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Microorganisms Associated with Selected Fresh Fishes from River Niger, Lokoja and their Antibiotic Susceptibility

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Abstract **– A microbiological study of microorganisms associated with four species of fishes namely; *Orochromis niloticus* (Tilapia fish), *Clarias gariepinus* (Catfish), *Carcharodon chacharias* (Shark fish) and *Rastrelliger branchysoma* (Short mackerel fish) obtained from River Niger, Lokoja, Kogi State, Nigeria was carried out using standard bacteriological and mycological methods. Samples from the skin, gut and gill were cultured in four media; nutrient agar, MacConkey agar, Salmonella shigella agar and potato dextrose agar and on examination the bacterial count obtained from the skin, gut and gillranged between 132.0 ± 1.0 - 149.0 ± 3.0 x 10^6cfu /ml (skin), $108.0 \pm 0.0 - 138 \pm 1.0$ x 10^6cfu/ml (gut) and 104 ± 4.0 - 127.0 ± 3.5 x 10^6cfu/ml (gill). Enteric count ranged between 105.0 ± 1.5 - 138.0 ± 1.7 x 10^6cfu /ml (skin), $85 \pm 4.0 - 129 \pm 2.0$ x 10^6cfu/ml (gut) and 76.0 ± 4.0 - 122.0 ± 5.0 x 10^6cfu/ml (gill). For Salmonella Shigella the count ranged between 84.0 ± 0.7 - 110.0 ± 4.0 x 10^6cfu /ml (skin), $73.0 \pm 4.5 - 102.0 \pm 5.5$ x 10^6cfu/ml (gut) and 64.0 ± 3.0 - 88.0 ± 2.0 x 10^6cfu/ml (gill) while the fungal count ranged between 18.0 ± 1.0 - 32.0 ± 2.5 x 10^6cfu /ml (skin), $12.0 \pm 0.5 - 21.0 \pm 2.5$ x 10^6 cfu/ml (gut) and $4.0 \pm 1.5 - 14.0 \pm 2.5$ x 10^6 cfu/ml (gill). A total of ten bacteria species were isolated from the samples, *Escherichia coli*, *Bacillus subtilis*, *Klebsiella* sp., *Serratia mercenses*, *Staphylococcus aureus*, *Pseudomonas* sp., *Shigella dysenteriae*, *Salmonella typhi*, *Staphylococcus epidermis* and *Streptococcus.* The fungi isolated include; *Penicillium* sp., *Aspergillus flavus, Aspergillus niger, Fusarium* sp., *Mucor* sp., and *Rhizopus stolonifer* the highest colony count was obtained from the skin of all samples whilegill had the lowest count. Antibiotic sensitivity pattern showed that Perfloxacin (83.3%) and Gentamicin (66.7%) exhibited significant inhibition against the bacterial isolates as compared with Chloramphenicol (75%) and Tarivid (75%) which showed resistant to the isolates. The study showed the presence of multidrug resistant bacteria in these fresh fish samplesand poses a serious health concern to the consumers. It is therefore recommended that better handling should be adopted to eliminate health risks to the fresh fish consumers.**

Keywords **– River Niger, Antibiotic, Susceptibility, Fishes.**

I. INTRODUCTION

Fish has been one of the main foods for humans for many centuries and still constitutes an important part of the diet in most countries, it as become an increasingly important source of protein and other elements necessary for maintenance of healthy body (Sinkafi and Ukwaja, 2010; Mahendra *et al*., (2016). In Nigeria, the short supplies of animal protein with the increasing human population have raised the cost of animal protein to a level almost beyond the reach of the low income group (Ezeri*et. al*., 2001). The resultant effect is a considerable increase in the demand for fish as an alternative source of animal protein in the face of the ever increasing population. It is comparatively cheaper and highly acceptable with little or no religious bias, which gives it an advantage over pork or beef (Shinkafi and Ukwaja, 2010).

Fishes are vertebrates, poikilotherms and live predominantly in water. Their bodies may be elongate, dorsoventrally, laterally compressed or rounded in cross section but recognizable into head, trunk and post anal tail. Fish are highly important in the development of Nigeria both economically and health wise (Ibemenuga and Okeke, 2014).

The freshwater or rivers and lakes have a complex flora of microorganisms which include genuinely aquatic species as well as component introduced from terrestrial, animal and plant sources (Shinkafi and Ukwaja, 2010). Initial microflora on the surface of fish is directly related to the surrounding aquatic environment while the bacterial flora in the gastrointestinal tract corresponds to the condition of the fish. The aquatic medium is extremely vulnerable to pollution that could result from domestic, industrial and agricultural discharges, contamination from soil and airborne infections. Hence, fishes and other aquatic life are prone to environmental hazards. Although infection as a result of microbial contamination may not usually result in disease, however, environmental stresses may upset the balance between the potential pathogens and their hosts. Some of these microflora may not be pathogenic for the fish but when they are consumed by man, a disease condition ensues, e.g., typhoid fever, bacillary dysentery and bacterial food poisoning (Liston, 1980).

The public health significance of fish contamination lies not only in their ability to cause diseases but also their possible role in the transfer of antibiotic resistant strains to other pathogens. Cross-contamination of household utensils and other foods by such fishes could aid the spread infection at home. Their microflora, especially those of the gastrointestinal tract, can be of economic importance as they are capable of effecting rapid post-mortem deterioration and also in aquaculture because of their growth-depressing effect (Novotny *et al*., 2004).

Various studies conducted on microorganisms associated with fresh fishes have shown different types of both bacterial and fungal microbes associated with these fishes. Shinkafi and Ukwaja (2010) conducted a research at Sokoto Central Market, Sokoto State, Nigeria on bacteria associated with fresh Tilapia fish indicated the presence of *Listeria monocytogenes*, *Staphylococcus saprophyticus*,

Serratia mercescens, *Salmonella* spp. among other microbes while Wogu and Maduokor (2010) also reported the presence of fungal species such as *Aspergillus niger*, *Rhizopus* spp., *Pennicillium* spp., as well as bacterial species such as *Staphylococcus aureus*, *Klebsiella* spp., *Escherichia coli* and *Pseudomonas* sp. in aquacultured fresh fish in Benin City, Nigeria these microbes are known to cause food poisoning leading to diseases such as Listeriosis, Urinary Tract Infections, Wound Infections, Typhoid fever, etc.

This study in particular seeks to identify those microorganisms that are associated with fresh fishes obtained from the River Niger, Lokoja outlining their significance to the health of consumers and also assessing the antibiotic susceptibility profile of these isolates.

II. Materials and Methods

Study Area

The study was carried out at Lokoja metropolis, Kogi State, Nigeria which is located within 7.49-7.817^0 North latitude, 6.45-6.75^0 East longitude and 55 meters elevation above sea level. It is also a confluence town where both River Niger and Benue meet. The study areas are Lokoja Old Market along Lokoja-Abuja expressway (site 1) and Ganaja Water Site at Ganaja Village, Lokoja (site 2).

Sample Collection

Four different samples of fishes namely; *Orochromis niloticus* (Tilapia fish), *Clarias gariepinus* (catfish), *Carcharodon chacharias* (Shark fish) and *Rastrelliger branchysoma* (Short mackerel fish) were purchased from both sites from the fisher men within the study area between the hours of 7:00 am and 10 am. The skin surface of each fish was swabbed with a swab stick immediately after been caught from the river the swab stick was inoculated into a test tube containing an already prepared peptone water. The fish was then put into sterile polythene bag and taken immediately to the Advanced Microbiology Laboratory of Salem University, Lokoja for analysis.

Microbiological Analysis:

Preparation of Stock Cultures:

Section of the gills and gut of each sample collected were aseptically removed by means of a sterile scalpel and pair of scissors and kept in sterile Petri dishes. Four (4) gram of the sections were pounded with mortar and pestle. Homogenization was carried out to obtain uniform distribution of cells through stock culture by dissolving the grounded section in 40ml of sterile distilled water. The solution obtained was then used as the stock culture for the experiment.

Isolation and Enumeration of Microorganisms

One milliliter of 10^{-6} dilution of each sample was inoculated on Nutrient agar (for total Viable bacteria), MacConkey agar (for coliform) Salmonella Shigella agar (for salmonella and shigella) and Potato dextrose agar containing 0.1% streptomycin (for fungi) using pour-plate technique. The plates were prepared in duplicates and incubated under aerobic condition at 37°C for 24 - 48 hours, with the exception of Potato dextrose agar plates which was incubated at 25^{0}C for 3-5 days. The number of colonies in each plate were counted using the Quebec colony counter (Reichert, USA) and expressed as colony forming unit per ml of sample homogenate (cfu/ml) (Clarence *et al*., 2009).

Identification of Isolates

The isolates were purified by sub culturing and characterized based on colonial morphology, cellular morphology, stainning and biochemical reactions. Identification was done using Bergey's Manual of determinative bacteriology (Cheesebrough, 2006).

Methods for Fungi Isolation

The fungi were characterized based on colonial morphology and cellular morphology as described by Cooper (1995).

Sensitivity Test

The antibiotics susceptibility of the isolate was determined by the disc diffusion method on Muellar Hinton Agar. The antibiotic multi-disc; Made in Nigeria by Maxicare Medical Laboratory, containing Gram negative (G-ve); septrin, Chloramphenicol, sparfloxacin, ciprofloxacin, amoxicillin, augmentin, gentamycin, perfloxacin, tarivid, streptomycin and Gram positive (G +ve); perfloxacin, gentamycin, ampiclox, zinnacef, amoxicillin, rocephin, ciprofloxacin, streptomycin, septrin, erythromycin, was used. The inoculum was standardized by adjusting its density to equal to a barium sulphate ($BaS0_4$) at 0.5 McFarland turbidity standards, and incubated at 37^{0}C for 18hrs. The diameter of the zone of clearance was measured to the nearest millimeter (mm) (Cheesbrough, 2006).

Statistical Analysis

The data generated were analyzed by one way ANOVA and T- test of the SPSS version 20. All data were expressed as Mean ± SEM. P values less than 0.05 were considered statistically.

III. Results

The mean bacterial count obtained from the skin, gut and gill ranged between $143 \pm 4.0 \times 10^6$cfu /ml(skin) $115.25 \pm 0.0 \times 10^6$cfu/ml (gut) and $127.27 \pm 0.0 \times 10^6$cfu/ml (gill). Enteric count ranged between $121.75 \pm 4.0 \times 10^6$ cfu/ml (skin), $103.5 \pm 0.0 \times 10^6$cfu/ml (gut) and $96.25 \pm 2.0 \times 10^6$ cfu/ml (gill), for Salmonella Shigella the count ranged between $99.0 \pm 1.0 \times 10^6$cfu /ml (skin), $88.25 \pm 0.0 \times 10^6$cfu/ml (gut) and $76.50 \pm 4.5 \times 10^6$cfu/ml (gill) While fungal count ranged from $25.50 \pm 1.5 \times 10^6$ cfu/ml (skin), $15.0 \pm 2.5 \times 10^6$ cfu/ml (gut) and $9.25 \pm 0.0 \times 10^6$cfu/ml (gill) (Table 1). The trend of variation in colony count of the various parts of the fish sampled showed highest microbial count on the fish skin followed by gill and then the gut.

A total of ten bacteria species were isolated from the samples, *Escherichia coli*, *Bacillus subtilis*, *Klebsiella* sp., *Serratia mercenses*, *Staphylococcus aureus*, *Pseudomonas* sp., *Shigella dysenteriae*, *Salmonella typhi*, *Staphylococcus epidermis* and *Streptococcus.* The fungi isolated include; *Penicillium sp., Aspergillus flavus, Aspergillus niger, Fusarium sp., Mucor sp.,* and *Rhizopus stolonifer*.

The distribution of bacterial isolates within the samples are shown in Table 2. Skins of the samples contained six

out of the ten isolates while the gills only three. Table 3 shows the distribution of fungal isolates, it was observed that only the skin of *Carcharodon chacharias* having one of the isolates. Table 4 shows the antibiogram patterns of isolates to Gram positive (G +ve) antibiotics discs, while Table 5 shows the antibiogram for gram Negative organisims.

IV. Discussion

The results of the bacterial analysis of fresh fish from River Niger Lokoja, Nigeria indicate high levels of contamination with pathogenic bacteria. The total aerobic bacteria counts (TBC) exceeded the minimum acceptable limit ($<10^5$ cfu/g) for total aerobic counts (Refai, 1979). Total coliform and staphylococcal counts of the fish samples were also above the acceptable limit (coliform $<10^2$cfu/g, *Staphylococcus aureus* $<10^2$cfu/g) according to Whong *et al*., (2003). The high total aerobic counts is an indication of reduced shelf-life for the fish samples while the high coliform and staphylococcal counts is an indication of potential food infection/ intoxication (Buchanan, 1991). *M*ajority of the isolates are the major pathogens associated with post-harvest fish spoilage. This finding is in agreement with that of Gram and Huss (2001), who reported that these organisms were the major causes of microbial spoilage of fish after capture. Higher microbial counts in the skin samples comparative to the gill and gut may be attributable to handling and processing.

The gills had the lowest bacterial population compared to the gut and skin in all the samples analyzed. According to Ezeri*et al. (*2001), the number of bacteria associated with the gills are actively maintained at low level, thereby implying that fish probably had mechanism which enables it to keep the bacteria number low, and therefore afford it some degree of protection against bacterial infection by all the gill microflora. Walke*et al*. (2015) revealed some opportunistic pathogens in the mucus of skin, gills, fins and mouth of *Labeorohita.*

The presence of *Staphylococcus aureus* a normal flora of the skin and mucous membrane of man and animals in all the samples analyzed can be attributed to human contact during handling and processing (Dalgaard*et al.,* 2006). *Staphylococcus aureus* produces a variety of extracellular enzymes and toxins that have been found to be responsible for food poisoning and can rapidly develop resistance to many antimicrobial agents and pose therapeutic problems (Thrower, 2000).

Bacillus sp., *Escherichia coli*, *Salmonella* sp., *Streptococcus* sp and *Staphylococcus aureus* have been implicated in fish-borne diseases of humans (Babu, 2000). *Salmonella* sp. has been demonstrated to cause enteritis and systemic disease. This constitutes a food safety concern because fishes could be potential agent of transfer of these species to unsuspecting consumers.

The pathogenic state of species of *Streptococcus* is alarming. For instance, *Streptococcus parauberis* has become an important disease agent in the aqua culture industries of North East Asia (Korea, Japan and China), most especially among olive flounder aqua culture farms (Soeng*et al.,* 2013). Only recently, Nho*et al.,* (2009) reported that *S. parauberis* is the dominant etiological agent of *Streptococcus* characterized by clinical symptoms, such as chronic wasting syndrome, haemorrhagic septicaemia, exophtaimia and meningitis with abnormal swimming. Streptococcal diseases have been reported worldwide in wild and farm populations of diverse fresh water and marine fish (Austin and Austin, 1993). Other *Streptococcus* species that have been found to be associated with aquatic contamination include *Streptococcus pyogenes, Streptococcus pneumonia* etc.

The presence of *Escherichia coli* in all the samples analyzed may be due to its ubiquitous nature as it could be found in all environments including human skin, water and air during processing. This result corroborated that of Majeed and MacRae (1991) who observed that most of the bacteria flora associated with spoilage of fish were Gram negative rod bacilli such as *E. coli, Salmonella* sp and *Pseudomonas* sp.

The presence of *Klebsiella* and *Salmonella* sp. in all the fresh fish samples is an indication that the river where the fishes were sourced from was faecally contaminated.

The presence of *Bacillus subtilis* was not surprising since according to Okpokwasili and Alapiki (1990), fish lives in water habitat full of microorganism confirmed that bacteria flora associated with a Nigerian water culture include the genera *Bacillus, Lactobacillus, Staphylococcus, Escherichia, Micrococcus, Proteus* and others. *Bacillus* sp. are implicated in causing a wide range of infectious diseases including abcesses, bacterimia/septicaemia, wound and food borne infections, ear infections, endocardiatis, meningitis, ophthalmitis, osteomyelitis, peritonitis and respiratory and urinary tract infections (Morales *et al.,* 2004).

Serratia mercenses isolated is in collaboration with a similar study conducted by Shinkafi and Ukwaja (2010). The microorganism has been reported to cause lower respiratory tract infections and urinary tract infections in humans.

The fungal species encounted in the fresh fish (*Penicillium* sp., *Aspergillus flavus, Aspergillus niger, Fusarium* sp., *Mucor* sp., and *Rhizopus stolonifer* could come from the water habitat, environment, materials used in fishing and the handlers.

Tudor *et al.* (2009) reported that certain species of *Aspergillus* produced toxic metabolites, while *Mucor* sp. could degrade the biochemical structure of proteins and lipids thereby altering its organoleptic property. The presence of *Mucor* sp, *Penicillium* sp., *Aspergillus niger, Aspergillus flavus, Fusarium* sp. *and Rhizopus stolonifer* in the fish sample is not surprising as they disperse in the form of spores which is abundant in the environment and can be introduced through dust and soil (Apinis, 2003). Their presence in these food samples is of serious public health concern as these fungi have all been implicated with the production of mycotoxin (Makun *et al*., 2009).

The results of the antibiotics sensitivity pattern of the bacterial isolates using the agar disc diffusion method showed that , Pefloxacin and Gentamicin were more sensitive to 83.3% and 66.7% of gram negative isolates

respectively while gentamicin was 100% sensitive to gram positive isolates. Maximum resistance of the bacteria isolates were found in Chloramphenicol (83.5%) and ciprofloxacin (83.5%) for gram negative isolates while for gram positive isolates Chloramphenicol and Tarivid (75%) respective.

V. Conclusion

The presence of these isolates in fresh fish is indicative of the health risk encountered by mostly unsuspecting public in contacting diseases associated with these microorganisms if consumed directly or without proper cooking. Compliance with standard microbiological measures to prevent contamination by these organisms becomes very necessary and should therefore be encouraged. In view of the findings of this research it is therefore recommended that good hygienic conditions and use of clean water during processing should be strictly adhered to. After harvest, fresh fish should be properly stored at low temperatures so as to inhibit the growth of mesophilic bacteria.

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Table 1: Total Microbial Count from Skin, Gut and Gill of the Fresh Fish Samples

SAMPLE	PART OF FISH	COLONY COUNT (X10^{6}cfu/ml)			
		TOTAL BACTERIA COUNT	TOTAL ENTERIC COUNT	TOTAL SALMONELLA COUNT	TOTAL FUNGAL COUNT
Orochromis niloticus	Skin	149.0 ± 3.0	105.0 ± 1.5	84.0 ± 0.7	25.0 ± 1.0
	Gut	129.0 ± 1.0	90.0 ± 2.5	73.0 ± 4.5	12.0 ± 0.5
	Gill	108.0 ± 3.0	85.0 ± 2.0	70.0 ± 1.0	9.0 ± 2.5
Clarias gariepinus	Skin	132.0 ± 1.0	118.0 ± 3.0	96.0 ± 3.0	27.0 ± 3.5
	Gut	108.0 ± 0.0	85.0 ± 4.0	82.0 ± 3.0	13.0 ± 0.5
	Gill	104.0 ± 4.0	76.0 ± 4.0	64.0 ± 3.0	4.0 ± 1.5
Carcharodon chacharias	Skin	148.0 ± 3.5	126.0 ± 1.0	110.0 ± 4.0	32.0 ± 2.5
	Gut	136.0 ± 2.0	110.0 ± 2.5	96.0 ± 5.0	21.0 ± 2.5
	Gill	122.0 ± 3.0	102.0 ± 3.0	84.0 ± 4.0	14.0 ± 3.0
Rastrelliger branchysoma	Skin	146.0 ± 0.0	138.0 ± 1.7	107.0 ± 2.0	18.0 ± 1.0
	Gut	138.0 ± 1.0	129.0 ± 2.0	102.0 ± 5.5	14.0 ± 2.5
	Gill	127.0 ± 3.5	122.0 ± 5.0	88.0 ± 2.0	10.0 ± 2.0

Table 2: Distribution of bacterial isolates among various samples

MICROORGANISMS	FISH SAMPLES											
	Orochromis niloticus			*Clarias gariepinus*			*Carcharodon chacharias*			*Rastrelliger branchysoma*		
	Skin	Gut	Gill	Skin	Gut	Gill	Skin	Gut	Gill	Skin	Gut	Gill
Escherichia coli	+	+	-	+	+	-	+	+	-	+	-	+
Staphylococcus aureus	+	-	+	-	-	+	+	-	-	+	-	-
***Pseudomonas* sp.**	+	-	+	-	+	+	+	-	-	+	-	-
***Streptococcus* sp.**	-	-	-	-		-	+	+	-	+	+	-
***Klebsiella* sp.**	+	-	+	+	+	-	+	+	-	-	-	-
Salmonella typhimurium	-	+	-	-	+	-	-	+	-	-	+	-
Bacillus subtilis	-	-	-	+	-	-	-	-	+	+	-	+
Serratia mercenses	+	-	-	+	-	-	+	+	+	-	-	+
Staphylococcus epidermis	+	-	-	+	-	+	-	-	+	-	+	-
Shigella dysentariae	-	+	-	-	+	-	-	+	-	+	+	-

Key: + = Present, - = Absent

Table 3. Distribution of fungal isolates among various samples

MICROORGANISMS	FISH SAMPLES											
	Orochromis niloticus			*Clarias gariepinus*			*Carcharodon chacharias*			*Rastrelliger branchysoma*		
	Skin	Gut	Gill	Skin	Gut	Gill	Skin	Gut	Gill	Skin	Gut	Gill
***Penicillium* sp.**	+	+	-	+	+	+	+	-	+	-	-	+
Aspergillus flavus	-	+	+	-	-	-	-	+	-	-	+	+
Aspergillus niger	+	-	-	+	-	+	-		+	+	-	+
***Fusarium* sp.**	-	+	-	-	+	-	-	+	-	+	-	-
***Mucor* sp.**	-	+	-	-	+	-	-	-	+	-	+	+
Rhizopus stolonifer	+	-	+	+	-	-	-	-	+	+	+	-

Key: + = Present, - = Absent

Table 4. Antibiotics Susceptibility Profile of Gram positive isolates

Antibiotics	**Test Isolates**			
	Staphylococcus aureus	***Streptococcus* sp.**	***Bacillus subtilis***	***Staphylococcus epidermis***
Septrin (mm)	10.0 (R)	12 .0 (S)	6.0 (R)	14.0 (S)
Chloramphenicol (mm)	8.0 (R)	4.0 (R)	19.0 (S)	11.0 (R)
Sparfloxacin (mm)	20.0 (S)	6.0 (R)	16.0 (S)	10.0 (R)
Ciprofloxacin (mm)	16.0 (S)	8.0 (R)	8.0 (R)	20.0 (S)
Amoxacillin (mm)	8.0 (R)	12.0 (S)	12.0 (S)	8.0 (R)
Augmentin (mm)	10.0 (R)	12.0 (S)	4.0 (R)	15.0 (S)
Gentamycin (mm)	28.0 (S)	18.0 (S)	14.0 (S)	14.0 (S)
Perfloxacin (mm)	25.0 (S)	4.0 (R)	16.0 (S)	10.0 (R)
Tarivid (mm)	10.0 (R)	6.0 (R)	8.0 (R)	12.0 (S)
Streptomycin (mm)	12.0 (S)	12.0 (S)	4.0 (R)	10.0 (R)

(R) = Resistant (below 12mm), S = Susceptible (above 12mm)

Table 5: Antibiotics Susceptibility Profile of Gram negative isolates

Antibiotics	**Test Isolates**					
	Escherichia coli	***Pseudomonas* sp.**	***Klebsiella* sp.**	***Salmonella typhi***	***Serratia mercenses***	***Shigella dysentariae***
Septrin (mm)	9.0 (R)	10.0 (R)	12.0 (S)	5.0 (R)	18.0 (S)	2.0 (R)
Chloramphenicol (mm)	3.0 (R)	5.0 (R)	5.0 (R)	5.0 (R)	16.0 (S)	8.0 (R)
Sparfloxacin (mm)	16.0 (S)	18.0 (S)	8.0 (R)	7.0 (R)	4.0 (R)	15.0 (S)
Ciprofloxacin (mm)	8.0 (R)	8.0 (R)	4.0 (R)	16.0 (S)	6.0 (R)	5.0 (R)
Amoxacillin (mm)	25.0 (S)	10.0 (R)	7.0 (R)	2.0 (R)	14.0 (S)	3.0 (R)
Augmentin (mm)	25.0 (S)	0.0 (R)	6.0 (R)	8.0 (R)	12.0 (S)	8.0 (R)
Gentamycin (mm)	28.0 (S)	8.0 (R)	6.0 (R)	18.0 (S)	18.0 (S)	18.0 (S)
Perfloxacin (mm)	16.0(S)	14.0 (S)	21.0 (S)	16.0 (S)	8.0 (R)	16.0 (S)
Tarivid (mm)	8.0 (R)	4.0 (R)	14.0 (S)	8.0 (R)	4.0 (R)	15.0 (S)
Streptomycin (mm)	5.0 (R)	8.0 (R)	15.0 (S)	4.0 (R)	13.0 (S)	4.0 (R)

(R) = Resistant (below 12mm), S = Susceptible