

## Antibiotic Resistance Patterns of Bacteria flora Obtained from Selected Fresh Fish Samples from Eleyele and Asejire Dams, Southwestern Nigeria

A.A. OGUNJOBI, \*B.I. NWADIKE, I.M. IBOK AND I.O. OSAJI

Environmental Microbiology and Biotechnology Laboratory,  
Department of Microbiology, University of Ibadan, Ibadan- Nigeria

\*Corresponding Author:

Email: okolieblessing@yahoo.com

### Abstract

A bacteriological study was conducted on gills, skin and intestine of selected fresh fish samples- *Tilapia zilli*, *Ictalurus punctatus*, *Oreochromis* sp. and *Chrysichthys nigrodigitatus* from Eleyele and Asejire Dams. The fish samples were bought from fish vendors at the shorelines of Eleyele and Asejire dams. Pour plate technique was used to isolate bacteria as well as determine the presence of coliform in the fish samples over a period of two months. The bacterial isolates obtained were identified using their morphological and biochemical characteristics. These bacterial isolates were subjected to antibiotic susceptibility testing using disc diffusion technique against ten antimicrobial agents. The coliform count obtained for the first month was  $7.5 \times 10^2$  cfu/ml and the second was  $3.5 \times 10^2$  cfu/ml. A total of 53 bacteria isolates (body surface = 22, gills = 16, intestine = 15) belonging to the genera *Escherichia* (3), *Bacillus* (18), *Pseudomonas* (6), *Staphylococcus* (5), *Salmonella* (6), *Klebsiella* (4), *Citrobacter* (2), *Acinetobacter* (1), *Enterobacter* (4), *Shigella* (2), *Proteus* (1) and *Serratia* (1) were obtained. The antibiotic susceptibility pattern of the isolates showed that all the bacteria isolates were susceptible to Ciprofloxacin (CPX), Gentamycin (CN) and Pefloxacin (PEF) while all the Gram negative isolates showed varying degrees of resistance (ranging from 50-100 %) to Augmentin (AU) except *Proteus* sp. All the bacteria isolates obtained from fish samples in Asejire dam were susceptible to streptomycin; the Gram negatives were susceptible to Chloramphenicol (CH), Sparfloxacin (SP) and Tarivid (OFX) while the Gram positives were susceptible to Zinnacef (Z) and Rocephin (R) while in fish samples from Eleyele Dam, *Staphylococcus aureus* isolates were susceptible to all the antibiotics tested while *Salmonella* and *Klebsiella* species were susceptible to all the antibiotics except Augmentin. Nineteen isolates accounting for 44.19% showed resistance to single antibiotics while 24 (55.81%) showed Multiple Antibiotic Resistance (MAR). Among the antibiotics tested in this study, the overall resistance was highest to Amoxicillin (55.81%) followed by septrin (27.91%) and least in streptomycin (11.63%). In all, 12 different antibiotic resistance phenotypes were obtained with resistance to ampiclox and amoxicillin being the predominant antibiotype. There was high prevalence of bacterial pathogens in the fish samples and also presence of resistance to anti-microbial agents which might pose therapeutic problems as well as health risk to consumers.

### Introduction

Although there is no certainty about the existence of strictly aquatic bacteria, the most widespread opinion among the various authors is that the

majority of the bacteria found in aquatic environments are of soil origin and carried into the water due to rain or accidental introduction, whether they are natural or a direct consequence of human activity (de Sousa and Silva-Sousa, 2001). The microbial flora of freshly captured fish is usually a reflection of the environment in

**Keywords:** Antibiotic, Resistance, Susceptible, Antibiotype

which it was harvested (Grema *et al.*, 2015a). Generally, ponds and rivers that harbour fish may be the source of the microorganisms due to indiscriminate dumping of human and animal excreta as well as other environmental wastes into natural water bodies or washing of excreta from land into water during the rainy season (Cabral, 2010). Free roaming animals especially dogs and birds contribute to faecal contamination of surface water and ponds (Green *et al.*, 2012, Mauffret *et al.*, 2012). These microorganisms from faeces or environmental waste contain antibiotic resistant gene that may disseminate and contaminate aquatic environment. On the other hand, aquaculture represents one means that supplement wild fish due to the growing demand of fish protein in the population (Alday *et al.*, 2006). Hygiene is important and necessary for food and environment to reduce harmful microorganisms. This involves assessing or investigating the level of hygiene of food or water sources or samples as well as the environment for the safety of public. The affinity of microorganisms to liquid water for their survival or as habitat explains the importance of water to the survival and reproduction of microbes.

Fish has been a stable source of animal protein in many developing nations, and the high demand for fish has shifted farmers' interest from subsistence fish growers to larger, export-driven producers. Fishes inhabiting aquatic habitat are continuously exposed to a wide range of microorganisms present in the environment, and the microbiota of fish have been as a result of their symbiotic relationship with microorganisms (Ringoe and Gatesoupe, 1998). Generally, aquatic organisms include both macro and microorganisms inhabiting water. This gives these organisms opportunity for intimate symbiotic relationships either mutual or parasitic relationships. Bacterial cell, though small, possess elegant structures and mechanisms which provide for remarkable adaptation such that bacteria can exploit a variety of habitat and nutrient condition which aid them get associated with fishes by these adaptive features (Grimes, 1991). Gram negative rod-shaped bacteria

belonging to the genera *Pseudomonas*, *Moraxella*, *Acinetobacter*, *Shewanella* and *Flavobacterium* and members of the family *Vibrionaceae* (*Vibrio* and *Photobacterium*) and the family *Aeromonadaceae* (*Aeromonas* sp) are common aquatic bacteria and typical of the fish flora (Dalgaard, 1993).

The internal organs of apparently healthy fish should be sterile, but isolations of bacteria from kidney, liver and spleen have been reported (de Sousa and Silva-Sousa, 2001). The presence of microorganisms in internal fish organs could indicate the breakdown of immunological defense mechanisms. Moreover, under natural conditions, most infectious agents coexist with their host without causing significant disease (de Sousa and Silva-Sousa, 2001). Al-Harbi and Uddin (2005) reported viable count of bacteria flora of the intestine and gills of healthy tilapia in Saudi Arabia and the isolates were predominantly Gram-negative rods. Therefore, the knowledge of the infectious agents that exist in an aquatic ecosystem is of great importance if one is to, for instance, install an aquaculture facility. Subsequently, fish contamination with antibiotic-resistant bacteria can be a major threat to public health, as it can be transferred to other bacteria of human clinical significance (O'Brien, 2002).

This study therefore assessed the bacteriological quality of selected fresh fishes from Eleyele and Asejire Dams and the antibiotic susceptibility patterns of the bacteria isolates obtained.

## Materials and Methods

### *Sample Collection*

The fish samples were bought from fish vendors at the shorelines of Eleyele and Asejire dams. The fish samples were collected at 2 weeks intervals within the 2 months sampling period. The fishes were identified in the Fisheries unit, Department of Zoology, University of Ibadan as *Tilapia zilli*, *Ictalurus punctatus*, *Oreochromis* sp. and *Chrysichthys nigrodigitatus*. A total of 32 fish samples (8 of each species) were used for this study.

### Bacteria isolation and identification

Conventional methods of bacterial isolation such as growth on selective media (Plate Count Agar (PCA), Mannitol Salt Agar (MSA), Eosin Methylene Blue agar (EMB), MacConkey agar and Salmonella-Shigella Agar (SSA)), gram staining and biochemical tests were used for the identification of the different bacterial isolates. The pour plate technique was employed to evaluate coliforms in fish and water samples. A sterile dissecting set was used to dissect the fish samples. Samples were collected using sterile moist cotton swab from the surface of the fish skin. The operculum was lifted using sterile forceps and a part of the gill was cut out as a sample and the fish was dissected laterally to collect the intestinal sample. The gill and intestine samples of each fish were aseptically introduced into peptone water for about six hours. Serial dilution was carried out and 1 ml of water and fish samples of dilutions  $10^{-2}$  and  $10^{-4}$  were drawn aseptically from each bottle and inoculated into sterile Petri dishes with the different media and incubated at  $28 \pm 2^{\circ}\text{C}$  for 24-48 hours. Each distinct colony was further streaked on freshly prepared Nutrient agar plates for evaluation of purity and colonial morphology. The isolates were further subjected to Gram stain to determine their Gram reaction and biochemical tests as described by Cheesbrough (2006) to determine the identity of bacteria isolates.

### Antibiotic susceptibility testing

The test bacterial isolates were inoculated unto Mueller Hilton agar and followed by application of the discs (oxid Ltd) impregnated with different antibiotics namely; Streptomycin (S), Septrin (SXT), Ciprofloxacin (CPX), Amoxicillin (AM), Gentamycin (CN), Pefloxacin (PEF), Chloramphenicol (CH), Sparfloxacin (SP), Augmentin (AU), Tarivid (OFX), Erythromycin (E), Ampiclox (APX), Zinnacef (Z) and Rocephin (R). The zones of inhibition were translated using Clinical and Laboratory Standards Institute (CLSI), 2014. Agar disc diffusion method (Bauer *et al.*, 1996) was employed.

### Results and Discussion

A total of 53 bacteria isolates (body surface = 22, gills = 16, intestine = 15) belonging to the genera *Escherichia*, *Bacillus*, *Pseudomonas*, *Staphylococcus*, *Salmonella*, *Klebsiella*, *Citrobacter*, *Acinetobacter*, *Enterobacter*, *Shigella*, *Proteus* and *Serratia* were obtained from the fish samples from both dams. *Bacillus* spp. had the highest percentage occurrence of 33.96% followed by *Salmonella* and *Pseudomonas* species with 11.32% while *Serratia*, *Acinetobacter* and *Proteus* species had the least percentage occurrence of 1.89% each (Table 1). This is in contrast with the findings of Kato *et al.* (2016) in which *Proteus* species had high percentage occurrence of 63% from fish samples. The presence of these genera *Escherichia*, *Bacillus*, *Pseudomonas*, *Staphylococcus*, *Klebsiella*, *Enterobacter* and *Proteus* in this study was similar to those isolated by Kato *et al.* (2016) from both Tilapia and Catfish. The distribution of the bacteria species showed that 28 bacteria species (10 genera) were obtained from fish samples from Eleyele dam while 25 bacteria species (8 genera) were from fish samples in Asejire dam showing that those from Eleyele dam had more bacterial diversity (Table 2). The presence of *E.coli* and *Pseudomonas* spp. isolates which are microorganisms of public health significance in fish samples from Eleyele dam can be attributed to its urban nature, exposing it to inputs from different sources unlike the Asejire dam that is in a secluded area with less human activities. This agreed with the hypothesis advanced by Shewan (1977) that the bacteria flora of fish is a direct reflection of its environment (water). The body surface of the fish samples had the highest number of bacteria isolates (41.5%) among the sampled parts (Table 3) and this is similar to the works of Rocha *et al.* (2014) and Grema *et al.* (2015a). This high number may be attributed to their direct contact with the water.

Members of the family Enterobacteriaceae of different genera which are Gram negative rods were predominant in the fish samples. This result

correlates with the findings of Sadhukhan *et al.* (1997) where they reported the isolation of Gram negative rod organisms from fishes.

Microorganisms from human origin such as *E. coli*, *S. aureus* and *Klebsiella* have been found to survive and multiply in the gut and tissues of fish which render fish a potential source of human disease over long periods (Udeze *et al.*, 2012). These pathogens have been identified to be present

in the skin, gills and intestine of fish that were sampled in this study. The difference in the dominating microflora between sites of colonisation has been reported by previous investigation (Oloja *et al.*, 2010). *Bacillus* was present in virtually all fish samples tested in the study which is in agreement with the findings of Shinkafi and Ukwaja (2010). *Bacillus* species are considered medically significant and diseases caused by *Bacillus* isolates include self limited food poisoning, deep seated

**Table 1:** Frequency and percentage occurrence of bacteria isolates obtained from the selected fresh fish samples in Eleyele and Asejire Dams

Bacteria isolates	Frequency	Percentage frequency (%)
<i>Bacillus</i> spp.	18	33.96
<i>Pseudomonas</i> spp.	6	11.32
<i>E. coli</i>	3	5.66
<i>Staphylococcus aureus</i>	5	9.43
<i>Salmonella</i> spp.	6	11.32
<i>Shigella</i> spp.	2	3.77
<i>Enterobacter</i> spp.	4	7.55
<i>Serratia</i> sp.	1	1.89
<i>Acinetobacter</i> sp.	1	1.89
<i>Klebsiella</i> spp.	4	7.55
<i>Citrobacter</i> spp.	2	3.77
<i>Proteus</i> sp.	1	1.89
<b>Total</b>	<b>53</b>	<b>100</b>

**Table 2:** Distribution of the different genera of bacteria isolates in the fish samples from Eleyele and Asejire Dams

Bacteria isolates	Eleyele	Asejire
<i>Bacillus</i> spp.	10	8
<i>Pseudomonas</i> spp.	6	-
<i>E. coli</i>	3	-
<i>Staphylococcus aureus</i>	2	3
<i>Salmonella</i> spp.	2	4
<i>Shigella</i> spp.	-	2
<i>Enterobacter</i> spp.	1	3
<i>Serratia</i> sp.	1	-
<i>Acinetobacter</i> sp.	1	-
<i>Klebsiella</i> spp.	1	3
<i>Citrobacter</i> spp.	1	1
<i>Proteus</i> sp.	-	1
<b>Total</b>	<b>28</b>	<b>25</b>

**Table 3:** Bacteria Isolates associated with the different parts of the fish samples (body surface, gills and intestine) from Eleyele and Asejire Dams

Bacteria isolates	Site of occurrence (%)		
	Body surface	Gills	Intestine
<i>Bacillus</i> spp.	6 (27.27)	8 (50.00)	4 (26.67)
<i>Pseudomonas</i> spp.	4(18.18)	1(6.25)	1(6.67)
<i>E. coli</i>	2(9.09)	0	1(6.67)
<i>Staphylococcus aureus</i>	2(9.09)	2(12.50)	1(6.67)
<i>Salmonella</i> spp.	1(4.55)	2(12.50)	3(20.00)
<i>Shigella</i> spp.	2(9.09)	0	0
<i>Enterobacter</i> spp.	3(13.64)	1(6.25)	0
<i>Serratia</i> sp.	0	0	1(6.67)
<i>Acinetobacter</i> sp.	1(4.55)	0	0
<i>Klebsiella</i> spp.	0	1(6.25)	3(20.00)
<i>Citrobacter</i> spp.	1(4.55)	1(6.25)	0
<i>Proteus</i> sp.	0	0	1(6.67)
<b>Total</b>	<b>22 (41.5)</b>	<b>16 (30.2)</b>	<b>15 (28.3)</b>

soft tissue infections and systemic infections (Tena *et al.*, 2007). *Klebsiella sp.* causes a wide range of community associated diseases. The classical clinical presentation ranges from localized abscesses to pneumonia and more generalized infections (Botelho-Nevers *et al.*, 2007; Elemam *et al.*, 2009; Seki *et al.*, 2013). While for *Proteus sp.*, urinary tract infections, endocarditis and septicemia has been reported (Endimiani *et al.*, 2005; Cohen-Nahum *et al.*, 2010; Kalra *et al.*, 2011). The presence of *S. aureus*, *E. coli*, *Klebsiella* and *Proteus* species in fish may result from indiscriminate deposition of human and animal excreta as well as other environmental wastes into ponds and rivers that harbour fish or through washing of land surfaces into water bodies during the rainy season (Cabral, 2010). These microorganisms in water may carry gene of multi-drug resistance that are transferable between human, animals and the environment (da costa *et al.*, 2013).

The antibiotic susceptibility patterns of the isolates are shown in Tables 4 and 5. The

antibiotic susceptibility pattern of the bacterial isolates showed that all the bacteria isolates from both dams were susceptible to Ciprofloxacin (CPX), Gentamycin (CN) and Pefloxacin (PEF) while all the Gram negative isolates showed varying degrees of resistance (ranging from 50-100 %) to Augmentin (AU) except *Proteus sp.* (Tables 4 and 5). The finding in this study on *Proteus sp.* being susceptible is in contrast to the result obtained by Grema *et al.* (2015a) where *Proteus spp.* showed resistance to 4, 5 and 6 antibiotics used in the study. From Asejire dam, all the bacteria isolates were susceptible to streptomycin; the Gram negatives were susceptible to Chloramphenicol (CH), Sparfloxacin (SP) and Tarivid (OFX) while the Gram positives were susceptible to Zinnacef (Z) and Rocephin (R) (Table 4). From Eleyele Dam, *Staphylococcus aureus* isolates were susceptible to all the antibiotics they were subjected to while *Salmonella* and *Klebsiella* species were susceptible to all the antibiotics except Augmentin (Table 5). Also all *E. coli* isolated in this study were found to be resistant to 3, 5 and 6 antibacterial agents and this is similar to the findings of Grema *et al.* (2015a); while

**Table 4:** Antibiotic susceptibility pattern of bacteria isolates obtained from the fish samples from Asejire Dam

Bacteria isolates	Number of Antibiotic resistant bacteria isolates (%)													
	S	SXT	CPX	AM	CN	PEF	CH	SP	AU	OFX	E	APX	Z	R
<i>Bacillus spp.</i> (n=8)	0	3 (37.5)	0	4(50)	0	0	NA	NA	NA	NA	1 (12.5)	4(50)	0	0
<i>Staphylococcus aureus</i> (n=3)	0	0	0	2 (66.7)	0	0	NA	NA	NA	NA	0	3 (100)	0	0
<i>Salmonella spp.</i> (n=4)	0	1(25)	0	2(50)	0	0	0	0	2(50)	0	NA	NA	NA	NA
<i>Shigella spp.</i> (n=2)	0	0	0	0	0	0	0	0	2 (100)	0	NA	NA	NA	NA
<i>Enterobacter spp.</i> (n=3)	0	3 (100)	0	0	0	0	0	0	3 (100)	0	NA	NA	NA	NA
<i>Klebsiella spp.</i> (n=3)	0	0	0	0	0	0	0	0	2 (66.7)	0	NA	NA	NA	NA
<i>Citrobacter sp.</i> (n=1)	0	0	0	0	0	0	0	0	1 (100)	0	NA	NA	NA	NA
<i>Proteus sp.</i> (n=1)	0	0	0	0	0	0	0	0	0	0	NA	NA	NA	NA

**Key:**

S=Streptomycin, SXT=Septrin, CPX=Ciprofloxacin, AM=Amoxicillin, CN=Gentamycin, PEF=Pefloxacin, CH=Chloramphenicol, SP=Sparfloxacin, AU=Augmentin, OFX=Tarivid, E=Erythromycin, APX=Ampiclox, Z=Zinnacef, R=Rocephin. NA= Not Applicable

all the *Enterobacter* spp. tested were resistant to two antibiotics (Table 6), these findings are supported by earlier reports of Overdevest *et al.* (2011) that antibiotic resistance in Enterobacteriaceae has increased dramatically during the past decade.

Among the 53 bacterial isolates obtained, 43 (81.13%) of the isolates showed resistance to one antibiotic or more (Table 6). Out of these 43 isolates, 19 accounting for 44.19% showed resistance to single antibiotics while 24 (55.81%) showed Multiple Antibiotic Resistance (MAR). Among the antibiotics tested in this study, the overall resistance was highest to Amoxicillin (55.81%) followed by septrin (27.91%) and least in streptomycin (11.63%). Among the Gram positives, resistance was highest to ampiclox (52.63%) followed by rocephin (21.05%) and least in erythromycin (10.53%) while for the Gram

negatives, resistance was highest to augmentin (91.67%) followed by chloramphenicol (20.83%) and least in sparfloxacin (4.17%).

Comparing resistance in bacteria flora of the fish samples from both dams, it was observed that isolates from the fish samples from Asejire dam had 84.9% resistance (21 out of 25 isolates) while those from Eleyele dam showed 78.57% resistance (22 out of 28 isolates). From Asejire dam, 52.38% (11) of the isolates showed single antibiotic resistance and 47.62% (10) showed MAR while from Eleyele dam, 36.36% (8) showed single antibiotic resistance and 63.64% (14) showed MAR. Thus, more of the bacterial isolates from fish samples from Eleyele dam showed MAR and highest number of MAR (7) was equally from there. Equally, there are differences in the distribution of the MAR

**Table 5:** Antibiotic Susceptibility Pattern of Some of the Bacteria Isolates obtained from the Fish Samples from Eleyele Dam

Bacteria isolates	Number of Antibiotic resistant bacteria isolates (%)													
	S	SXT	CPX	AM	CN	PEF	CH	SP	AU	OFX	E	APX	Z	R
<i>Bacillus</i> spp. (n=10)	1 (10)	3 (30)	0	6 (60)	0	0	NA	NA	NA	NA	2 (20)	2 (20)	2 (20)	2 (20)
<i>Staphylococcus aureus</i> (n=2)	0	0	0	0	0	0	NA	NA	NA	NA	0	0	0	0
<i>Salmonella</i> spp. (n=2)	0	0	0	0	0	0	0	0	1 (50)	0	NA	NA	NA	NA
<i>Pseudomonas</i> spp. (n=6)	2	2	0	2	0	0	2	1	3 (50)	2	NA	NA	NA	NA
<i>Klebsiella</i> sp. (n=1)	0	0	0	0	0	0	0	0	1 (100)	0	NA	NA	NA	NA
<i>E. coli</i> (n=3)	2 (66.7)	2 (66.7)	0	3 (100)	0	0	3 (100)	0	3 (100)	1 (33.3)	NA	NA	NA	NA

**Table 6:** Antibiotic Resistant Patterns of the Bacterial Isolates from the Fish Samples from both Dams

Isolates (n)	Number of antibiotics to which organisms were resistant							
	1	2	3	4	5	6	7	8
<i>Bacillus</i> spp. (16)	6	4	3	1	2			
<i>Staphylococcus aureus</i> (3)	1	2						
<i>Salmonella</i> spp. (6)	5	1						
<i>Shigella</i> spp. (2)	2							
<i>Enterobacter</i> spp. (3)		3						
<i>Klebsiella</i> spp. (3)	3							
<i>Citrobacter</i> sp. (1)	1							
<i>Pseudomonas</i> spp. (6)	1	3				1	1	
<i>E. coli</i> (n=3)			1		1	1		

**Table 7:** Antibiotic Resistance Types and Pattern among the Bacterial Isolates from Fish Samples from Asejire Dam

Isolates (n)	Single R-Type	Antibiotic	Multiple R-Type	Number of isolate	Antibiotic resistance pattern (Phenotype)
<i>Bacillus</i> (6)	1	SXT	2	2	APX, AM
	1	E	3	2	APX, AM, SXT
<i>S. aureus</i> (3)	1	APX	2	2	APX, AM
<i>Salmonella</i> spp. (4)	2	AM	2	1	AU, SXT
	1	AU			
<i>Shigella</i> spp. (2)	2	AU			
<i>Enterobacter</i> spp. (3)			2	3	AU, SXT
<i>Klebsiella</i> spp. (2)	2	AU			
<i>Citrobacter</i> sp. (1)	1	AU			

**Table 8:** Antibiotic Resistance Types and Pattern Among the Bacterial Isolates From Fish Samples from Eleyele Dam

Isolates (n)	Single R-Type	Antibiotic	Multiple R-Type	Number of isolate	Antibiotic resistance pattern (Phenotype)
<i>Bacillus</i> (10)	3	AM	2	1	APX, AM
	1	R		1	AM, R
			3	1	AM, APX, R
			4	1	AM, R, S, SXT
			5	2	AM, SXT, E, APX, Z
<i>Salmonella</i> spp. (2)	2	AU			
<i>Pseudomonas</i> spp. (6)	1	AU	2	3	AM, AU
			6	1	AM, AU, OFX, S, SXT, CH
			7	1	AM, AU, OFX, S, SXT, CH, SP
<i>Klebsiella</i> spp. (1)	1	AU			
<i>E. coli</i> (3)			3	1	AM, AU, CH
			5	1	AM, AU, S, SXT, CH
			6	1	AM, AU, S, OFX, SXT, CH

**Key:**

S=Streptomycin, SXT=Septrin, CPX=Ciprofloxacin, AM=Amoxicillin, CN=Gentamycin, PEF=Pefloxacin, CH=Chloramphenicol, SP=Sparfloxacin, AU=Augmentin, OFX=Tarivid, E=Erythromycin, APX=Ampiclox, Z=Zinnacef, R=Rocephin.

isolates; it was observed that 13 (54.17%) were resistant to two antibiotics, 4 (16.67%) to three, 1 (4.17%) to four, 3 (12.5%) to five, 2 (8.33%) to six and 1 (4.17) to seven antibiotics but none of the isolates showed resistance to all 10 of the antibiotics tested in this study. In all, 12 different antibiotic resistance phenotypes were obtained with resistance to ampiclox and amoxicillin being the predominant antibiotic type (Tables 7 and 8).

Although the use of antibiotics in human medicine has influenced the emergence of resistant bacteria,

the use of antibiotic in animals has contributed to the problem of resistance and complicates the choice of antibiotic for treatment in human diseases (Novotny *et al.*, 2004). According to Grema *et al.* (2015b), transfer of resistant bacteria between aquatic animals and humans through food production line has been documented and can pose a threat to public health. Although there is records of antimicrobial resistance from fish and fish handlers, the world organization for animal health (OIE), aquatic animal health code recommends the continuous monitoring and surveillance of

antimicrobial resistance in microorganism associated with aquatic animals (Smith *et al.*, 2013). This is important due to the fact that transfer of resistant bacteria between aquatic animals and humans through consumption or handling has been documented and can pose a serious hazard to human health (da costa *et al.*, 2013). Therefore presence of multiple drug resistant bacteria from fish poses not only risk of disease to the fishes but public health hazard to fish handlers and consumers in general. The result of this study recommended ciprofloxacin, gentamycin and pefloxacin as good choice antibiotics for treatment of infection in the study area.

## Conclusion

In conclusion, this study has revealed that although fish could provide huge culinary and health benefits for mans' sustenance and development, it could also harbour antimicrobial resistance genes that could be transferred to the consumers causing widespread resistance to the usual antibiotics. While the presence of potentially pathogenic bacteria species as observed in the study may not present a serious human health hazard because of heat treatment accorded fish before consumption, the presence of antibiotic resistant strains should not be ignored because of the potential for horizontal gene transfer in the food chain. Given the significance of this study to the public health managers, it is advocated that inputs into these water bodies be properly monitored in other to eliminate/reduce contaminations and antibiotic resistance gene transfers.

## References

- Alday, V., Guichard, B., Smith, P. and Uhland, C. (2006). Towards a risk analysis of antimicrobial use in aquaculture. *Proceeding of the Joint FAO/WHO/OIE Expert Consultation on Antimicrobial Use in Aquaculture and Antimicrobial Resistance Seoul*, South Korea.
- Al-Harbi, A.H and Uddin, N. (2005). Bacterial diversity of tilapia (*Oreochromis niloticus*) cultured in brackish water in Saudi Arabia. *Aquaculture* 250:556-572.
- Bauer, A. W., Kirby W.M.M., Sherris, J.C. and Turck, M. (1966). Antibiotic susceptibility testing by a standard single disc diffusion method. *American Journal of Clinical Pathology* 45: 493-496.
- Botelho-Nevers, E., F. Gouriet, H. Lepidi, A. Couvret, B. Amphoux, P. Dessi and D. Raoult, (2007). Chronic nasal infection caused by *Klebsiella rhinoscleromatis* or *Klebsiella ozaenae*: Two forgotten infectious diseases. *International Journal of Infectious Disease* 11: 423-429.
- Cabral, J.P.S. (2010). Water microbiology, bacterial pathogens and water. *International Journal of Environmental Research and Public Health* 7: 3657-3703.
- Cheesbrough, M. (2006). District laboratory practice in tropical countries: Cambridge university press.
- CLSI (Clinical Laboratory Standards Institute) (2014). Performance Standards for Antimicrobial Susceptibility Testing; Twenty-Third Informational Supplement. CLSI Document M100-S23, Wayne, PA.
- Cohen-Nahum, K., L. Saidel-Odes, K. Riesenber, F. Schlaeffer and A. Borer. (2010). Urinary tract infections caused by multi-drug resistant *Proteus mirabilis*: Risk factors and clinical outcomes. *Infection* 38(1): 41-46.
- Da costa, P.M., L. Loureiro, J. Augusto and F. Matos (2013). Transfer of multidrug-resistant bacteria between intermingled ecological niches: The interface between humans, animals and the environment. *International Journal of Environmental Research and Public Health* 10(1): 278-294.
- Dalgaard, P. (1993). Evaluation and prediction of microbial fish spoilage. Ph.D Thesis. The Technological Labouring of the Danish Ministry of Fisheries and the Royal Veterinary and Agricultural University, Denmark.
- de Sousa, J. A. and Silva-Souza, Â. T. (2001). Bacterial Community Associated with Fish and Water from Congonhas River, Sertaneja, Paraná, Brazil. *Brazilian Archives of Biology and Technology* 44.4 <http://dx.doi.org/10.1590/S1516-89132001000400007>.

- Elemam, A., J. Rahimian and W. Mandell (2009). Infection with Pan resistant *Klebsiella pneumoniae*: A report of 2 cases and a brief review of the literature. *Clinical Infectious Diseases* 49: 271-274.
- Endimiani, A., F. Luzzaro, G. Brigante, M. Perilli, G. Lombardi, G. Amicosante, G.M. Rossolini and A. Toniolo, (2005). *Proteus mirabilis* bloodstream infections: risk factors and treatment outcome related to the expression of extended-spectrum beta-lactamases. *Antimicrobial Agents and Chemotherapy* 49(7): 2598-2605.
- Green, H.C., L.K. Dick, B. Gilpin, M. Samadpour and K.G. Field (2012). Genetic markers for rapid PCR-based identification of gull, canada goose, duck and chicken fecal contamination in water. *Applied Environmental Microbiology* 78 (2): 503-510.
- Grema, H.A., Geidam, Y.A., Suleiman, A., Gulani, I. A and Birma, R.B. (2015a). Multi-Drug Resistant Bacteria Isolated from Fish and Fish Handlers in Maiduguri, Nigeria. *International Journal of Animal and Veterinary Advances* 7(3): 49-54.
- Grema, H.A., Y.A. Geidam, G.B. Gadzama, J.A. Ameh and A. Suleiman. (2015b). Methicillin Resistant *Staphylococcus aureus* (MRSA): A review. *Advances in Animal and Veterinary Sciences* 3(2): 79-98.
- Grimes, D.J. (1991). Ecology of Estuarine Bacteria Capable of Causing Human Diseases: a review. *Estuaries* 14: 345-360.
- Kalra, A., C. Cooley and C. Tsigrelis (2011). Treatment of endocarditis due to *Proteus* species: A literature review. *International Journal of Infectious Diseases* 15: 222-225.
- Kato, Charles Drago; Ruth Kabarozi, Samuel Majalija, Andrew Tamale, Nathan Lubowa Musisi and Asuman Sengooba. (2016). Isolation and identification of potential probiotic bacteria on surfaces of *Oreochromis niloticus* and *Clarias gariepinus* from around Kampala, Uganda. *African Journal of Microbiology Research* 10(36):1524-1530.
- Mauffret, A., M. Caprais and M. Gourmelon (2012). Relevance of bacteroidales and F-specific RNA bacteriophages for efficient fecal contamination tracking at the level of a catchment in France. *Applied Environmental Microbiology* 78 (15): 5143-5152.
- Novotny, L., L. Dvorska, A. Lorencova, V. Beran and I. Pavlik (2004). Fish: A potential source of bacterial pathogens for human beings. *Veterinary Medicine Czech* 49(9): 343-358.
- O'Brien, T.F. (2002). Emergence, spread and environmental effect of antimicrobial resistance: How use of an antimicrobial anywhere can increase resistance to any antimicrobial anywhere else. *Clinical Infectious Diseases* 34(3): 78-84.
- Oloja, E.A.A., N.A. Amusa, A. Osho and V.O. Badejo. (2010). Commensal bacterial flora of synodontis nigrita and *Clarias gariepinus* from River Osun, Southwestern Nigeria, Nigeria. *Research Journal of Applied Sciences* 5(3): 231-235.
- Overdeest, I., I. Willemsen, M. Rijnsburger, A. Eustace, L. Xu, P. Hawkey, M. Heck, P. Savelkoul, C. Vandenbroucke-Grauls, K. van der Zwaluw, X. Huijsdens and J. Kluytmans, (2011). Extended spectrum  $\beta$ -lactamase genes of *Escherichia coli* in chicken meat and humans, the Netherlands. *Emerging Infectious Diseases* 17(7): 1216-1222.
- Ringoe, E. and Gatesoupe, F.J. (1998): Lactic acid bacteria in fish: A Review. *Aquaculture* 161 (3-4): 177-203.
- Rocha, R.D., Leite, L.O., de Sousa, O.V and Vieira, H.S.D. 2014. Antimicrobial Susceptibility of *Escherichia coli* Isolated from Fresh-Marketed Nile Tilapia (*Oreochromis niloticus*). *Journal of Pathogens* 2014: 756539-756543. <http://dx.doi.org/10.1155/2014/756539>.
- Sadhukhan, P.C.; Gihosh, S.; Chaudhuri, J.; Ghosh, D.K.; Mandel, A. (1997). Mercury and organomercurial resistance in bacteria isolated from freshwater fish of wetland and fishery around Calcutta. *Environmental Pollution* (1-2): 71-78.
- Seki, M., K. Gotoh, S. Nakamura, Y. Akeda, T. Yoshii, S. Miyaguchi, H. Inohara, T. Horii, K. Oishi, T. Iida and K. Tomono. (2013). Fatal sepsis caused by an unusual *Klebsiella* species that was misidentified by an automated identification system. *Journal of Medical Microbiology* 62: 801-803.
- Shewan, J.M. (1977). *The bacteriology of fresh and spoiling fish and the biochemical*

- changes induced by bacterial action.* In: *Proceedings of the conference on Handling, processing and marketing of Tropical Fish.* Tropical Products Institute, London: 51-66.
- Shinkafi, S.A. and V.C. Ukwaja. (2010). Bacteria associated with fresh Tilapia fish (*Oreochromis niloticus*) sold at Sokoto central market in Sokoto, Nigeria. *Nigerian Journal of Basic and Applied Sciences* 18(2): 217-221.
- Smith, P., V. Alday-Sanz, J. Matysczak, G. Moulin, C.R. Lavilla-Pitogo and D. Prater. (2013). Monitoring and surveillance of antimicrobial resistance in microorganisms associated with aquatic animals. *Revue Scientifique Et Technique* 32(2): 583-593.
- Tena, D., J. A'ngel Marti'nez-Torres, M.T. Pe'rez-Pomata, J.A. Sa'ez-Nieto, V. Rubio and J. Bisquert. (2007). Cutaneous infection due to *Bacillus pumilus*: Report of 3 cases. *Clinical Infectious Diseases* 44: 40-42.
- Udeze, A.O., M. Talatu, M.N. Ezediokpu, J.C. Nwanze, C. Onoh and I.O. Okonko, (2012). The effect of *Klebsiella pneumoniae* on catfish (*Clarias gariepinus*). *Researcher* 4(4): 51-59.

