Clonal relationship between high-level vancomycin resistant *Enterococcus faecium* of human and food origin

Delpech, G.¹, Sparo, M.^{1*}, Pourcel, G.¹, Corso, A.², Gagetti, P^{.2}, Sánchez Bruni, S.¹ ¹ Universidad Nacional del Centro de la Provincia de Buenos Aires (Av. Pringles 4375 (7400)-Olavarría, Argentina), ² ANLIS-"Dr. Carlos G. Malbrán" (Av. Vélez Sarsfield 563 (1281)-Ciudad de Buenos Aires, Argentina), *E-mail: <u>msparo@salud.unicen.edu.ar</u>

Enterococci are part of the indigenous microbiota of human and food of animal origin. When these bacteria behave as etiologic agents of invasive diseases, eradication is difficult due to their natural and acquired resistance to antimicrobials. Enterococcus faecium is one of the most frequently recovered species in food of animal origin and in patients with health-care associated infections. E. faecium with high-level vancomvcin resistance (VRE) represents a significant therapeutic problem. especially in patients with invasive infectious diseases. VRE strains have been reported for human and food of animal origin isolates. In Argentina, specifically in Central region of Province of Buenos Aires there is a lack of information about clones that colonize food of animal origin. The aim of this study was to investigate the clonal relationship between VRE of human and food origin. Bacterial isolates were recovered from food (artisanal salami, 1; artisanal cheese, 2) produced in mediumsized establishments in the region and from different patients with rectal colonization or invasive infections from Intensive Care Unit (ICU), Hospital Ramón Santamarina Tandil (HRS), Buenos Aires (blood culture, 3; abdominal fluid, 1; liver biopsy, 1; leg cellulitis, 1, rectal swabs, 2; mattress, 1) during 2013. Isolates were stored (triplicate) in 30% glycerol-broth at -70 ° C. Study of encoding vancomycin resistance gene (vanA) was carried out by DNA amplification (PCR). For molecular typing, Pulsed-Field Gel Electrophoresis (PFGE) was performed. Total DNA was digested with Smal and obtained band patterns were analyzed. In all VRE isolates, vanA gene was detected. Isolates could be differentiated in 6 clonal types: A, B, C, D (1 and 2), E and F. Clone A: 3 isolates of clinical origin (blood cultures). Clone B: 3 isolates of clinical origin (rectal swabs, mattress). Clone C: 2 clinical isolates (abdominal fluid, liver biopsy). Clone D: 2 subtypes were observed, D1 (artisanal salami) and D2 (artisanal cheese). Clones E and F: respectively, a clinical (leg cellulitis) and a food origin (cheese) isolates. In VRE isolates from different origin, concordance of vancomycin resistance encoding gene was found. Clonal spread among clinical strains was observed. Spread of VRE clones between humans and food was not detected. However, carry out of extended resistance monitoring protocols on the regional ecosystem is needed since its relevance for Public Health.

Key words: *E. faecium*, vancomycin, clonal relationship