Abstract

Characterization of Genetic Determinants Involved in Antimicrobial Resistance in *Aeromonas hydrophila*, *Escherichia coli* and *Vibrio cholerae* Isolated from Different Aquatic Environments [†]

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Abstract: *Aeromonas hydrophila*, *Escherichia coli* and *Vibrio cholerae* are among a myriad of bacteria pathogen commonly found in natural water bodies that cause serious waterborne infection while antibiotic resistance genes are emerging contaminants posing potential worldwide human health risk. This study was designed to determined genetic determinants involved in antimicrobial resistance in bacteria isolates from aquatic environments. A total of 372 water samples, comprising of 111, 144 and 117 ponds, rivers and streams were collected from three local governments areas (Abakaliki, Ebonyi and Ikwo) of Ebonyi State Nigeria over a period of twelve (12) months. Bacteria Isolates obtained from water bodies were identified and characterized by polymerase chain reaction (PCR) analysis using 16S rRNA specific primers. The susceptibility of the isolates to different antibiotics was determined using disc diffusion technique. Total DNA was extracted and sequenced on Genetic Analyzer 3130 xl sequencer and the amplified 16S rRNA gene sequence. The presence of antibiotic resistance genes was determined by PCR using specific primers. Bacteria isolated were *Aeromonas hydrophila* (103), *Escherichia coli* (118) and *Vibrio cholera* (87). The isolates were susceptibility to gentamicin (96.12%), meropenem (94.17%), ciprofloxacin (89.32%) imipenem (85.44%) and chloramphenicol (84.47%) while they showed 94.17%, 93.20%, 90.29%, 89.32%, 88.35%, 86.41% and 83.5% resistance to penicillin, sulphamethoxazole, kanamycin, azithromycin, streptomycin cephalothin and cefuroxime respectively. The isolates were found to harbor the following antibiotic resistance genes, blaCTXM, blaSHV, class 1 Integron Ac, Intl1, blaTEM and TetB. These findings deserve serious attention, as the presence of bacteria coliforms in water harbouring antibiotic resistance genes are potential risk to the health of people. Keywords: aquatic environment resistant genes characterization.