Title: GENETIC DIVERSITY OF *Enterococcus* spp. FROM FECAL SAMPLES OF MAGELLANIC PENGUINS FROM THE NORTH COAST OF RIO GRANDE DO SUL, BRAZIL.

Authors: Prichula, J.[1,2], Pereira, R. I.[1,2], Cardoso, L. A.[1], Wachholz, G. R.[2], Santestevan, N. A.[1], Cunha, G. R.[2], Tavares, M.[3], d'Azevedo, P. A.[2], Frazzon, A. P. G.[1]

Affiliations: [1]UFRGS - Universidade Federal do Rio Grande do Sul (Sarmento Leite, n° 500, Porto Alegre, RS, Brasil). [2]UFCSPA - Universidade Federal de Ciências da Saúde de Porto Alegre (Sarmento Leite, n° 245, Porto Alegre, RS, Brasil). [3]CECLIMAR - Centro de Estudos Costeiros, Limnológicos e Marinhos da UFRGS (Av. Tramandaí, 976, Imbé, RS, Brasil).

Abstract:

Enterococcus spp. are commensal organism of the gastrointestinal tract of humans and others animals. Until today, limited studies have been evaluated the presence of enterococci in marine animals samples, probably due to the migratory habits of some species and the difficulty in obtaining samples from this environment. For this reason, this study aimed to evaluate the genetic diversity of enterococci by analyzing the chromosomal DNA fragmentation profiles using the pulsed-field gel electrophoresis (PFGE) technique, isolated from fecal samples of magellanic penguins (*Spheniscus magellanicus*). Cloacal swabs were collected from 11 magellanic penguins found along the North coast of Rio Grande do Sul, Brazil. A total of 172 enterococci were isolated. The chromosomal DNA of enterococci was purified, digested with *Sma*I restriction endonuclease. The separation of the fragments was performed on pulsed-field electrophoresis system using the CHEF DR lll (Bio-Rad) with the following running parameters established in previous studies. The analysis of the sample fragmentation profiles was performed using the *Bionumerics* 7.1 (Applied Maths) software. For this study, 17 distinct clonal profiles with 80% of similarity or higher and a *singleton* unrelated to the other profiles. The main clonal profile (C14) consisted of 54 *E. faecalis*, with 82.6% similarity between them, obtained from three penguins. The second profile that showed more clonal isolates was the C3 clone, 21 isolates of *E. faecium*, followed by the C9 clone with18 *E. mundtii*, and C8 clone containing 18 isolates of *E. faecium*. The clonal profile C13 showed 13 *E. faecium,* C15 clone contained 11 *E. faecalis*, C2 clone presented five *E. faecalis,* and C5 and C6 clones contained five *E. hirae*. Clonal profiles C4 and C11 consisted of four *E. hirae*, followed by the C12 clone with three *E. hirae*, the C16 clone that contained two *E. faecium*, the C7 and C17 clones that showed two *E. faecium*, and C1 and C10 clones that were formed by two *E. faecalis*. In conclusion, our data indicate that the results obtained by PFGE revealed a large number of clones and showed that this technique is effective to verify the clonal relationship of enterococci resistant and virulent strains isolated from marine animals, contributing to elucidate the trajectory of spread of resistant and virulent bacterial strains originating from these animals on marine ecosystems.

Keywords: enterococci, genetic diversity, magellanic penguins, PFGE

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