
Characterization of Antimicrobial Resistance and Virulence Profile of *Vibrio Parahaemolyticus* in Water and Bivalve Mollusk Samples

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Resumo

The objective of the present study was to characterize the antimicrobial susceptibility profile and virulence factors of *Vibrio parahaemolyticus* in water and bivalve mollusk samples in the estuary of the river São Francisco do Conde, Bahia, Brazil. Every month for 15 months collections were made of estuary water (45 samples), oysters and mussels (30 in natura and 15 processed samples). The strains were identified biochemically according to the identification key for environmental strains. The antimicrobial susceptibility tests were carried out with 11 pharmacons from seven families, the minimum inhibitory concentration (MIC) and metallo- β -lactamase (M β LS) enzyme production. To characterize virulence, exoenzyme production was used (amylase, caseinase, DNase, phospholipase, gelatinase, lipase and urease), hemolytic activity and the *tdh* and *trh* primers. Ten species were identified and 67% (30/45) belonged to *V. parahaemolyticus* (38% in water, 18%, in natura bivalve mollusks and 11% processed mussel). Antimicrobial resistance was observed of at least one of the 11 antimicrobials tested, with a high percentage for ampicillin (97%) (55% in water isolates, 27% in in natura bivalve mollusks and 17% in processed mussel) and 400 μ g MIC and cephalothin (93%) (53% in water isolates, 28% in in natura bivalve mollusks and 18% in processed mussel) and ≤ 100 μ g MIC. Multi-resistance was observed in 59% of the

Referência:

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water strains, 75% of the in natura bivalve molluscs and in 20% of the processed mussel. All the isolates produced the MβLs enzyme. For the phenotypic virulence profile the highest positivity percentage was for amylase (97%), DNase (83%), phospholipase (70%), β-hemólise (57%), gelatinase (43%), lipase (13%) and caseinase (7%). The *tdh* and *trh* virulence genes were not detected. Environmental strains are generally difficult to characterize because they live in an environment with intense variations and can insert or exclude traits. The high microbial resistance and MβLs production in *V. parahaemolyticus* showed that the environment under study has undergone human pressure. Although expression of the *tdh* and *trh* virulence genes was not verified, the high production of exoenzymes facilitates host tissue invasion and lesion by the microorganism and there is also toxigenic potential.

Palavras-Chave: antimicrobial susceptibility, metallo-β-lactamase , virulence, mussels

Agência de Fomento: