Scientia Africana, Vol. 23 (No. 4), October, 2024. Pp 51-60
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

PREVALENCE AND ANTIBIOGRAM STUDY OF *AEROMONAS* SPECIES ISOLATED FROM AQUACULTURE AND ABATTOIR SOURCES IN EBONYI STATE, NIGERIA

Onuoha, S.C.*[1], Nweke, R. N.[1], Ugwu, E.N.[2], and Ali, M.O.[1]
[1]Department of Biotechnology, Ebonyi State University, Abakaliki, Ebonyi State, Nigeria,
[2]Department of Science Laboratory Technology, Akanu Ibiam Federal Polytechnic, Unwana, Afikpo.

Received: 01-08-2024
Accepted: 28-08-2024

https://dx.doi.org/10.4314/sa.v23i4.4

Journal Homepage: http://www.scientia-african.uniportjournal.info
Publisher: *Faculty of Science, University of Port Harcourt.*

ABSTRACT

Aeromonas has been recognised as the primary source of bacterial sickness in aquaculture and agricultural animals. Thorough examination of these disorders and their detrimental effects on public health is lacking in Ebonyi State, Nigeria. Hence, it was imperative to evaluate the occurrence and resistance profiles of the bacteria present in particular aquaculture and abattoir environments against antimicrobial drugs. The technique encompassed the acquisition of wastewater samples from abattoirs and aquaculture plants located in different locations around Ebonyi State. The specimens were gathered utilising specimen containers and thereafter conveyed to the laboratory for subsequent examination. Aeromonas species were obtained from samples collected from aquaculture facilities and abattoirs. Aeromonas isolates were examined using Aeromonas agar and identified using morphological and biochemical analysis. The investigation revealed significant variations ($p<0.05$) in the microbial load among different locations, with values ranging from $4.0\pm0.33x10^6$ CFU/mL to $36.2\pm0.25x10^6$ CFU/mL. The prevalence of Aeromonas species showed substantial variance among different locales, ranging from 5.40% to 12.90%. The medications exhibited a range of susceptibility patterns, ranging from complete resistance (100%) to amoxicillin clavulanic acid, cefotaxime, tobramycin, and ceftazidime, to a 40% susceptibility to imipenem. The isolates displayed a MAR index ranging from 0.6 to 1.0, with an average value of 0.8. The study found that the abattoir and aquaculture environment can act as a possible reservoir for Aeromonas, which could potentially pose a health hazard to humans who consume meat and fish from these farms.

Keywords: Aquaculture, Abattoir, Aeromonas species, Ebonyi State

INTRODUCTION

Aeromonas are Gram-negative bacilli that are frequently present in diverse aquatic environments (Janda & Abbot, 2010, Beez-Hildago *et al*, 2010). *Aeromonas* species are omnipresent bacteria frequently encountered in various settings, such as freshwater, brackish water, sewage, wastewater, and soil. This particular strain of bacteria has also been identified in food and is associated with a variety of illnesses (Altwegg & Geiss, 2009, Araujo *et al*, 2010).

Aeromonas has been highlighted by several authors as a highly significant causal factor in extraintestinal infections in humans, especially in those with compromised immune systems, young children, and the elderly. This cluster of bacteria has been associated with wound

infections, meningitis, pericarditis, endocarditis, septicaemia, urinary tract infections, and respiratory tract infections (Altwegg & Geiss, 2009). The mobile strains of Aeromonas commonly display pathogenicity towards both people and animals. *Aeromonas* species have the potential to induce gangrenous ulcers and sepsis in individuals with burn injuries (Kuhn *et al.,* 2017). The prevalence of antibiotic-resistant bacteria, such as *Aeromonas* species, has led to many clinical repercussions. This issue has also been attributed to the uncontrolled use of antibiotics in animal farming to meet the nutritional needs of people. According to Fainstein *et al* (2012), multiple authors have verified that *Aeromonas* species are rapidly adapting to commonly used medications, which could potentially endanger public health. Moreover, the genomic analysis of selected species offers proof that chromosomes regulate both resistance and new virulence factors (Goni-Urriza*et al*, 2010). Hence, it is imperative to carry out environmental surveillance to evaluate the existence of contamination resulting from pathogenic *Aeromonas* species.

The presence of *Aeromonas* species in wastewater from abattoirs and aquaculture indicates the possible presence of these disease-causing microorganisms and the associated risk of infection. Studies have indicated that certain strains of Aeromonas bacteria are progressively being acknowledged as a source of gastrointestinal diseases (Altwegg & Geiss, 2009). The presence of *A. hydrophila* and *A. sobria* in drinking water is considered noteworthy due to its association with gastrointestinal diseases (Krovacek *et al*, 2014). Hence, the presence of this harmful bacterium suggests the possibility of an epidemic in farm animals and produced fish. Moreover, the contaminated wastewater has the capacity to infiltrate aquatic ecosystems, intensifying their pollution and making them unfit for human consumption. Ingesting meat or seafood that is tainted with this bacterium might result in serious gastrointestinal diseases.

The presence of antibiotic-resistant bacteria in wastewater is widely acknowledged (Igbinosa & Okoh, 2012). Sewage and wastewater, being environments rich in nutrients, create favourable conditions for promoting horizontal gene transfer processes. Therefore, the wastewater environment is regarded as a focal point for the spread of antibiotic resistance factors (Kummerer, 2009). Aeromonas bacteria are exemplary microorganisms that are frequently present in aquatic environments and have acquired resistance to antimicrobial treatments. Although Aeromonas is commonly found in aquatic habitats and has the potential to acquire antimicrobial resistance, there is currently a paucity of detailed research regarding the resistance patterns of the Aeromonas genus in aquaculture and slaughterhouse environments in Ebonyi State. Hence, this research is imperative to fill this void in knowledge.

MATERIALS AND METHODS

Sample Collection and Procession

A total of 50 samples were obtained from the waste-water of an abattoir and the aquaculture environment in Abakaliki Metropolis, Ebonyi State. The waste water from the abattoir was collected from the drainage system, butcher tables, and wash water. While the aquaculture samples were obtained from the different fish ponds. The samples were obtained using aseptic technique and stored in sterile universal containers. The containers were filled, leaving a gap of approximately 2.5cm at the top. The samples were processed and incubated within a time frame of 5 hours from the moment of sampling. The samples were transported to the laboratory of the Applied Microbiology Department at Ebonyi State University for analysis of Aeromonas using isothermal boxes with ice.

Scientia Africana, Vol. 23 (No. 4), October, 2024. Pp 51-60
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

Isolation, Enumeration, and Identification of *Aeromonas* species

The isolation, identification and enumeration of Aeromonas were carried out using standard microbiological/biochemical methods (Cheesbrough, 2006, Abrahim *et al*, 2010).

Antibiotics Sensitivity Testing

Susceptibility patterns of the isolated *Aeromonas* were tested against a wide range of antibiotics namely; Imipenem (10 µg), cefoxitin (30 µg), cefotaxime (30 µg), cefeprime (30 µg), meropenem (10 µg), tobramycin (10 µg) ceftazidime (30 µg) and amoxicillin clavulanic acid (30 µg) on Muller Hinton Agar (Oxoid, UK) using Kirby and Bauer disc diffusion methods of determining susceptibility (CLSI, 2019). All the antibiotics disks were procured from Oxoid limited (Oxoid, UK).

Multiple Antibiotic Resistance (MAR) Index

MAR index was determined by following the procedure described byAyandele *et al.,* (2020)

$$\text{MAR index for an isolate} = \frac{\text{Number of antibiotics to which isolate is resistant}}{\text{Total number of antibiotics against which isolate was tested}}$$

Statistical Analysis

The percentage frequency of occurrence of the *P. aeruginosa* isolated from abattoir and aquaculture environment was calculated using

$$\text{Frequency (\%)} = \frac{n}{N} \times \frac{100}{1}$$

Where n = Number of occurrence of bacteria species, N = Total number of bacteria isolated.

Experimental data was presented as mean±standard deviation, while one way ANOVA procedure was used to analyze statistical difference in the data generated.

RESULTS

An analysis of the microbial load of the isolated Aeromonas specie from abattoir samples revealed that waste water samples from abattoir Butcher's Table with sample code AB_3 (36.2±0. 25 x 10^6 cfu/ml) showed the highest microbial load, followed by AB_5 (27.5±0. 35 x 10^6 cfu/ml) and AB_6 (26.8±0. 39 x 10^6 cfu/ml), while AB_1 (12.0±0. 39 x 10^6 cfu/ml), and AB_2 and AB_4 (7.0±0. 14 x 10^6 cfu/ml) had the least microbial load respectively (Table 1). Drainage samples with sample code AB_3 showed the highest microbial load (21.6±0.19 x 10^6 cfu/ml), followed by AB_1(20.6±0. 19 x 10^6 cfu/ml), AB_4 (16.8±0.04x10^6cfu/ml) and AB_5 (15.0±0. 98 x 10^6 cfu/ml), while AB_2 recorded the least microbial load (10.2±1.32 x 10^6 cfu/ml). AB_6 revealed the highest microbial load of 36.2±0. 14 x 10^6 cfu/ml from wash water samples followed by AB_5 (27.5±0.35x10^6cfu/ml), while AB_3 (4.0±0. 33 x 10^6 CFU/mL) had the least microbial load

Table 1 : Microbial load (CFU/mLx10^6) of the isolated *Aeromonas* species from abattoir samples

Sample code	Wash Water	Drainage	Butcher Table
AB_1	22.0±0. 28	20.6±0. 19	12.0±0. 39
AB_2	6.6±0.67	10.2±1.32	7.0±0. 14
AB_3	4.0±0. 33	21.6±0.19	36.2±0. 25
AB_4	22.5±0. 35	16.8±0.04	7.0±0. 14
AB_5	27.5±0.35	15.0±0. 98	27.5±0. 35
AB_6	36.2±0. 14	12.0±0. 39	26.8±0. 39

Key: AB= Abattoir, Values were mean ± standard deviation (SD)

The highest microbial load of *Aeromonas* species (26.8±0. 39x10^6cfu/ml) was observed in earthen pond water with the sample code PW_1, followed by earthen pond water PW_2 (22.0±0. 28 x 10^6 cfu/ml), while concrete pond water PW_1 and PW_2 revealed the least microbial load of *Aeromonas* specie (10.2±0.39 x 10^6 cfu/ml) respectively (Table 2).

Table 2: Microbial load (x10^6cfu/ml) of the isolated *Aeromonas* species from aquaculture samples

Sample code	Earth Pond	Concrete Pond
PW_1	26.8±0. 39	10.2±0.39
PW_2	22.0±0. 28	10.2±0.39
PW_3	14.4±0.50	12.0±0. 96
PW_4	19.2±0.33	16.0±0. 19
PW_5	12.0±0. 67	15.0±1.97
PW_6	19.9±0.65	12.0±0. 96

Key: PW= Pond water, Values were mean ± standard deviation (SD)

The result of distribution of *Aeromonas* species showed that waste water samples from Wash waters had the highest percentage distribution (35.14%), followed by Drainage samples and Butcher's table which are (32.43%) respectively (Table 3). On the basis of sample code, AB_3 had highest percentage of *Aeromonas* species (18.90%), while the rest of the samples AB_1.AB_2,AB_4,AB_5 and AB_6 had (16.22 %) respectively

Table 3: Distribution of the *Aeromonas* specie isolates from waste water samples from abattoir

Sample code	Wash water (%)	Drainage (%)	Butcher Table (%)	Total (%)
AB_1	2(5.40)	2(5.40)	2(5.40)	6(16.22)
AB_2	2(5.40)	2(5.40)	2(5.40)	6(16.22)
AB_3	3(8.10)	2(5.40)	2(5.40)	7(18.90)
AB_4	2(5.40)	2(5.40)	2(5.40)	6(16.22)
AB_5	2(5.40)	2(5.40)	2(5.40)	(16.22)
AB_6	2(5.40)	2(5.40)	2(5.40)	6(16.22)
Total	13(35.14)	12(32.43)	12(32.43)	37 (100)

Key: % = Percentage

Aquaculture samples showed a slightly higher prevalence among species from concrete pond (51.61**%),** while earthen pond showed least prevalence of (48.39 %) as shown in Table 4. Pond water PW_1 showed highest percentage of *Aeromonas* specie (22.57%), while PW_4 had the least percentage of *Aeromonas* species (12.9 %) as shown in Table 4.

Table 4: Distribution of the *Aeromonas* specie isolates from waste water samples from aquaculture

Sample code	Concrete Pond Number (%)	Earth Pond Number (%)	Total Number (%)
PW_1	3(9.67)	4(12.90)	7(22.57)
PW_2	3(9.67)	2(6.45)	5(16.12)
PW_3	3(9.67)	2(6.45)	5(16.12)
PW_4	3(9.67)	3(9.67)	6(19.34)
PW_5	2(6.45)	2(6.45)	4(12.9)
PW_6	2(6.45)	2(6.45)	5(12.90)
Total	16(51.61**%)**	15(48.39**%)**	**31 (100%)**

Key: PW = Pond water, % = Percentage.

Scientia Africana, Vol. 23 (No. 4), October, 2024. Pp 51-60
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

An assessment of the antibiotic's susceptibility of *Aeromonas* specie to the respective antibiotics used revealed that the isolates showed highest resistance to amoxicillin/clavulanic acid, cefotaxime, tobramycin, ceftazidime (100 % to all) and the lowest resistance was shown to imipenem (40%). Highest susceptibility was observed to imipenem (40%) and meropenem (19%).

Table 5) Antibiotics Susceptibility Pattern of the *Aeromonas* Isolates

ANTIBIOTICS	RESISTANCE(%)	INTERMEDIATE(%)	SUSCEPTIBILITY(%)
Imipenem	27(40)	14(20)	27(40)
Amoxillin/ clavulanic acid	68(100)	0(0)	0(0)
Cefuroxime	63(93)	5(7)	0(0)
Cefotaxime	68(100)	0(0)	0(0)
Tobramycin	68(100)	0(0)	0(0)
Cefepime	50(73)	18(27)	0(0)
Meropenem	42(61)	14(20)	12(19)
Ceftazidime	68(100)	0(0)	0(0)

Key: FOX = Cefoxitin, CTX = Cefotaxime, MEM = Meropenem, CAZ = Ceftazidime, AMC = Amoxicillin/Clavulanic acid, TOB = Tobramycin, IPM = Imipenem, FEP = cefoxitin

From the abattoir samples obtained, highest MAR index of 1.0 was obtained with AB_4, followed by AB_5 (0.9), while the lowest MAR index was obtained with AB_1 (0.4) and AB_2 (0.4) as indicated in Table 6.

Table 6: Multiple antibiotics resistance indices (MARI) of *Aeromonas* species from Abattoirs samples

Sample Code	MARI	Antibiotics
AB_1	0.6	AMC, CXM, CTX, TOB, CAZ
AB_2	0.6	AMC CXM, CTX, TOB, CAZ
AB_3	0.7	AMC, CXM, CTX, TOB, FEP, CAZ
AB_4	1.0	IPM AMC CXM, CTX, TOB, FEP, MEM, CAZ
AB_5	0.9	IPM, AMC, CXM, CTX, TOB, FEP, MEM
AB_6	0.7	AMC, CXM, CTX, TOB, FEP, CAZ

Key: AB = Abattoir, FOX = Cefoxitin, CTX = Cefotaxime, MEM = Meropenem, CAZ = Ceftazidime, AMC = Amoxicillin/Clavulanic acid, TOB = Tobramycin, IPM = Imipenem, FEP = cefoxitin, MARI = Multiple antibiotics resistance index

From the aquaculture samples obtained, highest MAR index of 1.0 was obtained with PW_5, followed by PW_1 (0.7), PW_3 (0.7), while the lowest MA index was obtained with PW_2 (0.6) and PW_4 (0.6) as indicated in Table 7.

Table 7: Multiple antibiotics resistance indices (MARI) of *Aeromonas* species from aquaculture samples

Sample Code	MARI	Antibiotics
PW_1	0.7	AMC CXM, CTX, TOB, FEP, CAZ
PW_2	0.6	AMC CTX, TOB, FEP, CAZ
PW_3	0.7	CTX AMC FOX TOB, CAZ, MEM
PW_4	0.6	AMC CXM, CTX, TOB, CAZ
PW_5	1.0	IPM,AMC,CXM,CTX,TOB,FEP,MEM, CAZ

Key: PW, Pond water, FOX = Cefoxitin, CTX = Cefotaxime, MEM = Meropenem, CAZ = Ceftazidime, AMC = Amoxicillin/Clavulanic acid, TOB = Tobramycin, IPM = Imipenem, FEP = cefoxitin, MARI = Multiple antibiotics resistance index

DISCUSSION

The prevalence of multidrug resistant infections, namely those caused by *Aeromonas* species, has led to a multitude of clinical ramifications. This issue has also been attributed to the uncontrolled use of antibiotics in animal agriculture to meet the need for human consumption. Several researchers have verified that *Aeromonas* species are rapidly adapting to commonly prescribed drugs in the field of medicine, which could potentially endanger public health (Fainstein *et al*, 2012). Moreover, the examination of genetics in typical species clearly demonstrates that the chromosomes regulate the resistance and development of new virulence factors (Goni-Urriza, *et al*, 2010). Hence, it is imperative to carry out environmental surveillance to evaluate the existence of pathogenic *Aeromonas* species and ascertain the occurrence of contamination. Hence, this investigation was carried out to evaluate the antibiotic resistance potential of *Aeromonas* species discovered in aquaculture and abattoir environments in Ebonyi State.

The investigation revealed a significant discrepancy in the quantity of detrimental bacteria in the samples collected from different locations. The levels varied between a maximum of $4.0\pm0.33x10^6$ CFU/mL and a maximum of $36.2\pm0.14x10^6$ CFU/mL in both the aquaculture and slaughterhouse environments. The data obtained from the abattoir indicated elevated levels of bacteria, which can be attributed to the insufficient sanitary and hygienic practices of the abattoir's management and staff, as well as the unsanitary state of the cows being slaughtered. The unprocessed abattoir waste is being released into the drainage channel, both during and after the slaughter operation. This contamination presents a risk to public health as it has the capacity to pollute water sources, making the water unfit for human consumption and capable of transmitting diseases. At their study, Onuoha *et al*. (2017) observed that effluent from slaughtering and dressing slabs at abattoirs is commonly released into open drainage systems without undergoing any form of treatment. This untreated wastewater has the capacity to infiltrate adjacent surface and groundwater reservoirs. This was the prevailing condition at the present research location.

Moreover, the substantial prevalence of bacteria in the fish pond suggests that the bacteria are consistently infiltrating the pond from a certain origin, rather than being supplied randomly. Onuoha *et al* (2017) found that farmers commonly utilise chicken excreta and intestines, as well as extracts from cows and pigs, to enhance the pond's nutrient content instead of relying on costly feeds. These compounds are expected to have elevated quantities of bacteria and could be a significant contributor to the presence of these organisms in the pond. It is crucial to emphasise that these compounds are not subjected to any form of treatment prior to being discharged into the pond. However, Evangelista *et al* (2010) conducted a study that reported a colony count ranging from fewer than 10 to 1.4×10^4CFU/mL, which was lower than the results of the present inquiry. An examination of the bacteriological count results for both the earthen pond and the concrete pond indicated marginally elevated counts in the earthen pond in comparison to the concrete pond. The disparity can be ascribed to the increased probability of pollution in the adjacent water bodies in earthen ponds in contrast to concrete ponds.

The study sought to determine the spatial distribution of *Aeromonas* sp. in the sampled areas. The results revealed that Aeromonas was detected in every sample examined from both the abattoir and aquaculture locations, with a prevalence percentage of 5.88%.

Scientia Africana, Vol. 23 (No. 4), October, 2024. Pp 51-60
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

Aeromonas is widely distributed in various ecosystems, with a greater occurrence seen in a range of aquatic settings (Janda & Abbot, 2010; Salvat & Ashbolt, 2019). The bacteria have also been isolated from several environmental and clinical samples (Janda & Abbot, 2010, Pessoa *et al*, 2019). Previous studies have shown that the rate of isolating *Aeromonas* spp from abattoir and aquaculture sources was greater or lower than what we found in our research. The prevalence rate of 12.90% found in this study is somewhat lower compared to the prevalence rates reported by other researchers doing similar investigations. The changes in the amount of Aeromonas can be ascribed to differences in geographical distribution, sample origin, sampling period, analysis methodology, sample size, and insufficient cleanliness methods in the environment (Sarker *et al,* 2020).

A study conducted by Yakubu *et al* (2005) in Zaria, Nigeria, revealed the presence of *Aeromonas* species in the gastrointestinal tract, gills, and skin of various fish species. The fish were obtained from several water sources, including fresh water, sewage water, chlorinated water, and non-chlorinated water. Furthermore, a study conducted by Fawoyo and Achimugu (2019) suggested that the presence of *Aeromonas hydrophila* in the intestines, kidneys, livers, skin, and guts of fish aligns with the findings of Reyes-Becerril *et al* (2015). This study focusses on identifying *Aeromonas* species in Ebonyi State, which raises concerns about the safety of public meals.

The results of the antibiotics susceptibility test showed a significant variance ($p<0.05$) in the susceptibility of the pathogens across the different isolates, with a range of 0% to 100%. The results demonstrated that all of the samples showed resistance to amoxicillin-clavulanic acid, tobramycin, cefotaxime, and ceftazidime. Our work contradicts the findings of Abulhamd (2009) and Bizani and Brandelli (2001) by showing that the *Aeromonas* species found in environmental water sources are responsive to the same antibiotics. The isolates in this study demonstrated absolute resistance, 100%, to the medicines. This result was predictable, given many antibiotics are readily accessible without a prescription in pharmacies and are marketed by patent private medications vendors (PPMVs). Furthermore, livestock farmers frequently employ them as feed additives without exercising caution. Based on a recent investigation, it was found that these Aeromonas species acquired resistance to β-lactam antibiotics by synthesising lactamases in their chromosomes (Tayler *et al*, 2010). This observation is hypothesised to be due to a notable intrinsic resistance to β-lactam antibiotics, which is reinforced by an active mechanism of expelling the antibiotics from the cell or by collaborating with external factors that hinder the antibiotics from entering the cell membrane. β-lactamases or antibiotic efflux pumps are the external variables referred to in the statement (Janda & Abbot, 2010). The differences in antibiotic resistance patterns among the isolates from the abattoir and aquaculture sources can be attributable to changes in sampling locations, human activities, and different environmental factors. The discrepancies can potentially be attributed to the specific environmental pressure placed on Aeromonas isolates from the two sampling locations.

According to the data, 40% of the isolates were found to be susceptible to imipenem, while the majority showed intermediate susceptibility, as shown in Table 3. Nevertheless, this outcome is in direct opposition to the findings reported by Igbinosa *et al* (2017). The results of the multiple antibiotics resistance index varied significantly, ranging from 0.6 to 1.0, with an average MARI value of 0.8. The study found a high MAR score, which suggests that there is a significant risk to public health due to the spread of drug resistance in aquaculture and abattoir settings. The results of this experiment are consistent with the findings of Onuoha *et al* (2016) in the abattoir setting. Both studies yielded MAR index values exceeding 0.20, with the highest values falling

within the range of 0.90. This resemblance was also observed in our investigation. The study conducted by Igbinosa *et al* (2017) in abattoir and aquaculture environments produced similar findings to the current study, with a MAR index ranging from 0.4 to 0.8. The worldwide health community is alarmed by the rising prevalence of multi-drug resistance in environmental sources, such as abattoirs and aquaculture. This presents a problem to healthcare systems since it restricts the efficacy of therapeutic treatments and complicates the administration of antibiotics, especially in countries with little resources. To summarise, this work provides essential information on the antibiotic resistance traits of *Aeromonas* species collected from the abattoir and aquaculture environment in Ebonyi State. The analysis found that all of the isolates showed substantial resistance to the antibiotics used, as indicated by a high MAR index ranging from 0.6 to 1.0, with an average MAR index value of 0.8. This is consistent with recent studies on the antibiotic resistance of Aeromonads. Continual surveillance and investigation in slaughterhouses and aquaculture fish ponds across the entire southeastern region are of utmost importance. Further investigation is necessary to explore the antibiotic resistance genes and genetic similarities of these isolates.

Author Contribution: OSC.; Conceptualization, Methodology, Formal Analysis, Resources, Writing (Reviewing & Editing), Supervision, NRN; Resources and Visualization, editing and analysis, Project Administration. OSC, UEN, AMO AND NRN; Formal Analysis and Investigation

Conflict of Interest The authors declare that they have no known competing interest.

Acknowledgements We wish to acknowledge the owners of the various fish bonds and abattoir workers for granting accesses to collect samples for the work.

REFERENCES

Abrahim, A., Sergelidis, D., Kirkoudis, I., Anagnostou, V., Kaitsa-Tsiopoulou, E., Kazila, P. and Papa, A. (2010). Isolation and antimicrobial resistance of *Staphylococcus* spp. in freshwater fish and Greek market places. *Journal of Aquatic Food Product Technology*. 19: 93–102.

Abulhamd, A.T. (2009) Characterization of *Aeromonas hydrophila* isolated from aquatic environments using phenotypic and genotyping methods, *Research Journal of Agriculture and Biological Sciences,* 5(6): 923–931.

Altwegg, M. and Geiss, H.K (2009). *Aeromonas* as human pathogen. *Critical Review in Microbiology*, 16: 253-286.

Araujo, R.M., Pares, R. and Lucena, F (2010) The effect of terrestrial effluents on the incidence of *Aeromonas* spp. in coastal waters. *Journal of Applied Bacteriology*, 69: 439-444

Ayandele, A.A., Oladipo, E.K., Oyebisi, O. and Kaka, M.O. (2020) Prevalence of multi-antibiotic resistant *Escherichia coli* and *Klebsiella*species obtained from a tertiary medical institution in Oyo State, Nigeria. *Qatar Medical Journal*, 9: 1-6.

Beaz-Hidalgo, R., Alperi, A., Buján, N., Romalde, J.L. and Figueras, M.J. (2010). Comparison of phenotypical and genetic identification of *Aeromonas* strains isolated from diseased fish. *Systemic and Applied Microbiology*, 33: 149−153

Bizani, D and Brandelli, A. (2001) Antimicrobial susceptibility, hemolysis, and hemagglutination among *Aeromonas* spp. isolated from water of a bovine abattoir, *Brazilian Journal of Microbiology*, 32(4): 334–339.

Clinical and Laboratory Standards Institute (CLSI). (2019). Performance standards for antimicrobial susceptibility testing M100S, 26th Edition.

Cheesbrough, M. (2006) District laboratory practice in tropical countries, Part 2.

Scientia Africana, Vol. 23 (No. 4), October, 2024. Pp 51-60
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

Cambridge University Press, Cambridge, UK,. Pp. 23-78, 137-159.

Evangelista-Barreto, N.S., Carvalho, F.C.T.D., Vieira, R.H.S., dos Reis, C.M.F., Macrae, A. and Rodrigues, D.D.P. (2010) Characterization of *Aeromonas* Species Isolated from an Estuarine Environment. *Brazilian Journal Microbiology,* 41, 452-460

Fainstein, V., Weaver, S. and Bodey, G.P. (2012) In vitro susceptibilities of *Aeromonashydrophila* against new antibiotics. *Antimicrobial Agents and Chemotherapy*, 22: 513-514.

Fowoyo, P.T and Achimugu, F. (2019) Virulence of Aeromonas hydrophila Isolated from Fresh Water Catfish**,** *Journal of Biosciences and Medicines,* 7: 1-12

Goni-Urriza, L., Pineau, M., Capdepuy, C. Roques, P. Caumette, M. and Quentin, C. (2010) Antimicrobial resistance of mesophilic *Aeromonas* spp. isolated from two European rivers. *Journal of Antimicrobial Chemotherapy*, 46(2): 297–301.

Igbinosa ,I.H, Beshiru, A and Igbinosa, E.O (2017) Antibiotic resistance profile of *Pseudomnas aeruginosa* isolated from aquaculture and abattoir environment in urban communities. *Asian Pacific Journal of Tropical Disease,* 7(1): 47 – 52.

Janda, J.Mand Abbott, S.L (2010) The genus Aeromonas: Taxonomy, pathogenicity, and infection. *Clinical Microbiology Review*, 23: 35–73

Krovacek, K., Pasquale, V., Baloda, S.B., Soprano, V., Conte, M. and Dumontet, S. (2014) Comparison of putative virulence factors in *Aeromonas hydrophila* strains isolated from marine environmental and human diarrheal cases in Southern Italy. *Applied Environmental Microbiology*, 60: 1379-1382.

Kuhn, I., Albert, M.J., Ansaruzzaman, M., Bhuiyan, N.A., Alabi, S.A. and Neogi, P.K.B. (2017) Diversity, persistence and virulence of *Aeromonas* strains isolated from drinking water distribution systems in Sweden. *Applied Environmental Microbiology*, 63: 2708-2715.

Kummerer, K (2009) Antibiotics in the aquatic environment: A review-part II. *Chemosphere,* 75(4): 435–441.

Onuoha, S.C, Okafor, C.O., Aduo, B.C and Nwaka, F.C. (2016) Distribution of Antibiotic Resistant Bacteria from Abattoir Wastes and its Receiving Waters at Nkwo-Ezzamgbo, Ebonyi State, Nigeria, *World Journal of Medical Sciences,* 13 (4): 242-250

Onuoha, S.C. (2017) Assessment of Metal Pollution and Antimicrobial Resistance in Bacterial Species Isolated from Aquaculture Sources South Eastern Nigeria, *World Applied Sciences Journal*, 35 (2): 168-176.

Pessoa, R.B.G.; De Oliveira, W.F.; Marques, D.S.C.; Correia, M.T.D.S.; De Carvalho, E.V.M.M.; Coelho, L.C.B.B (2019) The genus Aeromonas: A general approach. Microbiology Pathogen., 130: 81–94

Reyes-Becerril, M., Angulo, C. and Ascencio, F. (2015) Humoral Immune Response and TLR9 Gene Expression in Pacific Red Snapper (Lutjanusperu) Experimentally Exposed to Aeromonasveronii. Fish and Shellfish Immunology, 42, 289-29

Salvat, M.J.F and Ashbolt, N. (2019) Aeromonas . In Global Water Pathogen Project; University of Alberta: Edmonton, AB, Canada

Sarker, B, Arif, M, Eashmen, N, Akter, M.R and LutfulKabir, S. M. (2020) Isolation, identification and antibiogram profile of *Aeromonas hydrophila* from broiler chickens in Mymensingh Sadar, Bangladesh, Asian Australas. *Journal of Food Safety and Security,* 4 (1): 22-30.

Tayler, A.E., Ayala, J.A., Niumsup, P., Westphal, K., Baker, J.A., Zhang, J.A., Zhang, L., Walsh, T.R., Wiedemann, B., Bennett, P.A., Avison, M.B. (2010) Induction of β-lactamase production in *Aeromonas hydrophila* is responsive to β-lactam-mediated changes in peptidoglycan composition. *Microbiology*, 156(8): 2327-2335

Yakubu, S.E., Olanike, O.O. and Wong, C.M.Z. (2005) Survey of Aeromonas hydrophila from Tilapia zillii in Zaria Dam. Journal of scientific Research, 2: 59-63