Abstract—Foodborne Salmonella infections have become a major problem world wide. Salmonellosis transmitted from fish are quite common. Established quality control measures exist for export oriented fish, none exists for fish consumed locally. This study aimed at characterization of Salmonella isolated from Nile tilapia. The study was carried out in selected beaches along L. Victoria in Western Kenya between March and June 2007. One hundred and twenty fish specimens were collected. Salmonella isolates were confirmed using serotyping, biochemical testing in addition to malic acid dehydrogenase (mdh) and fliC gene sequencing. Twenty Salmonella isolates were confirmed by mdh gene sequencing. Nine (9) were S. enterica serotype typhimurium, four (4) were S. enterica Serotype, enteritidis and seven (7) were S. enterica serotype typhi. Nile tilapia have a role in transmission of Salmonellosis in the study area, poor sanitation was a major cause of pollution at the beach inshore waters.

Keywords—fliC, mdh, Salmonellosis, Serotype

I. INTRODUCTION

Salmonella causes a wide range of human diseases such as enteric fever, gastroenteritis and bacteremia. Gastroenteritis has the greatest adverse effect on children’s growth and development [1]. In normal host, bacteremia accompanies gastroenteritis about 5% of the time, whereas in Acquired Immune Deficiency Syndrome (AIDS), the incidence of bacteremia is much higher [2]. The majority of 1.3 billion annual cases of Salmonellosis – caused human gastroenteritis result from ingestion of contaminated food products such as undercooked beef, pork, eggs, milk, shell fish and fish [3,4,5]. Salmonella infections can also be contracted following consumption of fresh fruits or vegetables contaminated by fertilizer [6]. Birds and flies are important vectors for rapid widespread dissemination of Salmonella in the environment [7]. Compared to E.coli, Salmonella withstands a wider variety of stresses associated with environmental fluctuations and may persist in water environment for sometime. Salmonella can be disseminated as a result of water currents, underground springs and rain run off carrying contaminated material [8], [9]. Like E.coli, Salmonella is constantly released into environment from infected human, farm animals, pets and wildlife [10].

Pathogenic and potentially pathogenic bacteria associated with fish and shell fish include Mycobacteria, Streptococcus iniae, vibrio vulnificus, vibrio spp, Aeromonads, Salmonella spp, Shigella and the others [11],[12],[13]. Human infections by these fish pathogens are usually through contact with infected fish while handling them, water or other constituents of fish life environment [14]. The initial microflora on the surface of fish is directly related to the water environment while the flora in the gastrointestinal tract corresponds to the type of food and condition of fish [15]. Most of the animal protein consumed by the local population in western Kenya comes from L. Victoria [16]. Mitigation of environmental problems in L. Victoria indicates four immediate microbiological pollution sources, namely municipal untreated sewage, run off, storm water, animal waste and maritime transport wastes. Municipal untreated sewage, run off and storm water are the most important immediate microbiological pollutants [17]. The low standard of health in the winam gulf region is caused by a general lack of awareness of good hygiene practices, direct contamination of beach waters through bathing and washing and uncontrolled waste disposal around the shoreline [17]. Other sectors like wildlife, agriculture, forestry, urban and rural settlements have been implicated to contribute to microbiological pollution of the lakes [17]. These activities increase eutrophication process thus creating a vast conducive environment for the survival of microbes which eventually infect fish. Analysis of fish tissue slurry indicated that fish harvested from landing beaches along Winam gulf are infested with Enterobacteriaceae namely, Salmonella, Shigella and E. coli [41].

Veterinary authorities from Spain and Italy detected unacceptable level of bacteriological contamination in fish from all the three East African counties [16]. In 1998, European Union (EU) banned fish exports from East Africa and Mozambique due to cholera outbreak. While established quality control measures exist for export oriented fish according to the European Union Directive on Hygiene (91/493/EEC), that deals with handling and processing of fish from the point of capture to its eventual arrival on the market. None exists for the fish consumed locally and this poses a great danger to the health of local consumers [18].
Prevalence of *Salmonella enterica* serotype *typhimurium* was found to be 23.3% and 60% among immunocompromised and immunocompetent children in western Kenya [19]. Septicemic Salmonellosis due to *Salmonella enterica* serotype *typhimurium* is documented to occur seven times more frequently than typhoid infections, with mortality rate of 18% in malaria endemic areas [20]. Clinic based surveillance by CDC/KEMRI for diarrheal diseases (May 1997 – April 1998) in Asembo along Winam gulf found 14% of the total isolates to be *Salmonella* [21]. [22],[23], also found 12% of nontyphoidal diarrhoea in the same region. In Kenya on average 6.6% of pediatric inpatient present with bacteremia. NTS has been second in importance only to invasive pneumococcal disease. However, there is scant information on likely reservoirs and sources of infection [24]. Given the prevalence of water and foodborne disease; Salmonellosis in western Kenya, it was important that all possible infection routes of the pathogens be investigated and prevention measures recommended. This study aimed to characterize *Salmonella* isolated from Nile tilapia (*Oreochromis niloticus*) along L. Victoria beaches in western Kenya as a purported source of Salmonellosis.

II. MATERIALS AND METHODS

A. Study Site

Lake Victoria is the second largest fresh water lake in the world, with an area of 69,000 sq km [16]. The lake is shallow with a maximum depth of 84 m, and a mean depth of 40 m. It has a catchment area of 193,000 Km² shared between Kenya, Tanzania and Uganda. Kenya owns 6%, Uganda 45% and Tanzania 49% of the total area. The basin supports over 30 million people. The major portion of Kenyan water of L. Victoria is a narrow gulf known to various authors by several names; the Victoria Nyanza, Kavirondo gulf, Nyanza gulf and Winam gulf. Winam gulf lies south of the Equator between 0°6' S – 0°32'S and 34°13’ - 34°52’E at an altitude of 1134 m above sea level and covers an area of 1,920 sq. km (approximately 6% of whole lake) between 6 km and 30 km [16]. It has a catchment area of 3,600 km² drained by five major rivers (Nzoia, Kuja, Nyando, Yala, Sondu) through which it contributes approximately 30% of total riperrine inflow into L. Victoria [25]. It receives a mean annual rainfall of about 1,153 mm and a mean annual potential evaporation of 1968 mm. Winam gulf experiences long rains from March – June and short rains in August and October. Sample collection was done in four selected beaches, Uhanya to the northern end of the lake, Luanda Kotieno; an open inshore beach, Homabay to the southern end of the lake and Dunga beach in Kisolmu city; a closed shore in industrialized area (Fig 1).

Working surface was cleaned using 10% jik solution and 70% ethyl alcohol before and after inoculation work. Fish samples were externally disinfected by dipping them in ethyl alcohol for 2 minutes followed by three washings with sterile distilled water.

Whole fish excluding bones was macerated using a sterile mortar and pestle, immersed in phosphate buffered saline (PBS) of pH 7.5 to achieve, 10% w/v suspension of fish. Five milliliters of each fish tissue was used to inoculate selenite F medium (Himedia laboratory Pvt Ltd Mumbai India), incubated at 37°C overnight (18-24h) for maximum recovery of the *Salmonella* pathogen. Isolates in selenite F medium
were subcultured onto both MacConkey agar (Oxoid No. 3 CM 115 Basingstoke, England) and Deoxycholate citrate Agar (DCA) (Himedia laboratories pvt Mumbai India), by streaking technique and incubated at 37°C for 18 – 24 hrs. Colonies from DCA were transferred to Nutrient broth (CDH JO 0003-Himedia laboratories pvt Mumbai India) and preserved at 4°C for later use in genetic analysis.

Biochemical tests (IMViC – Indole, Methyl red, Voges, proskauers, Citrate), was performed to identify bacteria genus based on their biochemical activities in different culture media. Isolates from Triple Sugar iron (TSI) were subcultured in methyl red medium and incubated at 35°C for 48± 2h. To obtain agglutination test for ‘O’ antigen of Salmonella, circular areas were marked off on surface of a glass slide using a crayon pencil marker heavily marked, circular areas containing cell suspension inhibits running onto each other or off the slide. A drop of cells suspended in normal physiological saline (0.9% ml NaCl) was placed in each circle and a drop of antisera was added to each. Agglutination will only occur when there is reaction between antibodies in the antisera and their homologous antigens on cell wall of bacterium. The ‘H’ antigen test was done in a test tube following same procedure as in ‘O’ antigen. The serovars were grouped according to their ‘O’ antigen reaction according to Popoff et al., [27] and Kauffman et al., [28] and Brenner et al., [29].

D. Genotypic Isolation and Analysis of Salmonella

Pure isolates of Salmonella obtained from a series of subcultures in selective medium DCA and stored in nutrient broth (CDH JO 0003 -Himedia laboratories pvt Mumbai India) were picked from solid agar plates using heat sterile broth (CDH JO 0003-Himedia laboratories pvt Mumbai India) and preserved at 4°C ready for DNA extraction. Pure isolates of 1.5 ml were spinned at 15,000 x g for 2 minutes in 0.9% NaCl solution ready for DNA extraction. The pellet was dried for 24 hrs and re – suspended in 100ul TE buffer ready for PCR.

The cycling conditions were as follows 94°C for 5 minutes, followed by 94°C for 25 sec, 54°C for 45 sec then 72°C for 1 min for 30 cycles and post elongation 72°C C for 7 minutes. The amplicons were then loaded onto a casted 2% agarose gel alongside 50 bp DNA marker, a negative control and resolved at a constant voltage of 100 for 25 min prior to UV visualization.

III. RESULTS

Out of 120 fish specimens collected, 63 were positive for various bacteria isolates from fish tissue slurry, Shigella spp (39.6%) was the most isolated Enterobacteriaceae followed by Salmonella (31.7%), E.coli (25.3%), proteus (1.58%) and E. aerogenes (1.58%). A total of twenty Salmonella spp were isolated, 9(14.3%) were Salmonella enterica serotype typhimurium, 4(6.3%) S. enterica serotype enteritidis, 7(11.1%) S. enterica serotype typhi. Dunga beach had the highest Salmonella spp. 8(40%) isolated as compared to Uhanya 6(30%), Homabay 4(20%) and Luanda Kotieno 2(10%) (Table 1).

### TABLE I

**DISTRIBUTION OF SALMONELLA ISOLATES WITHIN SELECTED BEACHES ALONG WINAM GULF**

<table>
<thead>
<tr>
<th>Salmonella serotype</th>
<th>Dunga</th>
<th>Uhanya</th>
<th>Homabay</th>
<th>Luanda Kotieno</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. typhimurium</td>
<td>4</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>N=9</td>
<td></td>
<td>(44.4%)</td>
<td>(33.3%)</td>
<td>(11.1%)</td>
</tr>
<tr>
<td>S. enteritidis</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>N=4</td>
<td></td>
<td>(25%)</td>
<td>(25%)</td>
<td>(50%)</td>
</tr>
<tr>
<td>S. typhi</td>
<td>13</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>N=7</td>
<td></td>
<td>(42.8%)</td>
<td>(28.5%)</td>
<td>(14.2%)</td>
</tr>
<tr>
<td>Total</td>
<td>8</td>
<td>6</td>
<td>4</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td>(100%)</td>
<td>(100%)</td>
<td>(100%)</td>
<td>(100%)</td>
</tr>
</tbody>
</table>

A. Genotypic characterization of Salmonella

Phenotypic identification was confirmed by amplification of Salmonella housekeeping gene matic acid dehydrogenase (mdh) that gave a band of 261bp (Fig 2). For identification of S. enterica serotype (typhimurium), primer combination of fli15 and Tym were used to amplify fliC gene and a band of 559bp was obtained for 9 samples (Fig 3). S.enteritidis identification was genotypically confirmed by 312bp gene amplification of sef A. (Fig 4).

IV. DISCUSSION

Lake Victoria basin is one of the areas where environment has continued to deteriorate [40]. Microbiological pollution through wildlife, agricultural activities, forestry, agribased industries, rural and urban settlement as well as surface runoff and storm water in the Kenyan catchment side of the lake, have negative effects on water quality of rivers draining into
lake Victoria [30]. These activities have contributed to the rising population of fish microbes within Winam gulf.

### Primer pair:

\[ \text{mdh - F, 5'} - \text{CGGACGGAGAAGGTGATG - 3'} \]
\[ \text{mdh - R, 5'} - \text{CGATTCCACCACGCGCTTC - 3'} \]

**M Ø 3 4 5 6 7 8 9 10 11 12 13**

Fig. 2 PCR gel showing *Malic cid dehydrogenase* gene products for *Salmonella*. Isolates from Dunga (Lane 3, 4, 5 & 6), Uhanya (Lane 7 & 8), Luanda Kotieno (Lane 10) and Homa Bay (Lanes 11, 12 & 13). Molecular DNA maker 50bp (lane 1), Ø; negative control (lane 2)

<table>
<thead>
<tr>
<th>Primers</th>
<th>Oligonucleotides sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>FliC</em></td>
<td>- CGGTGTTGCCAGGTTGGTAAT - 3'</td>
</tr>
<tr>
<td><em>Tym</em></td>
<td>- ACTCTTGTGGCGGTGAGCTT - 3'</td>
</tr>
</tbody>
</table>

**M Ø 3 4 5 6 7 8 9 10 11 12 13 14**

Fig. 3 PCR gel showing *fliC* gene products for *Salmonella*. Isolates from Dunga (Lane 4, 5, 6 & 7), Uhanya (Lane 8 & 9), Luanda Kotieno (Lane 12) and Homa Bay (Lane 13 & 14). Molecular DNA maker 50bp (lane 1), Ø; negative control (lane 2)

<table>
<thead>
<tr>
<th>Primers</th>
<th>Oligonucleotides sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Sef</em></td>
<td>- AGGGTCAGGCGGTTACT - 3'</td>
</tr>
<tr>
<td><em>Sef</em></td>
<td>- GGGACATTAGCGTCTTCTTG - 3'</td>
</tr>
</tbody>
</table>

Fig. 4 PCR gel showing *sefA* gene products for *Salmonella*. Isolates from Homa Bay (Lane 3) Dunga (Lane 11 & 12), Uhanya (Lane 13), and. Molecular DNA maker 50bp (lane 1), Ø; negative control (lane 2)

In the present study, analysis of fish tissue slurry indicated that harvested Nile tilapia were infested by *Salmonella*. Twenty *Salmonella* spp were isolated. Dunga beach had the highest *Salmonella* distribution (40%) of the total isolates. The beach area is densely populated with a closed shoreline, this has led to poor water circulation in the shore line. The effects of urbanization have serious implications on L. Victoria along Dunga beach in Kisumu city. Kisumu city is littered with pools of sewage spills from broken sewage pipes and tanks. This forms part of the surface run off after heavy rainfall that ends up into the Lake [31]. This accounted for the high *Salmonella* distribution in Dunga. These results concur with findings of Onyango et al., [41], who found *Salmonella, Shigella* and *E. coli* as some of the serious pathogens associated with fish from Dunga fish landing beach. [32], also identified fish landing environment to be a major source of fish quality problems in L. Victoria. Homabay beach had 20% of total *Salmonella* isolates. Presence of *Salmonella* in fish at Homabay beach was due to pollution as a result of untreated sewage effluents disposed directly into the lake due to dilapidated sewage treatment system. These results are typical of what was found in previous studies by [33], [34], [35],[36] who isolated *Salmonella, Shigella*, and *E. coli* from fish harvested from waters subjected to human sewage pollution.

Distribution of *Salmonella* isolates at Uhanya beach was 30%. Lack of portable water supply in addition to high latrine density in overcrowded nuclear settlements were the causes of high *Salmonella* distribution. The beach area has a closed shoreline hence poor water circulation leading to high levels of *Salmonella* counts. Luanda Kotieno had the lowest distribution of *Salmonella* (10%) in fish collected. This was attributed to the lake area being an open inshore with adequate water circulation. Dilution effect at the shoreline led to low levels of *Salmonella*.

The results of this study indicated presence of *Salmonella* in fish harvested from lake Victoria, an indication of contamination of the lake waters by the pathogen. These results are consistent with the National Agricultural Research Organization of Uganda (NARO) [37] Report which indicated the presence of certain species of *Enterobacteriaceae* like *E. coli, Salmonella* species at some fish landing sites along the shores of L. Victoria [38]. Previous studies by NARO (1997) also established that faecul or thermo tolerant coliforms and therefore prevalence of *Salmonella* species were higher at the inshore waters where beaches are located than offshore water, especially beaches which are densely populated with inadequate sanitary facilities.

The most commonly isolated *Salmonella* serotype was *typhimurium*, followed by *typhi* and the least was *enteritidis*. There being probability that the main source of *Salmonella* contamination in the marine environment is of human or animal origin, the different population structures of *S. enterica* serotype *typhimurium, S. enterica* serotype *enteritidis* may be attributed, to the different rates of growth and survival of these serovars in the aquatic environment. *Salmonella* serovar *typhimurium* was the clinically important serovar mostly identified in this study which attests to its capacity of...
adaptation and survival in the environment as has been suggested by other authors [39],[10]. The presence of Salmonella in Nile tilapia was as a result of contamination of fish during off loading but not during loading offshore. For absolute safety, elimination of initial contamination of fish by Salmonella from the source should be ensured. Landing and marketing of fish from beaches with essential sanitary facilities can reduce the risk of cross contamination. Additional safety measures should include training in personal hygiene, sanitation and ensuring water quality.

ACKNOWLEDGMENT

The authors thank the technical staff of the Department of Zoology laboratory, technical staff of Department of Biomedical Science laboratory. Special thanks to Dr. Gedion Ngwena for facilitating molecular work at KEMRI and Mr. Mulaya for hosting us at K.E.M.R.I Laboratory. We also thank Dr. Rose Kakai of School of Public Health and Biomedical Science laboratory. Special thanks to Dr. Gedion C. Nyangiro for hosting us at the KEMRI Laboratory. We also thank the facilities can reduce the risk of cross contamination.

REFERENCES


