

Molecular Characterization of Bacteria Isolates Associated with Mosquito Infested Dump Sites at Communities in Anambra State, Nigeria

Authors : Ruth Asikiya Afunwa, Martins Chilua Obiora, Jeremiah Chukwuagoziem Felix- Ngige, Martin Chukwunonso Nwofia, Francis Ayodele Gbadamosi, Florence Chioma Mgbodile

Abstract : Microorganisms have long been known to support immunity, food webs, nutrient cycling, and the health of mosquito biological niches. The aim of this study is to identify bacteria associated with mosquito-infested dump sites. The mosquitoes associated with the study sites are the Aedes, Anopheles, and Culex mosquitoes. Six samples from two different mosquito-infested dump sites at Otoko and Umudioka in Awkuzu, Anambra East L.G.A of Anambra state in Southeastern Nigeria were cultured in MacConkey, cetrinide and mannitol salt agars and subsequently identified using their morphological features, biochemical tests (catalase test, Kovacs citrate test, indole test and oxidase test) and 16S rRNA gene sequencing. Antibiotic susceptibility test (AST) was done on Mueller-Hinton agar after standardizing to 0.5 McFarland turbidity. The diameter of the zones of inhibition was measured in mm and interpreted using the EUCAST breakpoint guidelines. Biofilm formation was determined in twenty (20) isolates and the biofilm scoring was assigned as weak/minute, moderate and strong/high. A total of forty five (45) isolates, namely: *Vagococcus fluvialis* (18)(40%), *Serratia fonticola* (12)(26.7%), *E. coli* (4)(8.90%) and *Pseudomonas aeruginosa* (11)(24.4%) were isolated and identified. The results of the Antibiotic susceptibility test showed 95-100% resistance to imipenem, amoxicillin-clavulanate, nitrofurantoin, ampicillin, cefixime, cefuroxime, and ceftriaxone. The isolates were susceptible to levofloxacin, ofloxacin and gentamicin. Biofilm evaluation showed 3.45% moderate and 46.6% strong biofilms from *Vagococcus fluvialis*, 3.45% moderate and 15.5% strong biofilms from *Pseudomonas aeruginosa*, and both 10.3% and 20.7% strong biofilms from *E. coli* and *Serratia fonticola* respectively. The study identified bacteria associated with mosquito-infested dump sites and highlighted the importance of considering the environmental microbiome when studying mosquito biology and developing control strategies for these pests in relation to human health.

Keywords : bacteria, dumpsite, mosquitoes, community, molecular

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