Tracking nosocomial Vancomycin-resistant Enterococcus faecium outbreak by clinical and molecular epidemiology in a teaching hospital in Bogota, Colombia. 2016.

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ABSTRACT

VRE was first isolated in Europe and the United States by the end of the 1990s because of misuse and overuse of antibiotics in livestock and hospital settings. (1) Enterococcus spp. genuses is ranked as the fifth most frequently identified pathogens among agents responsible for HAIs, according to the latest report of the Centers for Disease Control and Prevention (CDC) (2,3). It belongs to the ESXAF cep isolated bacteria which have the ability to “escape” from most of the currently available antibiotics. This is why, in March 2017, the WHO included Vancomycin-resistant Enterococcus (VRE) as priority pathogen for research and development of new therapeutic options within the health-care setting, as an urgent measure of global public health. (4) This tendency is also observed in Colombia where Enterococcus spp. was classified amongst the five most common microorganisms related to HAI s during the past years. (5) The purpose of this study is to describe the spread of VRE occurred at a 802-bed hospital in Bogota during 2016 using molecular and epidemiological approaches.

INTRODUCTION

The antimicrobial resistance (AMR) is a public health problem directly related with the attending medical practice and the abuse of prescribing antimicrobial drugs in situations they do not represent a health benefit. Microorganisms with extended antimicrobial resistance patterns are a threat to the current global epidemiological transition (communicable diseases to non-communicable diseases) and it is estimated for the year 2050 that infectious diseases could reemerge as main diseases) and it is estimated for the year 2050 that infectious diseases could reemerge as main causes of mortality in the world due to the limited therapeutic spectrum (6,7).

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MATERIAL AND METHODS

The present study was conducted in an 802-bed, tertiary-care teaching Hospital, in Bogota, Colombia. For the microbiology study and molecular typing, a total of thirteen nonduplicated VRE isolates were recovered in a 2-month period from the 15 outbreak patients. Isolates from the first and third patients of the outbreak were not included in the molecular approach since it was not possible to recover at least one sample. Antimicrobial drugs sensitivity was determined by two different techniques: automated method with VITEK 2 system (software version 1.02 bioMérieux, USA), and manual microdilution methods for glycylglycine susceptibility of Vancomycin and Teicoplanin, based on Clinical Laboratory Standards Institute (CLSI) 2014 criteria. Multiple locus Variable Number Tandem Repeats fingerprinting (MLVF) was the typing method we finally adapted to determine clonality, and presence or absence of resistant genes was evaluated by PCR.

RESULTS

For the transmission analysis, Hospital tracking information was obtained from medical records of all patients belonging the outbreak (15 patients). We adopted the time-location-molecular (TLM) algorithm described and implemented by Willmann et al (34) in Germany in 2015.

DISCUSSION

Molecular results obtained in this study allowed us to achieve our goal to describe the VRE spread; four (4) different clonotypes were identified by MLVF, 69% (9 isolates) belonged to clone (34) in Germany 2015. Further reasons for this almost unique clone spread could be explained by different factors, as virulence capacities associated to this clonal profile; nevertheless, this approach also contributed to an accurate evaluation of the effectiveness in the epidemiological measures taken for the outbreak control and we plan to keep on using in next opportunities.