TITLE: MICROBIOLOGICAL CONTAMINATION AND PREVALENCE OF RESISTANCE GENES TO BETA-LACTAMIC ANTIBIOTICS IN BIVALVE MOLLUSCS

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ABSTRACT:

The quality of bivalve molluscs in coastal production is directly influenced by the condition of the used habitats, since they are filters that retain pollutants and existing microbiological contamination. Thus, the present work aims to evaluate the presence of pathogenic bacteria in the production of oysters and mussels, and the existence of resistance genes to beta-lactam antibiotics using PCR and sequencing of target genes. To characterize the isolates, classical and molecular techniques will be used by the molecular taxonomy by sequencing the 16S ribosomal RNA gene in 864 samples from nine mollusc producing regions in coastal waters at north of the Brazilian Amazon. As a result, isolates of *Escherichia coli* were identified in 71% (40/56) with atypical enteropathogenic *E. coli* identification in 3% (2/56), in addition to *Vibrio alginolyticus* (58%, 33/56), *V. parahaemolyticus* (67%, 38/56), *V. fluvialis* (28%, 16/56), *V. vulnificus* (12%, 7/56) and *V. cholerae* non-O1, non-O139 (8%, 5/56). The presence of the bla^{TEM} gene was observed in 11% (5/42) of oyster samples and 100% (12/12) of mussels indicating that microorganisms in estuarine water had the ability to produce beta-lactamase. Twenty-six strains of the genus *Vibrio* amplified the bla^{TEM} gene distributed among *V. alginolyticus* species 21.4% (12/56), *V. parahaemolyticus* 21.4% (12/56) and *V. cholerae* 3% (2/56), suggesting that these species can act as reservoir for resistance genes in the aquatic environment. Analysis by molecular taxonomy allowed to identify 12 strains of the genus *Vibrio* as *V. parahaemolyticus* by comparing the 16S rRNA region sequences with data from the literature. The isolates of *V. parahaemolyticus* did not showed the pathogenicity genes tdh and trh while the species-specific tlh gene was present in 100% of the isolates. Studies to detect beta-lactam antibiotic resistance genes in bivalve mollusc isolates associated with the contamination of the aquatic environment by anthropic action are scarce or non-existent in the Brazilian Amazon. The observation of resistance genes in strains of *V. parahaemolyticus, V. alginolyticus* and *V. cholerae* may indicate a spread of antimicrobial resistance in the estuarine environment forming a cycle by new routes to man by ingestion of oysters and mussels in natura and dispersion in the environment, favoring the contamination of the production chain.

Keywords: bacteriology, bivalve molluscs, pathogenicity, bla^{TEM} ,public health

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