Molecular Characterization of *Van* Genes Found in Vancomycin-Resistant *Enterococcus* spp. Isolated from Hospital das Clínicas, FMUSP, São Paulo, Brazil

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Vancomycin-resistant enterococci strains (VRE) is an important pathogen related with hospital infections in many countries, presenting limited or no therapeutic options for treating serious infections. VRE has presented some different genotypes been *Van*A and *Van*B considered to be the most important in hospital environments. In the present study the authors investigated the prevalence of van genes (A, B an C) among clinical isolates of VRE in a five month period at a large tertiary hospital in Sao Paulo, Brazil. The results showed the presence of *van*A, but not *van*B or *van*C in all 43 strains of *E. faecalis* and five *E. faecium* studied. The results bring an important issue, due to the possibility of resistance spread of vanA genes, to be monitored and solved by the hospital infection control team and the microbiology and molecular biology laboratories at tertiary Hospitals.
Key Words: Enterococci, vancomycin resistance, hospital infections.

Enterococcus spp. are part of the normal gastrointestinal flora, together with close to 100 other species of aerobic and anaerobic bacteria [1]. Initially, the enterococci were considered to be only slightly virulent, however the rapid emergence and dissemination of vancomycin-resistant enterococci strains (VRE) has completely changed the clinical relevance of these pathogens. Presently, VRE are an important cause of hospital infections in many countries, with limited or no therapeutic options for treating serious infections [2,3]. There is concern that resistance genes in VRE might be transferred to other gram-positive microorganisms, making the situation even worse. In addition, VRE has caused outbreaks and became endemic in several hospitals, presenting a challenge for hospital infection control teams [2-4]

Till now, six different genotypes of VRE have been found (*Van* A, B, C, D, E and G) [3,5,6]. *Van*A and *Van*B vancomycin resistance determinants are considered to be the most important, due to conjugative transfer, which may occur via plasmids or transposons. Also, glycopeptide resistance could be passed on to other pathogens, such as methicillin-resistant *Staphylococcus aureus*, transforming them into highly dangerous, difficult to treat, pathogens [2,3,7].

We investigated the prevalence of *van* genes among clinical VRE strains found during a 5 month period at the Hospital das Clínicas da Faculdade de Medicina da Universidade de São Paulo (HCFMUSP). The samples were isolated from 48 different patients between May and September 1999, 12 of which were from surveillance cultures and 36 from patients. Five strains were identified as *Enterococcus faecium* and 43 *as Enterococcus faecalis*.

The oligonucleotide primers directed towards *van*A, *van*B and *van*C genes in enterococci and the

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Polymerase Chain Reaction (PCR) techniques used were as described by CDC's Antimicrobial Resistance Working Team [8-11].

All the strains presented the *van*A gene and produced the expected 1030 bp amplicon with *vanA* primers. None of the strains with the v*an*A gene gave positive PCR results with *van*B or *van*C primers.

In Brazil, the first vancomycin-resistant *Enterococus faecium* was isolated in Curitiba, Parana in 1996. Subsequently, numerous isolates of VRE have been made throughout Brazil. However, only some of these have been reported in the literature [12-16].

As all the strains in our study presented the *van*A gene, there is a potentially high risk that they could spread to other hospitals (13Woodford, 1998; French, 1998; 2Centinkaya et al., 2000). Consequently, infection control measures to prevent the spread of VRE have been implanted. The HCFMUSP is a large, complex, tertiary hospital with 1500 beds that attends seriously ill patients at high risk for hospital infections. This fact increases the probability of the dissemination of VRE. Additionally, as enterococci are enteric bacteria and the intestinal lumen offers a favorable environment for bacterial conjugation, the *van*A gene could be disseminated to other enterococci species and to other bacteria genera. This is an important issue that needs to be monitored and resolved by the hospital infection control team and by microbiology and molecular biology clinical laboratories. Additional studies are in progress to help determine the impact of VRE and its patterns of transmission in our hospital.

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