EMERGENCE OF VanB PHENOTYPE-vanA GENOTYPE IN VANCOMYCIN-RESISTANT ENTEROCOCCI IN BRAZILIAN HOSPITAL

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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 vanA genotype and susceptible to teicoplanin. This is the first report of VanB phenotype-vanA genotype enterococci isolated from humans in Brazil.

Key words: enterococci, vanA 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 vanA phenotype is characterized by high-level resistance to vancomycin and teicoplanin, whereas the VanB phenotype by vancomycin resistance and teicoplanin susceptibility. Genes encoding the vanA- and VanB-phenotype resistance are located on transposons Tn1546 and Tn1547, respectively, or in closely related transferable genetics elements (1).

In Brazil, the first vanA 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 vanA 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 vanA, VanB, vanC1 and vanC2-3 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...
MIC were 8 μg/mL for both isolates. The \textit{vanA} genotype was confirmed by PCR assay with specific primers for the \textit{vanA} and \textit{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 \textit{vanA} resistance elements of those isolates has shown a deletion on right terminal inverted repeated nucleotides in the Tn\textit{1546}.

According to some reports, the VanB phenotype-\textit{vanA} genotype incongruence is result of mutations in the regulatory \textit{vanS} gene (4-6) or \textit{vanA} (7) cluster rearrangements. In the VRE strains described in the study the loss of part of Tn\textit{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-\textit{vanA} enterococci in Brazil.

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Palavras-chave: enterococos, genótipo \textit{vanA}, fenótipo VanB, vancomicina, VRE

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RESUMO

Emergência de enterococos resistentes à vancomicina com fenótipo VanB e genótipo \textit{vanA} em hospital brasileiro

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

Palavras-chave: enterococos, genótipo \textit{vanA}, fenótipo VanB, vancomicina, VRE

REFERENCES