MOLECULAR CHARACTERIZATION OF GLYCOPEPTIDE-RESISTANT *Enterococcus faecium* (VREfm) FROM 30 HOSPITALS IN ARGENTINA

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OBJECTIVES

@ TO DETERMINE THE RESISTANCE PATTERNS TO DIFFERENT ANTIMICROBIAL AGENTS.

@ TO CHARACTERIZE THE MECHANISM OF GLYCOPEPTIDE RESISTANCE.

@ TO DETERMINE THE CLONAL RELATION-SHIP BETWEEN ISOLATES BY PFGE. Enterococci (Ent) as a cause of nosocomial infection have become more prevalent over the last 20 years, both in US and in western European countries. Moreover, strains of Ent have acquired resistance to almost all antimicrobial agents, including vancomycin (VAN). The first *Enterococcus faecium* vancomycin resistant (VREfm) clinical isolate in Argentina was detected during 1997. Since then, VREfm have emerged in our country as colonizing or infecting strains in many hospitals (Htals). Through the surveillance on antimicrobial resistance, conducted by the WHONET Argentina Network (37 Htals), we noted in the last three years, an increase in the prevalence of vancomycin resistance among non-mobile *Enterococcus* spp. (species other than *E. gallinarum* and *E. caselliflavus/flavescens*) from infecting samples (FIG. 1). From Jan. 1997 to Dec. 2000, we received at the Antimicrobial Division of the National Institute on Infectious Diseases, a total of 189 VREfm isolates from 30 Argentine hospitals (FIG. 2). Names and locations of the Hatls., and number of strains recovered from the particular Htal. are listed in TABLE.



MATERIALS AND METHODS



STRAINS: From Jan.1997 to Dec. 2000, a total of 189 VREfm were isolated from 30 Argentinean hospitals (Htals.) (**FIG. 3**). 125 (66.1%) VREfm were collected from 20 Htals. in Cap. Fed., 52 (27.5%) from 6 Htals. in Buenos Aires and 12 (6.4%) from 4 Htals. in Cordoba, Stata Fe and Chaco (**FIG. 4**). Collected strains were identified in each Htal. to species level by biochemical characterization using Facklam 's recommendations (*1998. J. Clin. Microbiol. 36.1584-1587*). For each patient, only one isolate and one infection/colonization site was considered. Strains came from different clinical sources, but principally were from rectal swab (n/%) (145/76.7) (**FIG. 5**). Most of the VREfm were isolated from ICU (46.5%) and Medicine (36%) (**FIG. 6**). 80.5% patients from whom VREfm were recovered were colonized, 14.8 were infected and 4.7% was no possible to asses the clinical significance.

SUSCEPTIBILITY TESTING: Minimal inhibitory concentrations (MICs) to ampicillin (AMP), vancomycin (VAN), teicoplanin (TEI), gentamicin (GEN), streptomycin (STR), tetracycline (TET), chloramphenicol (CMP), erythromycin (ERY), ciprofloxacin (CIP) were determined by agar dilution according NCCLS M7-A5.

PCR: The presence of van genes was investigated by PCR with a Biometra thermal cycler, using specific primers for *van*A and *van*B (*Courvalain P. 1995. J. Clin. Microbiol. 33:24-27*) in standard conditions. Specific primers for 16S gene were used as control of DNA extraction (*Greisen, K.1994. J. Clin. Microbiol. 2:335-351*). DNA template was prepared by boiling, and 5µl of the supernant was used for the reaction mixture.

PFGE: Enterococcal genomic DNA was prepared and digested with *Sma*I, as previously described (*De Lencastre. 1999. Microb. Drug Resist... 5:113-128).* DNA fragments were separated in 0.8% agarose using a CHEF-DRIII (Bio-Rad Laboratories, CA), in same conditions that described by De Lencastre. Isolates were considered genetically indistinguishable and were assigned to the same strain type (e.g. type A) if their restriction patterns had the same number and size of bands. Isolates with 1-6 band differences in their restriction pattern were considered closely or possible related and were assigned to a subtype (e.g., subtype A1). Isolates whose restriction patterns differed by >6 bands were considered to be unrelated and were assigned to different strain types (e.g. A, B, C, etc.). The similarity between isolates was determined by visual comparation.

RESULTS



CONCLUDINGS REMARKS

× The percentage of resistance was high for VAN, TEI,

× 98% of the isolates were genotype vanA and only 3

A total of **35** different clonal types were identified

***** Almost 60% of the isolates belonged to VREfm CLONE

X VREfm CLONE 1 was classified in 24 clonal subtypes

CMP and TET (3.7 and 6.3% respectively) (FIG.7).

strains presented genotype vanB (FIG.8).

(FIG.9).

1 (FIG.10).

(FIG.11).

MP, STR, GEN, ERY and CIP, but relatively low for

X VREfm CLONE 1 was susceptible to TET and CMP, resistant to ERY, CIP and highly resistant to STR, GEN and AMP, avoiding the possibility of synergistic activity with aminoglycosides (FIG.12).

*** VREfm CLONE 1** was present during all the period in study (FIG.13)

X VREfm CLONE 1 was detected in 20/30 Htals (FIG.14).

X VREfm CLONE 1 was dominant in 10/20 Htals. from Capital Federal , 4/6 Htals. from Provincia de Buenos Aires and 3/4 from other cities (FIG. 15). * The increase in the incidence of VREfm in Argentina was due, at least in part, to the Clonal Dissemination of VREfm 1 within the Htals. and between different Htals.