TITLE: DETECTION OF vanA GENE IN ENTEROCCI ISOLATED FROM CLINICAL AND MUNICIPAL WASTEWATER

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Environmental dissemination of genes associated to antibiotic resistance bacteria is a worldwide concern since the potential risk for public health that it possesses. Vancomycin is an important antibiotic to treat serious nosocomial enterococci infections. Human activities, those related with clinical practices performed in hospitals, can potentiate the transfer and selection of clinically-relevant resistant bacteria such as vancomycin resistant enterococci (VRE). Species of enterococci acquire resistance to antibiotics with relative ease, and they diffuse these genes of resistance to other species. This resistance has increased in recent years due to an excessive use of this antimicrobial agent among ambulatory patients and general population, with a marked tendency toward self-medication. In this work we assess the presence of vanA gene in vancomycin resistant enterococci (VRE) isolated from hospital effluent and from municipal wastewater in Buenos Aires City (Argentina). In our study, although enterococci were detected in the samples from both sources, VRE were found in 30% of the samples from the hospital effluent and in 75% of the samples of municipal wastewater. Both sources showed a high prevalence of E. faecium. Twelve VRE isolated from Hospital de Clínicas José de San Martín wastewater and eighteen VRE obtained from Buenos Aires city municipal wastewater were studied using PCR to detect vanA gene. Results indicated presence of vanA gene in all VRE isolates from municipal wastewater and in eleven (92%) VRE isolates from clinical wastewater. This high presence of vanA gene in VRE isolated from wastewater is in accordance with clinical data that most nosocomial infections with VRE in Argentina is associated to vanA positive isolates. These results indicate that not only clinical but also municipal wastewater plays an important role in the dissemination of antibiotic resistant genes in environmental niches.