Characterization of antibiotic resistance in *Escherichia coli* isolates from abattoir effluents

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**Background:** The increase in antimicrobial resistance among pathogenic bacteria has emerged as an important risk in public health and in human medicine. This may lead to significant health risk to humans with records of disease outbreaks. The aim of this study was to characterize antibiotics resistance of *Escherichia coli* strains from abattoir effluents.

**Methods & Materials:** A total of 75 *Escherichia coli* isolates were isolated from abattoir effluents using standard culture-based, biochemical reactions and polymerase chain reaction (PCR) identification of the suspected colonies. The disc diffusion technique was used to screen for antimicrobial susceptibility against fifteen different antibiotics. The presence of class 1 integrons in each *Escherichia coli* strains was assessed using 3′-CS and 5′-CS regions specific primers. The sul1, sul2, and sul3 genes in all sulfonamide resistant isolates were investigated by PCR using primers specific.

**Results:** All the isolates were multi-resistance, defined as resistant to at least four different antibiotics with multiple antibiotic resistance (MAR) indexes ranging from 0.26 to 0.93, signifying that the isolates of high antimicrobial usage origin. Plasmid DNAs were found in 80% of the strains analyzed harbored plasmid DNA, size from 1.2 to 81.5 kb, separating the isolates into 8 different plasmid profiles were observed. The mechanism by which *Escherichia coli* have accumulated antibiotic resistance determinates is of interest. All strains showed resistance against sulfonamides. The presence of class 1 integrons was determined for all tested *Escherichia coli* strains. The relationship of sulfonamide resistance genes with integrons, it was revealed that *Escherichia coli* strains harbored class 1 integrons with variable regions. Antibiotic resistant *Escherichia coli* could be a major risk to public health as a significant reservoir of encoding antibiotic resistance genes that can be transferred intra or interspecies.

**Conclusion:** The increase of antimicrobial resistance signatures necessitates for adequate sanitation and proper surveillance programs towards monitoring of antimicrobial resistance determinants in abattoir environment.

http://dx.doi.org/10.1016/j.ijid.2016.02.512

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Detection of clusters and geographical hotspot for Lassa fever in Edo Central Senatorial district of Nigeria: A step into a nation-wide mapping of Lassa fever

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**Background:** Lassa fever is a viral hemorrhagic fever which occurs mainly in Nigeria and other African countries with high mortality during epidemics. Surveillance data shows that Edo Central Senatorial District of Nigeria has the highest number of cases recorded since 1969 when the disease was first discovered in Nigeria. Despite this, there is yet to be a detection of geographical clusters and hotspots of the disease since the first outbreak in 1969.

The objective of the study was to detect the geographical clusters and hotspots of Lassa fever in Edo Central District in order to develop a template for nation-wide mapping and sero prevalence study of Lassa fever and other related viral hemorrhagic fever in Nigeria and in West Africa.

**Methods & Materials:** Using a cross sectional study design, dataset of 213 cases of Lassa fever in Edo Central Senatorial District from 2008–2013 were visualized in space, queried and interpreted using ArcGIS 10.2, a Geographical Information System (GIS) software. Anselin Local Moran’s and Gertis-ord Gi* advanced geostatistical tools were employed in determining geographical clusters and hotspots of Lassa fever.

**Results:** The median age of Lassa fever patients was 30 years (IQR = 29 years). Statistical significant clusters (p < 0.05) and hot spots (p = 0.05) of all reported cases from 2008–2013 occurred in Ekpoma town, Esan West Local Government of Edo State, Nigeria. The hotspot of Lassa fever is a few meters away from Ambrose Alli University, Ujemen, Ekpoma. Clusters of Lassa fever are found at several locations within Ekpoma and Irrua.

**Conclusion:** Clusters and Hotspots of Lassa fever cases in Edo Central Senatorial District recorded from 2008 through 2013 were found in Ekpoma town. Based on the findings, both Local and regional and International disease control teams can now develop a national surveillance and control strategy to contain the outbreaks of Lassa fever and other related viral hemorrhagic fevers in Nigeria and other affected countries.

http://dx.doi.org/10.1016/j.ijid.2016.02.513