocomial pathogens with limited treatment options. They have low-level resistance to penicillins and aminoglycosides and are intrinsically resistant to cephalosporins. In addition, they can acquire high-level resistance to beta-lactam antibiotics, aminoglycosides and glycopeptides. Nine different types of vancomycin resistance gene clusters (*vanA*, *B*, *C*, *D*, *E*, *G*, *L*, *M*, and *N*) have been characterized on both a phenotypic and a genotypic basis in enterococci. Glycopeptide-susceptible, *vanA* positive *E. faecium* (VVE: vancomycin variable *E. faecium*) was described for the first time by Gagnon et al in 2011. The isolates were susceptible to vancomycin on phenotypic testing, although the presence of *vanHAXYZ* was demonstrated. Here, we report the identification of the first 2 VVE-strains in Belgium.

**Methods**

Species identification was performed using Malditof spectrometry (Bruker). MICs for ampicillin, linezolid, teicoplanin and vancomycin were determined according to EUCAST. Highlevel streptomycin and gentamycin resistance were determined by Etest according to the manufacturer's instructions (BioMérieux, France).

DNA was extracted using the NucliSens EasyMAG (BioMérieux). The presence of *vanA*, *vanB*, *vanD*, *vanE*, *vanG* was examined by PCR (Depardieu 2004). The same DNA extract was used for the qualitative detection each of the Tn1546 genes (Gagnon et al. 2011) to confirm the presence of the *vanA* operon. PCRs amplifying the seven loci used for MLST were done according to the reference (<http://efaecium.mlst.net/>). Typing was done by using PFGE.

**Results**

The two strains (20150189 and 20150190) were isolated in two different hospitals in Belgium in spring 2015. The Belgian National Reference Centre confirmed the identification of both *E. faecium* isolates. These isolates were susceptible to vancomycin, teicoplanin, tigecycline and linezolid. Both strains were found to be PCR positive for *vanA*. Both isolates were negative for the *vanB*, *vanC*, *vanD*, *vanE* and *vanG* genes.

A *vanA* confirmatory PCR was applied and confirmed the presence of *vanA*. In addition, both vancomycin susceptible isolates (20150189 and 20150190) contained the *vanH*, *vanX*, *vanY* and *vanZ* genes, whereas the *orf1*, *orf2*, *vanR* and *vanS* genes were absent. The strains represented 2 ST-types: 117 and 80. Two distinct PFGE-types were assigned to the strains.

**Conclusion**

Here we report on the first two Vancomycin Variable *E. faecium* strains.