TITLE: OCCURRENCE, ANTIBIOTIC-RESISTANCE AND PHYLOGENETIC PROFILE OF E. coli STRAINS ISOLATED FROM MANGROVE OYSTERS (Crassostrea gasar) FARmed IN ESTUARIES OF AMAZÔNIA

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ABSTRACT:
In recent years, the farming of mangrove oysters (Crassostrea gasar) has increased in the north of Brazil, especially in the state of Pará. Oysters are filter feeders that accumulate microorganisms in their gut becoming reservoirs of pathogenic bacteria and probably contribute to the widespread of antibiotic resistance genes. Therefore, these mollusks are considered good bioindicators of the health of aquatic environments where they live. Our work aimed to determine the occurrence, antibiotic-resistance and phylogenetic profile of Escherichia coli strains isolated from mangrove oysters farmed for food purposes in amazonic estuaries. Four sampling points localized at the northeast of the Pará state were selected: Lauro Sodré (LS); Pereru de Fátima (PF); Santo Antônio de Urindéua (SAU) and Nova Olinda (NO). The reference European MPN method for enumeration of E. coli in bivalves using MMGB and agar TBX medium were used. E. coli isolates were randomly recovered from the TBX plates and tested for their antibiotic susceptibility. Class 1 integron-integrase genes (intI1) were searched using PCR. Genomic fingerprint of the isolates was performed by REP-, BOX- and ERIC-PCR. E. coli phylo-groups were determined using a quadruplex PCR assay. SAU was the sampling point with the highest number of E. coli (16x10³ cells/100g of sample). According to the European legislation these oysters are not suitable for human consumption. The other sampling points showed <70 E. coli cells/100g of sample and thus animals were classified as suitable for human consumption. 24% percent of the isolates showed resistance to cephalexin and 17% to amoxicillin. Some isolates also showed resistance to ampicillin, gentamicin, tobramycin and amikacin. The gene intI1 wasn’t detected in the isolates. Five genotypes were found in SAU and PF while two genotypes were found in NO and LS. The majority of the isolates were assigned to the B1 and D phylo-groups which are composed of commensal or pathogenic strains. In this work, we found traces of human impact on SAU region since mollusks showed a high level of E. coli cells, and these isolates were mainly affiliated to pathogenic phylo-groups. SAU is the most densely populated region among the four ones analyzed. Some isolates showed a multi-drug resistance phenotype; however, all isolates were susceptible to last-resort antibiotics. The data indicate the importance of environmental health for the maintenance of oyster farming in the north of Brazil.

KEYWORDS: E. coli, Antibiotic-resistance, Oysters, Phylogenetic profile, Food surveillance.

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