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Paper Poster Session
The MDR enterococcus

Unexpected vancomycin-resistant Enterococcus faecium outbreak in a tertiary hospital in Madrid during a carbapenemase-producing Enterobacteriaceae active surveillance programme

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Background:. Incidence of vancomycin–resistant enterococci (VRE) infections remains low in Spain although sporadic outbreaks have been reported. Active surveillance programs may help to detect increases in VRE faecal colonization which frequently precede infections. The aim of this work was to characterize and describe a hidden VRE outbreak recently detected in our hospital.

Material/methods: In August 2015 an unexpected discover of VRE isolates on selective media for carbapenemase-producing Enterobacteriaceae (chromID CARBA, BioMèrieux, France) in stool samples from hospitalized patients prompted us to reinforce VRE surveillance and a VRE screening medium (chromID VRE, BioMérieux) was also incorporated. All isolates growing as tiny blue colonies after 24h-37ºC incubation in chromID CARBA agar as well as those compatible with enterococci colonies in VRE screening medium were screened for vancomycin resistance (Etest, BioMèrieux) and confirmed by PCR (*van* genes). Antibiotic susceptibility, and clonal relatedness (PFGE, MLST) were also performed. Tn*1546* was characterized by overlapping PCRs. Patient´s main clinical characteristics and admissions were recorded.

Results: A total of 2,190 patients were studied (August-October 2015). In 36 patients (1.6%) (72%, ≥65 years-old; 23 males) vancomycin-resistant *Enterococcus faecium* (VREfm) was detected in rectal swabs. Distribution of new cases of colonization over time was as follows: 13/36 (36.1%) in August, 17/36 (47.2%) in September and 6/36 (16.6%) in October. Thirty-three percent were admitted at internal medicine, 25% at nephrology and 16.6% at gastroenterology wards. During this period, 2 patients developed a urinary tract infection by VREfm. All but one characterized isolate (29/30) encoded for *vanA* gene and were resistant (>8 mg/L) to vancomycin and teicoplanin. The *vanB* gene was detected in a single colonization isolate from a haematological patient and was susceptible to vancomycin (MIC: 4 mg/L) and to teicoplanin (MIC: 0.5 mg/L). All isolates were susceptible to linezolid and daptomicin but resistant to levofloxacin. Five PFGE-types corresponding to 2 STs and were distributed as follow: ST17 (clone A) and ST117 (clones B, C and E) associated with VanA isolates and ST117 (clone D) associated with *vanB*. Clon A-ST17 was dominant (86.6%, 27/30) while the other ones

were detected in a single isolate each. VanA transposon Tn*1546* lacked ORF1 but *VanS, VanH, VanA, VanY* and *VanZ* genes were present.

Conclusions: A hidden VREfm outbreak was initially detected using a carbapenemase producing Enterobacteriacae selective media, allowing implementation of VRE specific surveillance and detection of a high colonization pressure. Most of the isolates were *vanA*. Unnoticed VRE outbreaks may occur in countries with low incidence of infection being a risk for subsequent infection development.