

Session: P069 Enterococcal infections: epidemiology and resistance

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Vancomycin-resistant *Enterococcus faecium* endemic outbreak in Trieste hospital

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Background: Enterococci are commensals of the gastrointestinal tract and an important cause of healthcare-associated infections, particularly in immunocompromised patients. Moreover they can also be shed into the environment, where they can persist for a long time. Acquired Vancomycin resistance has been found since the 1990's, been mostly detected in *Enterococcus faecium*. In the last 2 years a dramatic increase of glycopeptides resistance in Enterococci has been observed in Trieste hospital: in March 2014 the first VRE strains were found, and they rapidly spread in all the Hospital departments, soon broadened until an endemic state, still ongoing. Strong control measures have been settled from the beginning of the outbreak. Vancomycin usage in our hospital was 2.75 DDD/100 days in 2012 and it slightly increased every year until 3.38 DDD/100 days in 2015.

Material/methods: For this work we considered the *Enterococcus faecium* VRE (VREfm) strains found from March 2014 to October 2015 when 128 consecutive, nonreplicate VRE isolates were collected. They were all identified and tested by standard automatic systems (Vitek2, Biomerieux). All the strains were confirmed and characterized by PFGE in order to establish their clonal relationship. They were also tested for the glycopeptides resistance determinants *vanA* and *vanB* and investigated for two virulence genes encoding for Enterococcal surface protein (*esp*) and glycosidase (*hylEfm*) by hybridization. MLST was performed on some strains from every different PFGE cluster in order to determine the Sequence Type. PCR for the antibiotic resistance genes (*bla*; *ermB/C/TR*; *mefA/E*; *tetM/K/O*; *aadE/A*; *aphA3*; *aacA-aphD* and *aph(2'')*-Ic was performed on a restricted number of significant strains from the different STs.

Results: From March 2014 to October 2015 we collected 128 VRE strains, 6 *Enterococcus faecalis* and 122 *Enterococcus faecium*. The outbreak immediately spread around the hospital, but with a prevalence in the Emergency Department. Most of the patients were colonized as the infections counted for less than 10% of the cases. 90% of the strains (111/122) carried the *vanA* gene and 10% were *vanB* positive. The macrorestriction analysis demonstrated that the majority of the strains were genetically related and revealed by MLST to belong to ST17. Only one ST17 strain had *hyl* gene. Almost all the *VanB* strains (9 out of 12) were genetically related and belonged to ST780 and carried the *hyl* gene. We were able to characterize the genes that conferred the resistance to tetracyclin, aminoglycosides and macrolides on a very restricted number of strains.

Conclusions: Despite the strong control measures initiated from the beginning, the VRE outbreak soon reached an endemic state, mainly associated with colonizations. According to the antibiotic consumption data in our hospital, Vancomycin usage is disputable to be related with the outbreak.