

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

AUTHORS: MARCON, D. J.¹ ; OLIVEIRA, A. M.¹ ; LAGO, L. A. B.¹ ; SILVA, A.^{1,2} ; HENRIQUES, I.^{3,4} ; TACÃO, M.³ ; SCHNEIDER, M. P. C.¹ ; BARAÚNA, R. A.^{1,2} .

INSTITUTION: 1. CENTER OF GENOMICS AND SYSTEMS BIOLOGY, INSTITUTE OF BIOLOGICAL SCIENCES, FEDERAL UNIVERSITY OF PARÁ, 66075-110, BELÉM, BRAZIL; 2. LABORATORY OF BIOLOGICAL ENGINEERING, GUAMÁ SCIENCE AND TECHNOLOGY PARK, 66075-750, BELÉM, BRAZIL; 3. UNIVERSITY OF AVEIRO AND CESAM, DEPARTMENT OF BIOLOGY, 3810-193, AVEIRO, PORTUGAL; 4. UNIVERSITY OF COIMBRA, DEPARTMENT OF LIFE SCIENCES, 3000-456, COIMBRA, PORTUGAL.

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 Urindeua (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* (16×10^3 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 cephalothin 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.

DEVELOPMENT AGENCY: CAPES – Coordenação de Aperfeiçoamento de Pessoal de Nível Superior; FAPESPA – Fundação Amazônia de Amparo a Estudos e Pesquisas.