First Characterization of a Cluster of VanA-Type Glycopeptide-Resistant Enterococcus faecium, Colombia

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From August 1998 to October 1999, glycopeptide-resistant enterococci (GRE) were isolated from 23 infected patients at a teaching hospital in Medellín, Colombia. Identification at the species level and by multiplex polymerase chain reaction assay indicated that all isolates were Enterococcus faecium. The isolates were highly resistant to ampicillin, ciprofloxacin, gentamicin, penicillin, streptomycin, teicoplanin, and vancomycin; they were susceptible only to chloramphenicol, linezolid, and nitrofurantoin. Determination of glycopeptide genotype indicated the presence of the vanA gene in all isolates. Molecular typing by pulsed field gel electrophoresis showed that all isolates were closely related. This study is the first molecular characterization of GRE in Colombia.

Enterococci normally colonize the intestinal tract of humans and other animals, with urinary tract infection being the most common enterococcal infection reported in humans (1). In recent years, enterococci have become important nosocomial pathogens: the organisms have been reported as the second leading cause of urinary tract infections and the third leading cause of nosocomial bacteremia in hospitalized patients (2). The most commonly identified species is Enterococcus faecalis, followed by E. faecium (3). E. gallinarum, E. casseliflavus, and E. durans have been reported less often (4,5).

The most important characteristics of these organisms include their inherent resistance to several antimicrobial agents and their ability to acquire resistance determinants. Resistance against such diverse groups of drugs as β-lactams, macrolides, aminoglycosides, and glycopeptides continues to evolve. The ability to grow in the presence of glycopeptides results from the change of the C-terminal residue of peptidoglycan precursors (D-Ala) to D-lactate (VanA, VanB, and VanD phenotypes) (6,7) or D-serine (VanC, VanE, and VanG phenotypes) (8–10). The change alters the affinity of the glycopeptide for its natural target (6). Six different gene clusters have been described (vanA-B-C-D-E-G) (6,10–12). The most predominant phenotype in E. faecium is VanA; VanA strains are highly resistant to both vancomycin and teicoplanin. The vanA gene cluster is located on transposons or related elements (6) and has also been found in nonenterococcal species such as Arcanobacterium (Corynebacterium) haemolyticum, Oerskovia turbata, Bacillus circulans, and Streptococcus galolyticus (13–16). A van cluster with a high degree of homology to the vanA cluster (designated vanF) has been found in the bio-pesticide organism Paenibacillus popilliae (17).

Since the initial discovery of glycopeptide-resistant enterococci (GRE) in the United Kingdom (18), nosocomial isolates of GRE have been reported from around the world (14); these isolates have also been found in healthy people in the community outside the hospital (19). In Latin America, GRE have been reported in Argentina (20) and Brazil (21). We report here the first isolation and characterization of a cluster of VanA-type glycopeptide-resistant E. faecium in a teaching hospital in Colombia.

Materials and Methods

Bacterial Isolates

Hospital San Vicente de Paul is a 650-bed teaching hospital providing tertiary care for Medellín, Colombia, and neighboring towns, an area with a population of 1.5 million inhabitants. From August 1998 to October 1999, we collected organisms from 23 patients. Enterococci were isolated from infected patients by classical microbiologic techniques (3). Identification at the species level was performed by the Vitek gram-positive card (bioMérieux SA, Marcy l’Etoile, France), according to the manufacturer’s recommendations.

Antimicrobial Susceptibility Testing

Initial identification of resistance to vancomycin was performed by the Vitek system (bioMérieux SA). We confirmed resistance to vancomycin, determining MICs by an agar dilution method as recommended by the National Committee for Clinical Laboratory Standards (22) on Mueller-Hinton agar...
Polymerase Chain Reaction (PCR) for Species Identification of Enterococci and the van Genes

For species identification of enterococcal isolates, the genes encoding D-alanine-D-alanine ligases specific for *E. faecium* (ddl*E. faecium*), *E. faecalis* (ddl*E. faecalis*), vanC-1 (*E. gallinarum*), and vanC-2 (*E. casseliflavus*) were detected by a multiplex PCR assay, as described by Dutka-Malen et al. (23). Primers D1 (5´GCTTCTTCCTTTACGACC) and D2 (GTTC-CGAGTCCTAAAAAAC) for the multiplex PCR assay, as described by Dutka-Malen et al. (23). The protocol was performed separately for detection of genes encoding D-alanine-D-alanine ligases specific for *E. faecium*, *E. faecalis*, and *E. gallinarum*. A similar multiplex PCR protocol was performed for species identification of *E. faecium* BM4147, *E. faecalis* V583, and *E. gallinarum* BM4174 were used as control strains.

Genotyping

Molecular typing was performed by pulsed-field gel electrophoresis (PFGE). Chromosomal DNA was obtained by the procedure of Antonishyn et al. (24): a loopful of bacterial colonies from a 24-h isolate was grown until *A600* was 0.1 in brain heart infusion broth at 37°C. Bacteria were harvested by centrifugation at 4°C, and the pellet was resuspended in cell suspension buffer (1 M NaCl, 10 mM Tris-HCl, pH 8.0). The suspension was embedded in 1.5% agarose and disks were made. Disks were placed in lysis buffer (6mM Tris-HCl, pH 8, 1 M NaCl, 100 mM EDTA, 0.5% Brij-58, 0.2% Na deoxycholate, and 0.5% N-lauroyl sarcosine) with additional RNase (20 µg/mL) and lysozyme (1 mg/mL) and incubated for 4 h at 37°C. The disks were washed with EDTA-sarcosine buffer (0.5 M EDTA, pH 8, and 0.1% N-lauroyl sarcosine), placed in proteinase K solution (100 µg/mL), and incubated overnight at 50°C with mild agitation. Disks were washed four times with Tris-EDTA buffer (Tris 10 mM, pH 7.5, and 1 mM EDTA) for 30–60 min at room temperature on a rocker.

DNA was digested as described (25). Briefly, DNA fixed in the agarose disks was preincubated in 1 mL of buffer E (6 mM Tris, pH 8, 20 mM KCl, 6 mM MgCl2, and 6 mM 2-mercaptoethanol) at 25°C for 30 min. Restriction was performed for 17 h in 60 µL of restriction buffer containing *Sma*I (20 U) at 25°C. The reaction was stopped by addition of 10 µL of sterile loading buffer. Gels were prepared with 1% agarose in 0.5x TBE buffer (50 mM Tris, pH 8, 50 mM boric acid, 0.2 mM EDTA). A DNA ladder (50–1000 kb) was used as the molecular size marker. Fragments were separated by electrophoresis (CHEF-DR II system, Bio-Rad Laboratories, Inc., Richmond, CA) at 6 V/cm, with switch times ramped from 1 s to 35 s over 23 h at 14°C. After staining with ethidium bromide, the restricted DNA fragments were viewed under UV light and photographed. A vancomycin-susceptible strain of *E. faecium* isolated in the same hospital was included in the PFGE protocol as the control. We interpreted the band patterns by the criteria of Tenover et al. (26).

Results

GRE Isolates and Identification

From August 1998 to October 1999, 23 GRE were collected from the same number of patients hospitalized in various wards in Hospital San Vicente de Paul. The first isolate was recovered from the pleural fluid of a patient hospitalized in the surgical ward. Isolates came from urine (35%), peritoneal fluid (22%), surgical wound (17%), intra-abdominal abscess (13%), pleural fluid (9%), and bile (4%). Molecular identification by PCR showed that all isolates were *E. faecium*, in agreement with the results of the Vitek gram-positive identification card (bioMérieux SA).

Antimicrobial Susceptibility Testing

All isolates had high levels of resistance to ampicillin (MICs 128–256 µg/mL), ciprofloxacin (>32 µg/mL), gentamicin (1,024 µg/mL), penicillin (256–512 µg/mL), streptomycin (>2,000 µg/mL), teicoplanin (>32 µg/mL), and vancomycin (512 µg/mL). The isolates were susceptible to chloramphenicol (4–8 µg/mL), linezolid (1 µg/mL), and nitrofurantoin (<32 µg/mL).

PFGE and Glycopeptide-Resistant Genotype

Analysis of PFGE patterns obtained with the 23 *E. faecium* isolates showed that 21 isolates had the same banding pattern. The remaining two isolates had an additional band around 242 kb (Figure, lanes 2 and 15), indicating that all isolates were closely related (26). This finding suggests the presence of a bacterial clone spreading through different wards during the period of the study. The vanA gene was detected in all isolates, in agreement with the antimicrobial susceptibility tests (high-level resistance to both vancomycin and teicoplanin).

Discussion

The emergence of multiresistant GRE is a serious nosocomial problem with important implications for hospital infection control. Although the geographic distribution of GRE is worldwide, the epidemiology appears to differ within and across regions. For example, isolates from hospitalized patients in France were shown to be genetically unrelated...
The restriction patterns of the 23 VanA-type \(E.\) faecium isolates from Medellín, Colombia. Lane 1: a susceptible isolate of \(E.\) faecium. MWM, molecular weight marker.

As found by others (42–44), chloramphenicol was one of the two agents that retained in vitro activity against GRE in this investigation. In a retrospective study of 14 patients with clinical responses, 57% showed improvement after treatment with chloramphenicol (43). Microbiologic response was 73% in 11 patients evaluated in the same study (43). Although no lasting adverse effect related to use of the drug occurred, treatment with chloramphenicol was discontinued for two patients because of chloramphenicol-induced bone marrow suppression (43). In another study of 51 patients with bloodstream infection due to vancomycin-resistant \(E.\) faecium, 61% and 79% showed a clinical and microbiologic response to chloramphenicol, respectively, but no corresponding decrease in bloodstream infection occurred (45). In our study, patients with urinary tract infections (UTI) (eight cases) were initially treated successfully with nitrofurantoin (100 mg/6 h). Ampicillin (12 g/day) was used in patients with infections other than UTI. In the lat-
ter group, however, the death rate was 33%, mostly because of severe sepsis. Chloramphenicol was not used in this group of patients. Although no controlled trials have demonstrated the effectiveness of chloramphenicol for the treatment of GRE, this antibiotic could be a therapeutic alternative in Colombia.

Linezolid, a new compound from the oxazolidinone group, has just been launched in Colombia; our findings indicate that it was active against all isolates tested. Linezolid has emerged as a therapeutic alternative for multiresistant GRE in Colombia, as in other parts of the world where it is currently available. However, linezolid-resistant *E. faecium* clinical isolates have already been reported in relation to long courses of therapy (21–40 days) (46). A linezolid-resistant *E. faecium* isolated from a patient without prior exposure to an oxazolidinone has also been described (47).

In this study, we report the first isolation and characterization of a multiresistant cluster of VanA-type *E. faecium* in a Colombian hospital. The emergence of this problem and the limitation of therapeutic options require the implementation of specific infection control measures and antibiotic policies to avoid further dissemination.

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References


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