

TITLE: Antimicrobial resistance in Antarctic penguins microbiota: establishing a reference for antimicrobial resistance in bird's microbiota.

AUTHORS: MEREGALLI, R.T<sup>1</sup>.; KLEMBERG, V.S<sup>1</sup>.; PETRY, M.V<sup>2</sup>.; CARDOSO, M.R<sup>1</sup>., TAVARES, M<sup>1</sup>.; AMORIM, D.B<sup>1</sup>.; HORN, F. <sup>1</sup>

INSTITUTION: <sup>1</sup> UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL, PORTO ALEGRE, RS.

<sup>2</sup> UNISINOS, SÃO LEOPOLDO, RS

ABSTRACT:

Populations of Antarctic seabirds are considered sentinels of environmental changes in Southern Oceans. Because Antarctic penguins (AP) are among the wild birds with least contact with humans, they are potential indicators of antimicrobial resistance (AR) in the environment. The goal of this work was to identify the presence of AR genes in bacteria from the intestinal microbiota of *Pygoscelis antarcticus* and *P. papua* and to compare it with *Spheniscus magellanicus*, a penguin specie that inhabit the south of South America. Feces from *P. antarcticus* ( $n=46$ ), *P. papua* ( $n=12$ ) and cloacal swabs of *S. magellanicus* ( $n=19$ ) were enriched in BHI broth and submitted to growth in the presence of erythromycin(ER), vancomycin(VN), tetracycline(TE) or streptomycin (ST) according to the MIC (CLSI). Among the *P. antarcticus* samples ( $n=38$ ), 4 grew in the presence of ER; 1 in VN; 6 in TE and 1 in ST. Among the *S. magellanicus* samples ( $n=19$ ), 3 grew in the presence of ER, 1 in VN, 11 in TE and 2 in ST. All the *P. papua* samples ( $n=6$ ) were susceptible to all antimicrobials. The resistant isolates were screened by PCR for the presence of resistance genes *erm(B)*, *van(B)*, *tet(M)* and *int*, and the bacterial genus was determined by the 16sRNA sequence. From *P. antarcticus*, among isolates resistant to ER, we identified *Staphylococcus* sp., the *erm(B)* gene was absent. The VN resistant isolate has the *van(B)* gene but its genus has not yet been identified. Among isolates resistant to TE, we found *Staphylococcus* sp., *Serratia* sp., *Citrobacter* sp. and *Enterococcus* sp., the latter presenting *int* and *tet(M)*. The ST resistant isolate was *Enterococcus* sp., no resistance genes were found. From *S. magellanicus*, isolates resistant to ER were *Staphylococcus* sp., and *erm(B)* was absent. In the VN resistant isolate, the genus has not yet been identified and the *van(B)* was absent. In the TE resistant isolates, the genus were *Vagococcus* sp., *Aeromonas* sp., *Citrobacter* sp., *Enterococcus* sp., *Serratia* sp. and *Escherichia* sp.; the *tet(M)* has been found in the last 3 genera. Among ST resistant isolates, we found *Serratia* sp. and not yet identified microorganism; no resistance genes were found. In the DNA extracted from feces of *P. antarcticus* ( $n=25$ ), 1 sample had the *tet(M)*, 5 had *int*, 1 had *van(B)* and 1 had *erm(B)*. In the DNA extracted from feces of *P. papua* ( $n=8$ ), 1 sample had *erm(B)*, 5 had *tet(M)*, 7 had *int* and 1 had *van(B)*. According to our results, AR was higher in isolates from *S. magellanicus* than in AP.

KEYWORDS: *Pygoscelis antarcticus*, *Pygoscelis papua*, *Spheniscus magellanicus*, antimicrobial resistance, microbiota