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Poster Session VI
VRE: epidemiology and control

EPIDEMIOLOGY OF VANCOMYCIN-RESISTANT ENTEROCOCCI FROM FRANCE IN 2012

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Objectives: The aim of the study was to describe recent epidemiological features of vancomycin-resistant enterococci (VRE) collected from French hospitals in 2012.

Methods: The National Reference Center for Enterococci (NRC-Enc) received isolates suspected to be VRE from all French hospitals in 2012. All strains were identified by detection of species-specific *ddl* gene or sequencing of the *sodA* gene. Antimicrobial susceptibility testing was performed by the disc diffusion method, and following antibiotics were tested: ampicillin, streptomycin, kanamycin, gentamicin, erythromycin, lincomycin, pristinamycin, levofloxacin, chloramphenicol, doxycycline, vancomycin, teicoplanin, cotrimoxazole, linezolid, rifampicin and tigecycline. MICs of vancomycin, teicoplanin and daptomycin were determined by using E-test strips. Screening for all known *van* resistance genes was performed by multiplex PCR. All *vanA*- or *vanB*-positive *Enterococcus faecium* and *Enterococcus faecalis* isolates were typed by PFGE after *Sma*I restriction.

Results: In 2012, 369 clinical isolates (including 262 VRE) were received by the NRC-Enc from 33 different French counties. Note that 9 strains were imported from foreign countries (i.e. Bulgaria, Greece, USA, Morocco, Portugal and Turkey). The species *E. faecium* was largely predominant (n = 252; 96.2%) whereas a few isolates were *E. faecalis* (n = 7; 2,7 %) or belonged to uncommon enterococcal species (*E. hirae*, n = 1; *E. durans*, n = 1; *E. gallinarum*, n = 1). *vanA* was the most frequent resistance gene (89.3%), followed by *vanB* (10.7%). Amongst *E. faecium* isolates, 227 (90.1%), 14 (9.6%) and 1 (0.3%) were positive for *vanA*, *vanB* and *vanD* respectively. The *vanA* gene was detected in 4 *E. faecalis*, 1 *E. hirae*, 1 *E. durans* and 1 *E. casseliflavus*, whereas 3 *E. faecalis* strains were positive for *vanB*. All (except five) *E. faecium* isolates were highly resistant to ampicillin, and high-level resistance to gentamicin was detected among 76% of isolates, this proportion being much higher than that of 2011 (45%) and previous years (ca. 20%). No strain was resistant to linezolid or tigecycline, and none exhibited MIC values higher than 4 mg/L for daptomycin. By PFGE analysis, 90 different profiles were identified for *E. faecium* (including 77 *vanA*-positive clones and 13 *vanB*-positive clones), of which some spread regionally in different hospitals.

Conclusion: After an important peak in 2008-09, the number of VRE isolates received at the NRC-Enc has decreased and now remained stable. As described in previous years, some epidemic *E. faecium* clones diffuse at a regional level between closely located hospitals. Of note, there is a significant increase of gentamicin resistance in *E. faecium*, which should be kept under surveillance in the near future.