

RESISTANCE PATTERN OF URINARY TRACT INFECTION BACTERIAL ISOLATES TO SELECTED QUINOLONES

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ABSTRACT

The Quinolones inhibit bacteria by interacting with DNA topoisomerases (gyrases) of which four subunits (two A and B monomers) have been identified thus, inhibiting bacterial DNA gyrase. High level resistance to quinolones can be produced by serial exposure of bacteria to subinhibitory concentration. A Total of 408 suspected UTI and high vagina swab (HVS) samples were examined for bacteria and the isolates obtained tested against the newer quinolones. Prevalence of Bacterial isolates revealed *Escherichia coli* 110(92%) as the most isolated organism from urine, while *Staphylococcus aureus* 31(32%) was the most isolated species from HVS samples. Bacterial species such as coliforms 55(70%) and *Klebsiella* spp 42(84%), equally had high prevalence rate in urine samples. *Pseudomonas aeruginosa* 19(66%) was next to *Staphylococcus aureus* in terms of prevalence of isolated strains from HVS samples. The resistance pattern observed for these isolates, showed that the strains were least resistant to Ciprofloxacin, followed by Ofloxacin and Perfloxacin, while they were most resistant to Nalidixic acid. There was however no statistical significance ($P < 0.001$) between the use of Ofloxacin and Perfloxacin, however, ANOVA showed a significant difference ($P < 0.05$) between the pattern of *Klebsiella* spp resistance against Perfloxacin when compared to *Proteus vulgaris*.

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INTRODUCTION

The introduction of Nalixidic acid in 1962, began the history of the newer 4-quinolone antibacterial agents. The clinical significance of these drugs is based on their broad antibacterial spectrum, unique mechanism of action, good absorption from the gastrointestinal tract, excellent tissue distribution as well as low incidence of adverse reaction¹.

Recent studies indicate that the mechanism of action of these drugs is the inhibition of DNA topoisomerases (gyrases), thus inhibiting the bacterial DNA synthesis^{2,3}. The drugs are bacteriocidal, with a single most bacteriocidal concentration and in greater or lesser concentrations, kill few bacteria⁴. This Paradoxical effect of decreased killing at higher concentrations is most likely the result of dose-dependent inhibition of DNA synthesis⁵.

Antimicrobial Activity: Nalixidic acid has greater antibacterial activity against Gram negative rods than Gram positive bacteria. It is active against most strains of *Escherichia coli*, *Proteus mirabilis*, *Klebsiella* spp and other Coliforms at concentrations easily achieved in the

urine i.e. 16pg/ml or lower⁶ Gram positive organisms like *Staphylococcus aureus*, *Streptococcus pneumoniae* and *Streptococcus faecalis* are resistant to Nalixidic acid.⁷

Norfloxacin which is 100 times more active compared to Nalixidic acid, has a spectrum that includes enterococci, *Staphylococci* and *Pseudomonas* species.⁸ It is active against most Gram positive and Gram negative bacteria implicated in UTI at concentrations easily attained in the urine. Norfloxacin is active against *Haemophilus influenzae*, *Neisseria gonorrhoea*, regardless of beta-lactamase activity. However, it is less active against methicillin-resistant strains of *Staphylococcus aureus*.^{9,10}

Ciprofloxacin is said to be more potent than Norfloxacin, and is also active against most Gram positive and Gram negative infectious bacteria at concentrations easily attained in most tissues and body fluids.¹¹ Ciprofloxacin has excellent activity against *Chlamydia trachomatis* and genital Mycoplasma, inhibiting 90% of isolates at 1ug/ml concentrations.^{12, 13,14} However, reduced susceptibility of these organisms to Ciprofloxacin occurs following serial exposure of the organisms to subinhibitory drug concentrations, this invariably may lead to cross resistance to other quinolones by the organisms¹⁴.

Though, exact mechanism of bacterial resistance to the quinolones is unknown, it may occur when serine in position 83 of subunit A is replaced by tryptophan¹⁵. Or when inhibition of topoisomerase 1V interfere with replicated chromosomal DNA¹⁶. Finally, it could be due to a mutation in the gene coding for DNA gyrase or a mutation that alters the bacteria's outer-membrane porins¹⁷.

In this work, we identified and assessed the prevalence of bacteria in UTI as well as determined the current trend in the resistance pattern of the bacteria isolates to the selected quinolones.

MATERIALS AND METHODS

Specimen:

A total of 408 clinical specimens comprising of 305(75.25%) urine samples and 103(25.75%) of high vaginal swab (HVS) samples. All specimen were transported to the laboratory and were processed within 2hours of collection.

Isolation and identification:

The specimens were inoculated onto Nutrient agar, Blood agar and MacConkey agar plates by streaking. Inoculated plates were then incubated aerobically at 37°C for 24 hours. After 24 hours of incubation, discrete colonies were picked up and Gram stained and further subculturing was done to obtain pure cultures and biochemical tests carried out.

Antimicrobial Susceptibility Testing

This was done by the disc diffusion method. All isolates were subjected to testing using Nalidixic acid, Perfloxacin, Ciprofloxacin and Ofloxacin.

Staphylococcus aureus, Oxford stain NCTC 6751 was used as control for Gram-positive organisms while *Escherichia coli* NCTC 10418 was used as control for Gram negative organisms.

The results of the susceptibility test were interpreted as sensitive, intermediate or resistant, using the criteria below:

A zone's radius equal to or not more than 3mm smaller than the control was reported as sensitive.

A zone's radius more than 3mm smaller than the control but not less than 3mm was reported as intermediate or moderate.

A zone's radius of 2mm or less (i.e., no zone of inhibition) was reported as resistant.

RESULTS

A total of 408 suspected UTI and vaginitis samples were analysed during this study. Of these samples 305(75.25%) were urine samples and 103(25.75%) were high vagina swab (HVS) samples. Males contributed 156(51.51%) of the urine samples while a total of 103(100 *L) HVS samples were collected from females 18years and above.

Table 1: Prevalence of Bacterial Strains Obtained From Urine and HVS Samples

Bacterial Strains	No of Isolates obtained from	
	Urine Samples	HVS Samples
<i>Escherichia coli</i>	110(92%)	9(8%)
<i>Staphylococcus aureus</i>	67(68%)	31(32%)
<i>Coliforms</i>	55(70%)	23(30%)
<i>Klebsiella spp</i>	42(84%)	8(16%)
<i>Proteus mirabilis</i>	18(60%)	21(40%)
<i>Pseudomonas aeruginosa</i>	10(34%)	19(66%)
<i>Proteus vulgaris</i>	3(100%)	0(0%)
Total	305(75.25%)	103(25.75%)

Table 1.shows the prevalence of bacterial strains obtained from both urine and HVS samples. *Escherichia coli* has the highest prevalence among the bacterial isolates, with 119 samples. Of this total, 110(92%) were isolated from urine and 9(8%) was isolated from

HVS samples. *Staphylococcus aureus* were isolated in 98 samples, 67(68%) from urine samples and 31(32%) from HVS samples. *Klebsiella* species were isolated were isolated from 50 samples 42 from urine sample (84%) and 8 from HVS samples (16%).

Table 2: The Susceptibility Pattern of Bacterial Isolates and the Percentage (%) Resistance to the Selected Quinolones

Bacterial Strains	No (%) Resistance to the Quinolone				
	n	PER	CRP	OFX	NA
<i>Escherichia coli</i>	119	30(25.2%)	37(31.1%)	28(23.5%)	45(37.8%)
<i>Staphylococcus aureus</i>	98	16(16.3%)	8(8.2%)	8(8.2%)	37(37.6%)
<i>Coliforms</i>	78	18(22.8%)	6(7.6%)	18(22.8%)	45(60.0%)
<i>Klebsiella spp</i>	50	10(20.0%)	10(20.0%)	8(16.0%)	22(44.0%)
<i>Proteus mirabilis</i>	30	5(16.7%)	2(6.7%)	7(23.3%)	5(16.7%)
<i>Pseudomonas aeruginosa</i>	29	6(20.7%)	0(0.0%)	9(31.0%)	9(31.0%)
<i>Proteus vulgaris</i>	3	2(66.6%)	0(0.0%)	0(0.0%)	1(33.3%)

Key:

n = number of strains tested

PEF = Perfloracin
 CRP = Ciprofloxacin
 OFX = Ofloxacin
 NA = Nalixidic acid.

Table 2 shows the selected quinolones used and the isolates susceptibility pattern. *Escherichia coli* had 30 strains resistant to perfloracin, 37 were resistant to Ciprofloxacin, 28 and 45 isolates were resistant to Ofloxacin and Nalixidic acid.

Nalixidic acid unarguably is the least sensitive of the selected quinolones, virtually all other bacterial isolates showed increased resistance to Nalixidic acid than the other selected quinolones.

Table 3: *In-vitro* Antimicrobial Activity of the Selected Test Quinolones against Isolated Bacterial Species.

Bacterial Strains	Mic(μ g/ml)			
	n	PER	CRP	
<i>Escherichia coli</i>	0.039	0.250	0.125	5.000
<i>Staphylococcus aureus</i>	0.250	0.250	0.039	5.00
<i>Coliforms</i>	0.063	0.500	0.500	5.000
<i>Klebsiella spp</i>	0.250	0.500	0.250	10.000
<i>Proteus mirabilis</i>	0.250	0.500	0.250	10.000
<i>Pseudomonas aeruginosa</i>	0.500	5.000	5.000	10.000
<i>Proteus vulgaris</i>	0.063	0.250	0.250	0.500

In table 3, the minimum inhibitory concentration (MIC) in µg/ml of *Escherichia coli* to Nalixidic acid was observed to be 5.0µg/ml, 0.059µg/ml to Perfloxacin, 0.250µg/ml and 0.125µg/ml to Ciprofloxacin and Ofloxacin respectively.

Ofloxacin was observed to be a more potent for *Staphylococcus aureus* with the organisms having a MIC of 0.039 to Ofloxacin, and 0.250µg/ml to both Perfloxacin and Ciprofloxacin respectively and 5.00µg/ml to Nalixidic acid.

DISCUSSION

The selected quinolones proved to be of chemotherapeutic value against the 408 samples analysed in the cause of this work. Some strains however were resistant. This work agrees with other similar works, especially with respect to the incidence rates of *Escherichia coli*. *Escherichia coli* had earlier been reported as being the most prevalent organism implicated in UTI¹⁸. *Escherichia coli* was observed in this work to have 29.17% prevalent rate of 24.02%. These prevalent rates makes *Escherichia coli* and *Staphylococcus aureus* the two most implicated organism in UTI, as well as the most prevalent Gram-negative and Gram-positive organisms respectively.

Nalixidic acid was seen to be the least potent of the selected quinolones. However, there is no statistical significance ($p < 0.001$) between the use of Ofloxacin and Perfloxacin in the treatment of the isolated strains.

The pattern of *Klebsiella* spp resistance against Perfloxacin when compared to *Proteus vulgaris* was significant. In the same manner, the analysis of variance between the pattern of resistance against Perfloxacin shown by *Pseudomonas aeruginosa* compared to *Proteus vulgaris* was significant.

CONCLUSION

This study has been able to show that there is no real difference in therapeutic value between the selected quinolones, save for Nalixidic acid, which seen to have a wide range of resistance among the isolated organisms.

However, it is a first generation quinolone, compared to the other three which are second generation drugs.

The study has also shown that Gram-negative organisms, especially *Escherichia coli* are predominantly responsible for UTI, and *Staphylococcus aureus* is the most prevalent Gram-positive organisms implicated in UTI, although other Gram-positive organisms like *Streptococcus* species could be implicated.

It is hoped that findings from this study would be of help in:

Monitoring antimicrobial susceptibility, to ensure informed usage of antibiotics and usefulness of these drugs for longer period of time.

Assist in effective management of UTI cases.

Give a guide-line in choice of drug when certain related organisms are implicated in a UTI.

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