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INVITRO STUDY OF THE QUINOLONES ACTIVITY ON THE ISOLATES OF UPPER RESPIRATORY TRACT OF DELTA STATE UNIVERSITY STUDENTS

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ABSTRACT

The upper respiratory tract harbours various microorganisms. These microbes can cause severe debilitating health Conditions. This study is aimed at evaluating the Quinolones' pattern of activity on bacterial isolates of the upper respiratory tract of Delta State University Students. Eighty (80) swabs were collected as throat samples which yielded growth upon incubation at a temperature of 37C for 24 hours. Biochemical tests were carried out to characterise the bacteria isolates; antibiotic susceptibility testing was carried out using the Kirby-Bauer disc diffusion method. The results showed that Micrococcus species accounted for 26 (32.5%) while *Staphylococcus aureus* accounted for 16 (20%). While 38 of the swabs had no growth (47.5%), the micrococcus species was the most prevalent microorganism in the throat. Micrococcus species showed the highest susceptibility to ofloxacin (100%) and azithromycin (100%), followed by erythromycin (96.15%) and gentamycin (96.15%) and the lowest susceptibility to amoxiclav (3.84%) and CRO (3.84%). A similar result was obtained for *Staph aureus*, where the highest susceptibility occurred with ofloxacin (100%) and azithromycin (100%), followed by erythromycin (93.75%), gentamycin (93.75%) and the lowest susceptibility to amoxiclav (6.25%). This study revealed that micrococcus species and *Staph aureus* are significant health challenges regarding upper respiratory tract infections.

KEYWORDS: Quinolones; Susceptibility; Antibiotics.

1. INTRODUCTION

Quinolones and fluoroquinolones are broad-spectrum antibiotics, active against many bacteria and certain fungi. Quinolones are an important class of antibiotics used to treat various upper respiratory tract infections. Their success is not far-fetched from their excellent activity against most bacteria pathogens in the upper respiratory tract. Over the year, bacteria resistance has set in with conventional antibiotics, Quinolones inclusive. This resistance has called for various in-vitro studies to understand better the pattern of activity of quinolones on the isolates of the upper respiratory tract. Bacterial resistance to antibiotics has been recognised since the dawn of the antibiotic era. However, only within the past twenty years has the emergence of dangerous, resistant strains occurred with disturbing regularity. This escalating evolution of resistance, coupled with a diminished antibiotic pipeline, has led some to claim that a post-antibiotic era is imminent (Appelbaum, 2012). Though we are still far from that scenario becoming a reality, the trend in the antibiotics field has decidedly been negative for some time now. The upper respiratory tract is a harbour for the various bacterial pathogen that causes different community and hospital-acquired infections. Having efficient data on these pathogenic bacteria's local antimicrobial susceptibility pattern is necessary for selecting appropriate antibiotics for combating infections that may arise from bacteria pathogens residing therein, generally referred to as upper respiratory tract infections. (Watson-Williams, 2001). Upper respiratory tract infections (URTI) are among the most common diseases in individuals of all ages. These Upper respiratory tract infections include but are not limited to the following, Pharyngitis, nasopharyngitis, tonsillitis, otitis media and sinusitis. Although viruses generally cause these major Upper Respiratory infections, the subsequent secondary infection is caused by various types of bacteria resulting in chronic obstructive lung disease and high fever. The different bacteria involved in upper respiratory tract infections (RTIs) are Haemophilus influenza, Streptococcus pyogenes, Moraxella catarrhalis, Staphylococcus aureus, and Streptococcus pneumonia, amongst others. 2 The incidence of Bacteria resistance to

conventional antibiotics is increasing, and it is taking centre stage as a global problem in public health. Ten years ago, concern centred on Gram-positive bacteria, particularly methicillin-resistant S. aureus and vancomycin-resistant Enterococcus spp (Kumarasamy et al., 2010). However, many clinical microbiologists now agree that multidrug-resistant Gram-negative bacteria pose the most significant risk to public health (Ukpai et al., 2015). With this, it is clear that bacteria resistance is becoming very much complex in our present day than it ever was. Various studies have been conducted to better understand the cause of increasing bacterial antibiotic resistance. Although many reasons have been given, most researchers agree that it is mainly due to the mobile genes on the plasmids, which spread and transfer through bacterial populations (Bennett, 2009). The overuse and misuse of antibiotics for treating respiratory tract infections have been considered one of the primary reasons for the emergence of resistance of bacteria against antibiotics (Gonzales et al., 1997). Another reason for antibiotic resistance of bacteria has been considered to be the production of biofilms during a quorum-sensing-regulated mechanism which releases beta-lactamase responsible for the degradation of various antibiotics (Wilke et al., 2005). Nowadays, bacteria resistance against antibiotics has been at an alarming stage throughout the world, with a high mortality rate due to acute infections by various bacteria in respiratory infections. More studies are required to isolate the novel bacterial strains resistant to various antibiotics. The pool of isolated resistant bacteria will be used to develop the potential strategy to target the regulation of bacterial resistance mechanisms to enhance the potency of available drugs, restore the efficacy of available drugs and develop a new range of antibiotics specific to a new mechanism of drug resistance (Lister et al., 2009). In this study, bacterial isolates were obtained from Delta State University Students (DELSU), Abraka.

2. MATERIALS AND METHODS

2.1 Materials

Sterile swab stick, normal saline, syringe, test tubes, test tube racks, culture media (Nutrient agar, Sabouraud Dextrose agar, mannitol salt agar, MacConkey agar, Cetrimide agar, peptone water, nutrient broth, Miu agar, Urease broth base), sterile water, microscope, incubator, autoclave, refrigerator, beam balance, measuring cylinder, beaker, wire loop, glass holder, Bunsen burner, EDTA bottle. The various reagents and equipment used for this work were obtained from the laboratories of the Pharmaceutical Microbiology Department of the Faculty of Pharmacy Delta State University, Abraka (DELSU).

2.2 Methods

2.2.1 Collection of Clinical Specimens (Nasal swab)

Specimen collection was carried out from May 2022 to June 2022; 80throat swab samples from Delta State University male and female students were collected.

The patient was made to open the mouth and relax the tongue. A sterile flexible swab stick was inserted in the mouth and was then quickly and firmly rubbed on the tonsil area to obtain a good sample. The sterile swab sticks were labelled and transferred to microbiological investigation in the pharmaceutical microbiology laboratory, Faculty of Pharmacy, Delta State University, Abraka.

2.2.2 Sterilisation of materials

Glassware such as test tubes, beakers, and measuring cylinders was wrapped in foil paper and sterilised in an autoclave at 121 C for 15 minutes. Cork borers were sterilised by cleaning with cotton wool soaked with 99% methanol and flames over a Bunsen burner. The work area was also sterilised by cleaning it with cotton wool soaked in disinfectant before each work. Media used in the research was sterilised by autoclaving at 121 C for 15 minutes, and inoculating wire loops were sterilised by heating to redness using the Bunsen burner before each use.

2.2.3 Preparation of media

The various media for incubation of the microbial were prepared according to the manufacturer's instruction and were sterilised by autoclaving at 121 C for 15 minutes.

2.2.4 Isolation of test Microorganism and Preparation of Sub-cultures

Upon collection of samples, the throat swab was inoculated on the Nutrient agar plate and Sabouraud dextrose agar plate, respectively. The nutrient agar plates were at 37C for 24 hours, while the Sabouraud dextrose agar plate was incubated at 25°c for 48 hours (Housseiny et al., 2013). The emerging colonies on the nutrient agar were preserved on Slants.

These slants were made by pouring sterilised nutrient agar into sterile Bijou bottles and then kept in a slant position (the bottle laying at an angle resulting in a large surface area for spreading a culture) till they solidified in an aseptic environment.

The agar slant botties were inoculated, incubated at 37°C for 24 hours, and then stored in a refrigerator. The bacterial colonies were further subcultured into various agar, such as Mannitol Salt Agar, Centrimide agar and McConkey Agar. Further identification and biochemical tests for bacterial isolates were carried out using standard microbiological procedures (Cheesebrough, 2010).

2.2.5 Identification of microbial colonies

The identification of bacteria was based on morphological characteristics, and biochemical tests were carried out on the isolates. (Cheesbrough, 2006).

2.2.6 Biochemical reactions

Biochemical tests are performed on different bacteria for their identification based on their biochemical activities towards different biochemical compounds. Biochemical tests are one of the traditional methods for identifying

microorganisms, usually performed with phenotypic identification. (Cheesbrough, 2006).

2.2.7 Determination of antimicrobial activity

Antibacterial susceptibility was carried out using the agar well diffusion method to determine the antimicrobial activity of Quinolones on isolates of the upper respiratory tract.

Mueller Hinton Agar was prepared according to the manufacturer's instruction and poured into different sets of Petri dishes, and was allowed to solidify on the agar after cooling for some time. With the aid of a sterile swab stick, a 24hr broth culture was collected and swabbed all over the surface of the gelled Mueller-Hinton agar. (Cheesbrough, 2006).

With the aid of sterile forceps, an antibiotic disk containing Various Quinolone antibiotics was introduced into the plates and was left on the bench undisturbed for 30mins for pre-diffusion of the drug to occur and then it was incubated at 37C for 24hrs. The resulting zone of inhibition was then measured with a ruler calibrated in millimetres. The average reading was taken as a zone of inhibition of the bacterial isolate in question.

Isolates showing a Zone of Inhibition greater than 12mm were identified as Susceptible, and isolated zones of inhibition less than 12mm were identified as Resistant. (Cheesbrough, 2006).

2.2.8 Statical analysis

The data obtained were evaluated using Statistical Package for Social Sciences, Version 22 (SPSS 22) and then summarised using graphs, frequency tables, means and standard deviations.

2.2.9 Ethics approval

Ethical approval was obtained from the Research and Ethical Committee, Delta State University Teaching Hospital (DELSUTH), Oghara.

3. RESULTS

A total of 80 samples were collected from students of Delta State University, Abraka. On inoculation, 40 yielded growth and they were identified.

Table 3.1 gave the biochemical test result of the bacterial isolates, all of which were gram-positive. The gram-positive organisms identified; are micrococcus spp and Staphylococcus aureus.

Out of 80 samples, micrococcus spp. accounted for 26 (32.5%), and Staphylococcus aureus accounted for 16 (20%). In contrast, 38 swabs had no growth (47.5%) (Table 3.3).

As shown in Table 3.2, both Micrococcus spp and staphylococcus aureus were multi-drug resistant.

Table 3.1: Biochemical test on bacterial isolates.

ISO	Shape	GS	Motility	MRVP	SC	CATA	OXI	IND	H2S	UR	COA	G	L	S	Organism
1	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	AG	*Micrococcus*
2	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	A	*micrococcus*
3	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	A	*micrococcus*
4	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S.aureus*
5	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	AG	*micrococcus*
6	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	AG	*micrococcus*
7	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	A	*micrococcus*
8	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
9	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*micrococcus*
10	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
11	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
12	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*micrococcus*
13	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
14	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	AG	*micrococcus*
15	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
16	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
17	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*micrococcus*
18	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	A	*micrococcus*
19	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*micrococcus*
20	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
21	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	A	A	*micrococcus*
22	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	AG	*Micrococcus*
23	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	A	*micrococcus*
24	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	A	*micrococcus*
25	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S.aureus*
26	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	AG	*micrococcus*
27	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	AG	*micrococcus*

28	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	A	*micrococcus*
29	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
30	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*micrococcus*
31	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
32	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
33	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*micrococcus*
34	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
35	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	AG	*micrococcus*
36	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
37	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
38	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	AG	AG	*micrococcus*
39	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	A	A	*micrococcus*
40	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*micrococcus*
41	Cocci	+	Non-motile	+	-	+	-	-	-	+	+	AG	AG	AG	*S. aureus*
42	Cocci	+	Non-motile	+	+	+	-	-	-	+	+	AG	A	A	*micrococcus*

KEYS
ISO: Isolates
CATA: Catalase
UR: Urease test
MR/VP: Methyl Red/Voges-Proskauer
GS: Gram staining
G: Glucose fermentation test
SC: Simon Citrate test
L: Lactose fermentation test
OXI: Oxidase test
S: Sucrose fermentation test
IND: Indole test +: Positive
H2S: Hydrogen Sulphide -: Negative
COA: Coagulase

Table 3.2: Susceptibility result of bacteria isolates to routinely used Quinolone antibiotics.

ISO	AUG	CIX	CRO	ZEM	LBC	CIP	ERY	GN	AZN	IMP	CXM	OFX	Organism
1	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
2	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
3	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
4	R	R	R	R	S	S	S	S	S	R	R	S	S. aureus
5	R	R	R	R	S	R	S	S	S	R	R	S	Micrococcus
6	R	R	R	R	R	S	S	S	S	R	R	S	Micrococcus
7	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
8	R	R	R	R	S	S	S	S	S	R	R	S	S. aureus
9	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
10	R	R	R	R	S	S	S	S	S	R	R	S	S.aureus
11	R	R	R	R	S	S	S	S	S	R	R	S	S. aureus
12	R	R	R	R	S	R	S	S	S	R	R	S	Micrococcus
13	R	R	R	R	S	S	S	S	S	R	R	S	S. aureus
14	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
15	S	S	S	S	S	S	S	S	S	S	S	S	S. aureus
16	R	R	R	R	S	S	S	R	S	R	R	S	S. aureus
17	R	S	R	R	S	S	S	S	S	R	R	S	Micrococcus
18	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
19	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
20	R	R	S	R	R	R	R	S	S	R	R	S	S. aureus
21	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
22	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
23	R	R	R	R	S	S	S	R	S	R	R	S	Micrococcus
24	R	R	R	R	S	S	R	S	S	S	S	S	Micrococcus
25	R	R	R	R	S	R	S	S	S	R	R	S	S. aureus
26	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
27	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
28	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
29	R	R	R	R	S	S	S	S	S	R	R	S	S. aureus
30	S	S	S	S	S	S	S	S	S	S	S	S	Micrococcus
31	R	R	R	R	S	S	S	S	S	R	R	S	S.aureus
32	R	R	R	R	S	S	S	S	S	R	R	S	S. aureus
33	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
34	R	S	R	R	S	S	S	S	S	R	R	S	S. aureus

35	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
36	R	R	R	R	S	S	S	S	S	R	R	S	S. aureus
37	R	R	R	R	S	S	S	S	S	R	R	S	S. aureus
38	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
39	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
40	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus
41	R	R	S	R	S	S	S	S	S	R	R	S	S. aureus
42	R	R	R	R	S	S	S	S	S	R	R	S	Micrococcus

Percentage susceptibility

Organism	AUG	CIX	CRO	ZEM	LBC	CIP	ERY	GN	AZN	IMP	CMP	OFX
S. aureus[16]	1 6.25 %	2 12.5 %	3 18.75 %	1 6.25 %	15 93.75 %	14 87.5 %	15 93.75 %	15 93.75 %	16 100 %	2 12.5 %	2 12.5 %	16 100 %
Micrococcus spp[26]	1 3.84 %	2 7.69 %	1 3.84 %	1 3.84 %	25 96.15 %	24 92.3 %	25 96.15 %	25 96.15 %	26 100 %	2 7.69 %	2 7.69 %	26 100 %

Keys
ZEM: Cefixime -5ug
LBC: Levofloxacin – 5ug
CIP: Ciprofloxacin – 5ug
IMP: Imipenem – 10ug
CMX: Cefuroxime – 30ug
OFX: Ofloxacin – 5ug
ERY: Erythromycin – 15ug
GN: Gentamycin – 10ug
AZN: Azithromycin – 15ug
AUG: Augmentin – 30ug
CTX: Cefotaxime – 25ug
CRO: Ceftriaxone – 25ug
AG: Acid and Gas
A: Acid
S: Susceptible
R: Resistant

Table 3.3: Synopsis of microbial isolates and their frequency of occurrence.

Microorganisms	Frequency of occurrence
Micrococcus spp	26 (32.5%)
Staphylococcus aureus	16 (20%)

4. DISCUSSION

The nasal cavity, mouth, throat (pharynx), and voice box are the upper respiratory tract's main routes and structures (larynx) structures. A mucous membrane that secretes mucus lines the respiratory tract. The mucus captures smaller particles like smoke or pollen. Cilia, which resemble hairs, line the mucous membrane and transport mucus-trapped particles outside the nose. The skin lining the nasal cavity moistens, warms, and purifies the inhaled air. This study death with the quinolones pattern of activity of bacterial isolates of the upper respiratory tract of Delta State University students.

Eighty (80) swabs were collected as nasal samples, which yielded growth upon incubation at 37C for 24 hours. Biochemical tests were carried out to characterise the bacteria isolates. Antibiotic susceptibility testing was carried out using the Kirby-Bauer disc diffusion method. The results showed that Micrococcus species accounted for 26 (32.5%) while Staphylococcus aureus accounted for 16 (20%). While 38 of the swabs had no growth (47.5%), This was clearly shown in (Table 3.3). The result showed micrococcus specie to be the most prevalent microorganism present in the nostrils. Micrococcus species showed the highest susceptibility to Ofloxacin (100%) and Azithromycin (100%), followed by Erythromycin (96.15%) and Gentamycin (96.15%) and the lowest susceptibility to Augmentin (3.84%) and CRO (3.84%). A similar result was obtained for Staph aureus, where the highest susceptibility occurred with Ofloxacin (100%) and Azithromycin (100%), followed by Erythromycin (93.75%), Gentamycin (93.75%) and lowest susceptibility to Augmentin (6.25%). This study revealed that micrococcus species and Staph aureus are major health challenges as regards upper respiratory tract infections.

Resistance occurred with most of the beta-lactam antibiotics. This may have resulted from the presence of the beta-lactamase enzyme, which is responsible for the disruption of the Beta-lactam ring of the drug. This is one of the reasons why Quinolone antibiotics were introduced. This same study shows that they are still a viable class of antibiotics as there is 100% Susceptibility with both Staph aureus and Micrococcus specie.

Resistance of microorganisms to antibiotics can arise fr0m several ways, such as; Self-medication, resistance due to gene mutation, antibiotic inactivation, target modification, altered permeability and bypass of the metabolic pathway by the microorganism.

Multi-drug resistance for both Staph aureus and Micrococcus species may be due to reasons such as;

enzymatic deactivation of antibiotics, decreased cell wall permeability to0 antibiotics, altered target sites of antibiotics, efflux mechanism to remove antibiotics, increased mutation rate as a stress response etc.

As is the case with other incapacitating conditions like impaired respiratory system (asthma, chronic obstructive pulmonary disease [COPD]), diabetes etc. So also, nosocomial and community-acquired Upper Respiratory tract infections have been on the rise. These nosocomial Upper Respiratory tract infections are primarily caused by Gram-positive organisms (Staphylococcus aureus and Micrococcus specie). Although they are not recommended for viral infections, antibiotics are frequently administered to treat Upper Respiratory tract infections. It is crucial to employ the proper antibiotic based on the pathogen, and treatment must adapt when new diseases and resistance to standard treatments emerge.

One of the main reasons why the effectiveness of these antibiotics against microbial pathogens should be evaluated and confirmed is that Oral antibiotics are preferred and mostly prescribed by clinicians. Preference for Oral antibiotics is due to certain reasons such as increased patient compliance, and patients can be treated on an outpatient department (OPD) basis. Among oral antibiotics, quinolones are well absorbed, with moderate to excellent bioavailability. Serum drug levels achieved after oral administration are comparable to those with intravenous dosing, allowing an early transition from intravenous to oral therapy and potentially reducing treatment costs.

Thus, this study isolates the pathogens responsible for Upper respiratory tract infections and compares the *in vitro* efficacy of commonly prescribed fluoroquinolones and other commonly used first-line antibiotics by disc diffusion method.

The study evaluated the Quinolone antibiotics pattern of activity on bacterial isolates of the Upper Respiratory tract of Delta State university students. Having obtained the samples from throat swabs, the organisms were identified and confirmed by Cultural and Biochemical techniques. Staphylococcus was cream-coloured, appearing as small uniform colonies on nutrient broth agar. It was coagulase-positive, fermented glucose to acid and gas and was gram-positive, which showed cocci shapes in pairs, singles and clusters, while micrococcus species was cream in colour, appearing as circular tetrads on nutrient agar. It was coagulase-positive, catalase-positive, fermented glucose to acid and gas, and gram-positive.

Susceptibility studies were conducted using micrococcus Ofloxacin, Azithromycin, Erythromycin, Gentamycin, Augmentin, and Cefuroxime. The experiment was done in duplicate, and an intermediate zone of inhibition reading was taken. The study involved investigating the prevalence of Upper respiratory tract microbial pathogens in Delta State university students and also evaluating the pattern of activity of Quinolone antibiotics against the microbial isolates (Staphylococcus aureus and Micrococcus species) to ascertain the potential of these Quinolone antibiotics agents in the treatment of upper respiratory tract infections. The data collected were subjected to analysis, mean deviation, and standard deviation of the zones of inhibition exhibited by the antibiotic agents.

This study emphasises the importance of antimicrobial susceptibility testing of microbial isolates obtained. The emergence of the Resistant strain of Upper respiratory tract microbial pathogens is a global health problem and specifically a daunting challenge in African Countries like Nigeria and thus becoming a public health concern. Most microbial strains are multi-drug resistant, limiting the number of available effective drugs. The health care system depends majorly on a broad spectrum of orally administrable antibacterial, of which quinolones are an outstanding example. Moreover, as such, it is necessary to study the pattern of activity of these Quinolones to determine their effectiveness for use in combating Upper Respiratory Tract Infections.

Fluoroquinolone antimicrobial agents were introduced with high expectations as an effective alternative to older antibacterial compromised by resistance. Although resistance rates were lower for this class of drugs, the rate of Quinolone resistance of Staph aureus and micrococcus species has increased greatly over the past decade. Thus, the prudent use of antimicrobial agents is necessary to minimise the spread of these resistant genes.

Other factors include poor sanitation, contamination of food and water, use of other drugs concomitantly, and practices related to the use of antimicrobial agents that select for the growth of resistant strains.

5. CONCLUSION

The findings of this study have shown that the Upper Respiratory tract is associated with diverse species of microorganisms which inhabit the nostrils. These organisms are sources of potential pathogens and can cause serious infections. Microorganisms are ubiquitous and can be found in the nostrils, with micrococcus species being the most prevalent organism, according to the research. The twobacterial isolates, "micrococcus species and Staphylococcus aureus, showed multi-drugresistance. It is highly recommended that antibiotics should not be abused but used based on prescription in order to avoid resistance.

6. Contribution to Knowledge

This study will be highly important to healthcare practitioners and prescribers in ascertaining and prescribing effective drugs against upper respiratory tract pathogens such as Staphylococcus aureus and micrococcus species. Most Penicillin is no longer

effective in treatment combating Staphylococcus aureus and micrococcus species, so treatment should be focused on other classes of antibiotics, such as 2nd generation Quinolones; ofloxacin is a class, as the study has shown. This study is thus of great significance to keep healthcare practitioners abreast with the current trend of knowledge.

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