Brazilian Journal of Microbiology (2006) 37:117-118
ISSN 1517-8382

EMERGENCE OF VanB PHENOTYPE-*van*A GENOTYPE IN VANCOMYCIN-RESISTANT ENTEROCOCCI IN BRAZILIAN HOSPITAL

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Submitted: June 15, 2005; Approved: February 26, 2006

SHORT COMMUNICATION

ABSTRACT

In Brazil, vancomycin-resistant enterococci (VRE) have been reported as nosocomial pathogens since 1998. Recently, in a VRE surveillance in a hospital, we detected two *Enterococcus faecalis* isolates with *van*A genotype and susceptible to teicoplanin. This is the first report of VanB phenotype-*van*A genotype enterococci isolated from humans in Brazil.

Key words: enterococci, *van*A genotype, VanB phenotype, vancomycin, VRE

Vancomycin-resistant enterococci (VRE) were first reported in 1988 in Europe, and then they have emerged and disseminated as an important cause of nosocomial infections worldwide. Glycopeptide resistance in enterococci is associated with a variety of phenotypes and genotypes. Two principal phenotypes of resistance in VRE have been described and associated to nosocomial infections. In enterococci, the *van*A phenotype is characterized by high-level resistance to vancomycin and teicoplanin, whereas the VanB phenotype by vancomycin resistance and teicoplanin susceptibility. Genes encoding the *van*A- and VanB-phenotype resistance are located on transposons Tn*1546* and Tn*1547*, respectively, or in closely related transferable genetics elements (1).

In Brazil, the first *van*A *Enterococcus faecium* was isolated from a patient in São Paulo city in 1997, and the first VRE outbreak occurred in the same hospital one year after the first isolation (9). Furthermore, VRE isolates, *E. faecium* and *E. faecalis van*A genotype, were reported in São Paulo and in other states of Brazil (3,8). The Adolfo Lutz Institute (IAL), the public health laboratory of São Paulo State, in Brazil, performs the monitoring of the VRE isolates for hospitals by phenotypic and genotypic characterization. At the IAL, the VRE isolates are identified by conventional biochemical tests and by a multiplex PCR assay based on the specific detection of genes encoding D-alanine:D-alanine ligases (*ddl*) routinely used to confirm the identification of *E. faecalis* and *E. faecium* species. All isolates are initially tested by agar dilution screening method to vancomycin by CLSI recommendations (2). The MIC to vancomycin and teicoplanin are determined by broth microdilution method, according to CLSI interpretative criteria (2). The genotype is confirmed by PCR assay with specific primers for the *van*A, VanB, *van*C_1 and *van*$C_{2\text{-}3}$ genes. Molecular typing of the isolates is performed by PFGE-DR II (9).

Recently, during a VRE surveillance in a hospital located in São Paulo city, we detected two *E. faecalis* isolates resistant to vancomycin and susceptible to teicoplanin, consistent with the VanB phenotype (ET211 and ET217). These isolates were phenotypic and genotypically identified as *E. faecalis* and the resistance to vancomycin and susceptibility to teicoplanin were confirmed by two methods, the broth microdilution method and the E-test (AB Biodisk, Sweden). The MICs of vancomycin for the two isolates were above 128 μg/mL, and the teicoplanin

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MIC were 8 µg/mL for both isolates. The *van*A genotype was confirmed by PCR assay with specific primers for the *van*A and VanB genes. The molecular typing of those isolates have disclosed the same PFGE pattern for both isolates. However, this molecular pattern was different when compared with those PFGE patterns identified among the VRE isolates from the same hospital.

The phenotype and genotype results of those two isolates were confirmed by the "Laboratório Especial de Bacteriologia e Epidemiologia Molecular da Faculdade de Ciências Farmacêuticas de Ribeirão Preto - University of São Paulo". A preliminary study of characterization of the *van*A resistance elements of those isolates has shown a deletion on right terminal inverted repeated nucleotides in the Tn*1546*.

According to some reports, the VanB phenotype-*vanA* genotype incongruence is result of mutations in the regulatory *van*S gene (4-6) or *van*A (7) cluster rearrangements. In the VRE strains described in the study the loss of part of Tn*1546* can be responsible for this change in the phenotype. The data emphasize the importance on the characterization and monitoring of the resistance levels to vancomycin and teicoplanin among VRE for detecting the emergence of VanB-*van*A enterococci in Brazil.

ACKNOWLEDGMENTS

We are grateful to Dr. Nelson Ribeiro Filho and Eloisa Gagliardi, for sending the VRE isolates from the Hospital Paulistano, São Paulo, Brazil. This work had financial support from Brazilian Council for Science and Technology Development (CNPq-Grants 302628/2004-5 and 303348/2004-6 and FAPESP 05/50273-7).

RESUMO

Emergência de enterococos resistentes à vancomicina com fenótipo VanB e genótipo *van*A em hospital brasileiro

No Brasil, enterococos resistente à vancomicina (VRE) têm sido descritos como patógenos hospitalares, desde 1998. Durante um monitoramento de VRE em um hospital, foram detectadas duas cepas de *Enterococcus faecalis* com genótipo *van*A, e sensibilidade à teicoplanina. Este é o primeiro relato do isolamento de enterococo fenótipo VanB e genótipo *vanA* de amostra clínica no Brasil.

Palavras-chave: enterococos, genótipo *van*A, fenótipo VanB, vancomicina, VRE

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