

INVESTIGATION OF ANTIBIOTIC-RESISTANT ENTEROBACTERIALES IN SHELLFISH AND OYSTERS FROM BABITONGA BAY - JOINVILLE, SOUTHERN BRAZIL - FROM THE ONE HEALTH PERSPECTIVE.

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INTRODUCTION

According to the World Health Organization, more than 700,000 people worldwide die from infections resistant to antimicrobial therapy each year; if nothing is done, 10 million deaths are estimated by 2050. The misuse of antibiotics, whether in human therapy or animal husbandry, as well as inadequate sanitary conditions and food handling, contribute to this issue. Resistant bacteria are found in human, animal and environmental microbiota, and may be readily transmitted among them. In Brazil, not all citizens have access to basic sanitary conditions, leading to the dumping of waste into the environment, including strains showing phenotypic and genotypic resistance profiles. In aquatic environments, their dissemination can directly affect living organisms whose feeding strategy is filtration, such as molluscs that are consumed by humans. Therefore, such a food chain may play a role in the transfer of resistance genes among different microorganisms. In this sense, our aim was to investigate the occurrence of antibiotic-resistant Enterobacterales isolated from raw oysters and shellfish collected by fishermen for their own consumption at the Baía Babitonga estuary, Southern Brazil.

METHODOLOGY

Two samplings of shellfish (*Mytella* sp.) and oysters (*Sacostrea* sp. and *Crassostrea* sp.) were performed, in December 2020 and January 2021, near an island (Ilha do Mel) inside Babitonga Bay, totaling four mollusc samples. In the laboratory, they were washed with running water, brushed and sanitised with 70 % alcohol. The shells were opened under aseptic conditions. Peptone water (175 mL) was added to the intravalvar content of each shell (17.5 g). This was then incubated in duplicate for 24 h at 37°C. After this period, 1 mL of the enriched culture was transferred to 9 mL of saline solution (0.9 %), then inoculated with disposable loop into MacConkey Agar and cultivated under 37°C for an additional 24 h. The plates were analysed macroscopically and some representative colonies were picked for isolation. Another round of cultivation in MacConkey medium was performed. Bacterial isolates were identified through an automated system (Vitek II, bioMérieux), and their antimicrobial susceptibility testing was performed on the basis of EUCAST criteria.

RESULTS

From the sampling carried out in December 2020, three different Enterobacterales species were isolated in shellfish (*Escherichia coli*, *Klebsiella pneumoniae* and *Serratia fonticola*) and one species was isolated in oysters (*Klebsiella oxytoca*). Disregarding intrinsic resistance, the strains isolated from shellfish were resistant to colistin (*E. coli*, *K. pneumoniae*, *S. fonticola*), tigecycline (*E. coli*, *S. fonticola*), amoxicillin-clavulanic acid (*S. fonticola*) and ampicillin (*S. fonticola*), while *K. oxytoca* showed resistance to aztreonam, colistin and piperacillin. In the second sampling, two different Enterobacterales species were identified in shellfish (*E. coli* and *Proteus vulgaris*) and three different species were identified in oysters (*E. coli*, *K. pneumoniae* and *Providencia stuartii*). Similarly, the non-intrinsic resistance observed for *P. vulgaris* isolated from shellfish was to aztreonam, cefotaxime, ceftazidime, fosfomycin and piperacillin. The strains isolated from oysters showed resistance to ampicillin (*E. coli* and *P. stuartii*), chloramphenicol (*E. coli* and *P. stuartii*), piperacillin (*E. coli* and *K. pneumoniae*) and cefuroxime (*K. pneumoniae*).

DISCUSSION

The occurrence of antibiotic-resistant Enterobacterales in molluscs indicates that bacteria can circulate among humans, animals and environments. Some of these bacteria are of significant clinical interest, such as *E. coli*, *K. pneumoniae* and *P. aeruginosa*, which are commonly associated with community and nosocomial infections. Other bacterial species found in this study, although less well known, are also associated with human infections and demonstrate the existence of environmental pollution. Since the surroundings of Babitonga Bay are not extensively farmed, the source of contamination is likely to be the extensive use of antibiotics in clinics and hospitals. There is an urgent need to control the emission of raw waste into the environment, as the spread of Enterobacterales resistant to antimicrobial therapies may provide opportunities for the colonisation of humans and animals through food chain. It is necessary to expand our understanding of the relationships between animals, humans and their multiple shared environments, in application of the One Health concept, in order to control antimicrobial resistance dissemination and minimise this significant public health problem that affects the whole world.