



Bacteriological Water Qualities of Four Rivers in Ogbia Local Government Area of Bayelsa State, Nigeria

¹Ezenwaka, C. O. and ²Opara, C. N

¹Department of Biology, Faculty of Science, Federal University Otuoke, Nigeria

²Department of Microbiology, Faculty of Science, Federal University Otuoke, Nigeria

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ABSTRACT

The bacteriological quality of water from four different Rivers (Ologakpo, Iyeberia, Ekiritei and Oyai Rivers) in Ogbia Local Government Area of Bayelsa state was investigated. Water samples were collected in sterile bottles and analyzed for bacteriological parameters. On the basis of their morphological and physiological characteristics, bacterial isolates belonging to 5 genera were identified from Ogbia River. They are *Escherichia coli*, *Staphylococcus* spp, *Salmonella* spp, *Klebsiella* spp and *Shigella* spp. The Total viable counts were found in the range of 35 to 105 cfu per ml in Ologakpo River, 31 to 110 cfu per ml in Oyai River, 32 to 142 cfu per ml in Iyebena River and 20 to 91 cfu per ml in Ekiritei River. All the samples collected were found to have total viable count (TVC) higher than those prescribe by WHO. The occurrence of *E. coli* was higher than other bacteria isolated, *E. coli* 131 (41.3%), *S. aureus*, 101 (34.9%), *Salmonella* spp 70 (29.5%), *Klebsiella* spp 43(12.6%) and *Shigella* spp, 20 (5.8%). The consistently high load of the pollution indicator *E. coli* and its isolation from all the rivers indicated that the water body is undergoing severe sewage pollution. These results revealed that faecal coliform pollution were widely distributed in the selected rivers making it unsuitable, unsafe and not acceptable for human use or primary contact and there may be a potential risk of infection for users of waters from these Rivers.

Corresponding Author: xyo2000@yahoo.com

INTRODUCTION

Rivers are important to society, providing water for consumption, agriculture and carrying away human wastes. The bacteriological assessment of water is important in pollution studies, as it is a direct measurement of detrimental effect of toxic waste on human health. Water constitutes one of the most essential elements supporting the life of innumerable animals, plants and human beings. The total quantity of fresh water on earth could satisfy all needs of the human population if it were evenly distributed and accessible (Mahananda *et al.*, 2005). Fresh water resources are deteriorating day by day at a very faster rate. Now water quality has become a global problem (Mahananda *et al.*, 2005). Water is increasingly being threatened as human population grow and there is demand for more water of high quality for domestic purposes and economic activities (Kolawole *et al.*, 2011). Adequate quality, amount, time and place of water are vital for the environment and people's health (Ward and Velazquez, 2008). Pollution of surface and ground water is largely a problem due to

rapid urbanization and industrialization. Thus, gradual deterioration of water quality is as a result of increase in human population and urbanization (HO and Hui, 2001). Polluted water is also an important vehicle for the spread of diseases. In developing countries 1.8 million people, mostly children die every year as a result of water-related diseases (WHO, 2004). The most frequent microbial pathogens are bacteria that originate in wastewater, thus, it is necessary to assess the efficiency of the wastewater treatment and to perform microbiological analyses of the final effluent (Salem *et al.*, 2011).

A wide range of pathogenic microorganisms can be transmitted to humans via water contaminated with faecal material. These include unicellular parasites (such as the protozoan *Cryptosporidium*, *Microsporidium*, *Amoebae*) and enteropathogenic agents such as salmonellas, shigellas, enteroviruses and multicellular parasites as well as opportunistic pathogens like *Pseudomonas aeruginosa*, *Klebsiella*, *Vibrio parahaemolyticus* and *Aeromonas hydrophila* (Karanis *et al.*, 2002). Based on the study of WHO(2000), it has been estimated that waterborne

diseases kill more than 5 million people annually and the microbial pathogens responsible for most of these deaths originate from human and animal feces. Faecal Life Science, Environmental Science indicator bacteria like total coliforms, faecal coliforms (thermotolerant coliforms), *E. coli* and Faecal Streptococci (intestinal enterococci) are excreted by human and warm-blooded animals, pass sewage treatment plants to a great amount and survive for a certain time in the aquatic environment (Kavka and Poetsch, 2002). Faecal *E. coli* and Faecal *Streptococci* are most widely used indicator bacteria (Kistemann *et al.*, 2002).

Bacterial pollution in the river in ogbia local government is increasing day by day due to discharge of organic wastes, human excreta, sewage waste, municipal garbage and toxic discharge from petroleum factories. Escalating water pollution causes not only the deterioration of water quality but it also compromises human wellbeing and the permanence of aquatic ecosystems, economic growth and community affluence (Milovanovic, 2007). The dearth of reports on the bacteriological quality of these four River calls for attention. Therefore, it is important to carry out this study with the primary goal of determining the bacteriological qualities of these essential surface waters and to assess the public health risks emanating from the use of the contaminated water. The present study has been carried out with an objective to systematically examine the prevalence of indicator and pathogenic microorganisms of water from Ologakpo, Iyeberia, Ekiritei and Oyai Rivers flowing across Ogbia L.G.A, Bayelsa State Nigeria.

MATERIALS AND METHODS

To assess the bacteriological pollution in Rivers in Ogbia, four River sites were selected. These are Ologakpo, Iyeberia, Ekiritei and Oyai Rivers. Sampling was carried out from May to July 2016.

RESULTS AND DISCUSSION

The total bacteria count in each water sample was observed as shown in the Table 1: The sites were heavily contaminated, the highest count recorded was 142 CFU per ml and lowest was 31 CFU per ml. The analysis of total viable count in the water samples revealed the high presence of total bacteria in all the water sources. Which is similar to microbiological studies on the River Ganga and Gomti (India) and Densu River (Ghana) that also showed high microbial loads (Sood *et al.*, 2008; Srivastava *et al.*, 2010, Karikari *et al.*, 2006). Servais *et al.*, (2007)

Triplicate samples of surface water were collected in sterile glass bottles and immediately transported to the laboratory for analysis.

Sample analysis

The pour plate method was employed; one ml of each sample was take aseptically with sterile pipette and transferred into a sterile petri dish (duplicates) before aseptically pouring the media in the plate. For each water sample, there was a plate for maconkey agar, SSA, and TCBS agar. After pouring, the plates were incubated for 24hours at 37 °C. After 24hours incubation, colonies were counted using colony counter. The average number of colonies in particular dilution was multiplied by the dilution factor to obtain the total viable count. The results of the total bacterial count were expressed as the number of colony forming units (CFU) per gram of water samples (IS 5402, 2002). Organisms from the original plates were sub-cultured onto a fresh media- MacConkey agar, Salmonella-Shigella (SSA) agar and Thiosulfate citrate bile sucrose salt (TCBS) to obtain pure culture which was used for Gram staining and biochemical test. Enteric bacteria isolated on respective selective or differential media were identified on the basis of their colonial, morphological and Biochemical properties following Bergey's Manual of Determinative Bacteriology (Holt *et al.*, 1994).

Statistical Analysis

The data were elaborated statistically using the software package SPSS 18. The mean and standard deviation were calculated. Analysis of variance (ANOVA) was used to determine if there were differences in pattern of bacterial population among Rivers.

studied faecal contamination of the main Rivers of the Seine watershed (Seine, Marne, Oise Rivers) and found high levels of microbiological pollution which correspondence with the high level of bacteria in this work. Another similar report also indicated that higher bacterial population was obviously due to addition of more sewage and fecal matters through greater human activities (Bohra *et al.*, 2012). The results above exceeded the WHO permissible limit for drinking water which states that the total bacteria count should not be more than 100 CFU/ml (WHO, 2006).

The bacterial isolates were identified which comprised of *Salmonella* spp, *Staphylococcus* spp, *E. coli*, *Klebsiella* spp and *Shigella* spp (Table 2). The

presence of *E. coli*, *Shigella* and *Klebsiella* was an indication of faecal contamination of River water.

Table 1: The Total bacteria Plate Count (PCA) in CFU per ml

Media	Ologakpo River	Oyai River	Iyebena River	Ekiritei River
Maconkey agar	105	86	142	20
SSA	35	48	42	42
SSA	70	110	40	50
SSA	60	31	32	37
Maconkey agar	72	48	33	91

SSA = Salmonella Shigella Agar

Table 2: Cultural Characteristics, Morphological and Staining Properties of the Bacterial Isolates of Water Samples.

S/N	Media	Bacteria	Colony characteristics	Gram's Reaction	Shape	Motility
1	Maconkey agar	<i>E. coli</i>	Pink colonies	(-) ve	short plump rods	non motile
2	SSA	<i>Salmonella</i> spp	Colonies with blank centres	(-) ve	rod shape	Motile
3	SSA	<i>Shigella</i> spp	Circular, clear, colourless transparent colonies	(-) ve	short rods	non motile
4	SSA	<i>Klebsiella</i> spp	mucord/green colonies	(-) ve	shorter rods	non motile

SSA = Salmonella Shigella Agar

TCBS= Thiosulfate Citrate Bile Sucrose Salt

The most abundant bacterial isolate was *E. coli*, followed by *Staphylococcus*, *Salmonella* and while the least abundant bacteria was *Shigella*. The bacteriological analysis revealed that the entire samples collected from the Rivers were contaminated with coliforms and some pathogenic bacteria. Within the coliforms family *E. coli* is of the prime interest and reliable indicator for fecal contamination rather than total coliform, because its presence indicates recent fecal contamination with the possibility of enteric pathogens (Stevens *et al.*, 2003). Assessment of water quality depends on detection of indicators in water samples (Baudart *et al.* 2002). *E. coli* are a major indicator of faecal contamination of water. Therefore the findings of this study establish that there is sewage contamination of river because *E. coli* is found only in the mammalian intestinal tract including that of humans (WHO, 2011). The high coliform counts can be attributed to the unrestricted

inflow of domestic as well as industrial effluents especially petroleum products, livestock waste run-offs and open defecation along the river bank. The total percentage of bacterial count (Table 3) showed that *E. coli* had the highest percentage in all the rivers except Ekiritei River

McLellan *et al.*, (2001) stated that faecal pollution indicator organisms can be used to monitor a number of conditions related to the health of aquatic ecosystems and the potential for adverse health impacts among individuals using these aquatic environments. The presence of such indicator organisms may provide indications of water-borne problems and is a direct threat to human and animal health. As stated by Bohra *et al.*, (2012), presence of coliform simply indicates that pathogens are expected to be present. Gibson (2010), found out that pathogens associated with waterborne illnesses are

excreted in the feces of humans and animals. The alarming high number of coliforms showed in 34, in this study indicates high level of fecal pollution of the river which potentially poses a high health risk. Hamelin *et al.*, (2006) stated that, the presence of pathogenic *E. coli* in environmental waters poses a potential risk for infections in humans and animals especially since water is used for irrigation, drinking and recreational purposes.

Kolawole *et al.* (2011), reported gastrointestinal illness by swimmers who swam in water with a median coliform density of 2,300 coliforms per 100 ml. High total and fecal coliform counts in water are usually manifested in the form of diarrhea, fever and other secondary complications (Zamxaka *et al.*, 2004). These may result in fishes which live in these polluted rivers can easily take in these bacteria while feeding along with contaminated aquatic foods. Migration of the bacteria from water to fish may cause spoilage of fish and outbreak of disease (Rahman *et al.*, 2010). Based on the study of Karikari and Ansa-Asare (2004), poor microbiological quality of the river might be due to contamination caused by human activities and livestock. There is a usual practice for people living along the river catchment to discharge their domestic and agricultural wastes as well as human excreta/wastes into rivers. Wild and domestic animals that are drinking into the water can also contribute to the contamination of water through direct defecation and urination.

Klebsiella are natural inhabitants of many water environments and they may multiply to high numbers in waters rich in nutrients. Presence of these microorganisms implies that the water contains nutrients and this explains the high levels of phosphates. *Klebsiella* are excreted in the faeces of many healthy humans and animals and they are readily detected in sewage polluted water. The greatest microbial risks are associated with ingestion of water that is contaminated with human or animal feces (George *et al.*, 2001). *Staphylococcus aureus* was also identified in river water. It is a pathogenic bacterium responsible for several issues of severe health problems, e.g., chronic infections, abscesses, wound infection. In general, *S. aureus* occurs in water containing organic pollutants, (Tortora *et al.*, 1988). The high incidence of human pathogenic bacteria in the river may indicate their possible presence in fish and other foods derived from this source. Isolation and identification of other specific pathogens (*Salmonella*, *S. aureus* and *P. aeruginosa*, etc.) in water should be undertaken only for purposes of investigating and controlling outbreaks of disease (Abhishek *et al.*, 2015).

From Table 4: The statistical analysis carried out showed significant difference ($p < 0.05$) among Ologakpo, Oyai and Iyebena Rivers. The highest recorded mean concentration of isolates was 26.2 ± 12.66^b per ml from Oyai River and the lowest recorded mean concentration was 3.2 ± 2.39^b per ml from Iyebena River. The results indicated that there was a significance difference between the rivers.

Table 3: Total Percentage of Bacteria Count for Four Samples.

Isolated Organism	Ologakpo River	Oyai River	Iyebena River	Ekiritei River
<i>E.coli</i>	120(35.1%)	131 (41.3%)	72 (30.0%)	112 (38.8%)
<i>S. aureus</i>	89 (26.0%)	91 (28.7%)	87 (36.3%)	101 (34.9%)
<i>Salmonella</i> spp	70 (29.5%)	73 (23.0%)	60 (25.0%)	55 (19.0%)
<i>Klebsiella</i> spp	43 (12.6%)	20 (6.3%)	20 (8.3%)	16 (5.5%)
<i>Shigella</i> spp	20 (5.8%)	2 (0.6%)	1 (0.4%)	5 (1.7%)

Table 4: Total Mean Bacterial count isolated from four different samples per ml.

Bacteria Isolated	Ologakpo River	Oyai River	Iyebena River	Ekiritei River
<i>Esherichia coli</i>	19.0 ± 8.94 ^a	26.2 ± 12.66 ^b	22.4 ± 9.76 ^a	13.4 ± 9.63 ^c
<i>Staphylococcus</i> spp.	14.8 ± 7.29 ^a	18.2 ± 11.67 ^a	20.2 ± 4.55 ^a	15.4 ± 8.08 ^a
<i>Salmonella</i> spp.	10.0 ± 5.87 ^a	16.6 ± 10.60 ^a	13.6 ± 11.28 ^a	12.0 ± 7.58 ^b
<i>Klebsiella</i> spp	4.6 ± 3.65 ^a	4.0 ± 4.42 ^a	3.2 ± 2.39 ^b	4.0 ± 3.32 ^a

Values are Mean ± Standard deviation of 5 replicates per group.

Mean values in a column that do not share the same superscript differ significantly at $p < 0.05$.

Statistical analysis indicated that the four Ogbia Rivers are polluted almost to the same extent thus indicating an alarming situation that needs to be addressed.

In this study, water collected from the four community Rivers was not suitable for domestic uses as it exceeds maximum permissible limits of total coliform. McLellan *et al.*, (2001) stated that faecal pollution indicator organisms can be used to determine the number of cases related to the impacts on human health as well as health of aquatic ecosystems. Major factors affecting the microbial quality of surface and underground waters are improper sewage disposal, surface runoff, seepage from nearby sewage or septic tank (Fatoki *et*

CONCLUSION

The detection and isolation of *Salmonella* spp, *Staphylococcus* spp, *E coli*, *Klebsiella* and *Shigella* from Oyai, Iyebena, Ologakpo and Ekiritei Rivers indicates the frequent discharge of sewage containing pathogenic microorganisms into the Riverine ecosystem. The public health is at hazard as the community in this region depends on this water body for numerous domestic activities. Apart from it, this water body sustains major fish and shellfish resources. The people of Ogbia mainly depend on these Rivers for fish. There is a great chance of food-

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al.,2001).The presence of such indicator organisms may provide information regarding water-borne diseases and is a direct threat to human, animal and aquatic organisms. However, result on *E. coli* counts exceeded the WHO set limit of zero *E coli* in 100ml water sample (WHO, 2004). The study clearly exposes the fact that water becomes unhealthy for drinking as well as domestic purposes because of contamination due to industrial and domestic litter. The present study has obviously demonstrated that there is a significant occurrence of bacterial pollution indicators and pathogenic bacterial groups in the Ogbia River. The condition of the river is very alarming.

borne epidemics due to the presence of these pathogenic bacteria in fishes. The observations clearly indicate that all the studied sites of the Rivers have been contaminated with water-borne pathogenic bacteria. The bacteriological analysis of the four River water in Ogbia reveal that the water is polluted by sewage, faecal contaminants and industrial wastes and this water is not appropriate for drinking, fishing and recreational purposes. Regular monitoring of microbial contamination in the water of these Rivers should be an essential component for future public health protection strategies

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