Original Research Article

MOLECULAR CHARACTERIZATION AND ANTIMICROBIAL SUSCEPTIBILITY PATTERN OF MICROORGANISMS FROM PORT HARCOURT CORRECTIONAL CENTER, RIVERS STATE NIGERIA

ABSTRACT

Correctional centers have been reported to be associated with several conditions predisposing inmates to health challenges as a result of exposure to disease causing microbial population. This studytherefore targeted theMolecular Characterization and Antimicrobial susceptibility pattern of Microorganisms from Port Harcourt Correctional Center, Rivers State Nigeria. A total of 150 samples (100 from skin (upper arm) and 50 from wall surfaces) were collected using sterile swab sticks and immediately transported to Department of Microbiology Laboratory, Rivers State University for analyses, using standard microbiological techniques. Molecular characterization was done using Polymerase Chain reaction (PCR) and subjected to gene sequencing. The Kirby-Bauer Disc Diffusion method was used for the antimicrobial susceptibility test. Well in agar method was used toassess the susceptibility of the isolates to honey and Aloe Vera extract. Thestudy revealedthat 100% of all the bacterial isolates were resistant to Meropenem, Vancomycin, cefuroxime, and Ceftazidine, while 90% of the bacterial isolates were susceptible to Gentamicin, Cepftriaxone, Erythromycin, and Ciproflozaxine. Data showed the MAR index ranged from 0.3 to 0.8. Statistical analysis revealed there were no significant differences in the mean values of data obtained from the animate and inanimate surfaces ($p > 0.05$). Molecular identification confirmed the isolates to be*Kocuria palustris,Serretialiquefaciens,Klebsiella pneumonia*, *Enterococcus feacalis,Bacillus flexus,* and *Aspergillus niger*. The results revealed that honey was more effective (100%) than Aloe Vera extract which inhibited only one of the *Escherichia coli* isolates. Thestudy displayed the antimicrobial effect of honey against both Gram positive and Gram negative bacterial isolates. While adequate personal hygiene, proper sanitation, and spaced room should be encouraged, honey can be used in correctional centers to control bacterial skin infections.

Keywords: Antimicrobial, correctional center, molecular characterization,susceptibility.

INTRODUCTION

A correctional center is a place where individuals who have been convicted are kept for the period of time defined in relation to the crime committed [1].Correctional centres in Nigeria were initially referred “prisons”, until August 2019 when President Muhammadu Buhari signed the Nigerian Correctional Service Act of 2019 into law, and the agency's name was changed from the Nigerian Prisons Service to the Nigerian Correctional Service [2].However, the substandard prison conditions that

prisoners are subjected to can potentially increase the chances of the transmission of diseases or the decline of health[3].

Overpopulation, which is common in the Port Harcourt correctional center, combined with poor sanitary conditions and inadequate ventilation, can all contribute to the significant risks posed by the prison environment[4]. Also, contaminated surfaces have a significant role in the indirect spreading of infections.On average, for every single space in Rivers State prisons, there are three individuals present, as reported byAwopet, 2014[6].

Earlier data by Ohanekwu*et al.*, 2023 [7] identified Different microbial species recovered from the skin of inmates of a correctional center, which included *Staphylococcus*spp, *Escherichia coli*, *Streptococcus*spp, *Klebsiella*spp, *Bacillus*spp, and *Aspergillus* spp., with *Staphylococcus*spp showing the highest occurrence of 48%, while *Klebsiella*spp had the least occurrence (1%). The study indicated that the correctional center could pose serious environmental health concerns, requiring public health interventions.

Molecular tools have in recent time remained very vital in public health research, as they aid in the confirmation of microorganismscapable of causing disease in human population [8]. Genomic screening has therefore remain as a veritable tool in epidemiology as they enable the probing for the presence of special gene markers in the isolates. The detection of these gene regulators may point towards certain virulence characteristics of the organisms, including antibiotics resistance [9].

The intensifying issue of antibiotic resistance is a menace to public health[10]. Resistance has been witnessed to practically all the antibiotics developed by pharmaceutical companies. Overuse and misuse of medication, over the counter drug sale without prescription, and a scarcity of new drugs have all been connected to the antibiotic resistance emergency [11]. Vancomycin, which was created in 1972 to treat methicillin-resistant Staphylococcus aureus and coagulase-negative staphylococci [12; 13], was also reported to have a level of resistance.

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Due to the public importance of the microorganisms recovered from the inmates and the environment of correctional centers [7], it has become imperative to employ genomic characterization of these organisms and as well probe the antimicrobial susceptibility pattern of these organisms. The results from the study will be important in formulating public health intervention measures targeting the control of microbial infections among inmates. Understanding the susceptibility pattern of the isolates to antibiotics, honey and aloe vera,will be useful in establishing control protocolsof therapeutic values. The study therefore targeted the Molecular Characterization and Antimicrobial susceptibility pattern of Microorganisms from Port Harcourt Correctional Center, Rivers State Nigeria.

2.0 MATERIALS AND METHOD

2.1. Study Location and Sample Collection

The convenience sampling method was used in this analysis, which was carried out at the Port Harcourt maximum Security Correctional Center, Rivers State, Nigeria. A total of 150 (100 from inmates, 50 from the prison walls) samples were collected from the inmates and the prison walls. Skin (upper arm) of the inmates and the walls of the cells were swabbed using sterile swab sticks and immediately transported to Rivers State University Microbiology laboratory for analyses.

2.2. Isolation and Identification of Microorganisms

The specimens were inoculated into prepared/solidified agar plates by streak plate method and incubated for 18-24hrs at 37°C. Distinct colonies from the inoculated and incubated agar plates were sub-cultured onto different selective media for both bacterial and fungal growth. Finally, pure cultures were subjected to physiochemical and biochemical tests so as to identify the organisms.

2.3. Isolation and Cultural characterization of the isolates

Bacterial growth was examined using their colonial characteristics on the following selective media: MacConkey agar, Blood agar, and Mannitol salt agar. Pure cultures were subjected to the following physiochemical and biochemical tests: Indole production, Catalase, Coagulase, Oxidase, Starch hydrolysis, Sugar fermentation and Methyl Red Vogue’s Proskauer tests.

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Sabouraud dextrose agar (SDA) was used to observe the colony characteristics (color, shape, size, and hyphae) and macroscopically examine the fungi's morphology[15].The microscopy of the fungal isolates was done using lactophenol/cotton blue stain and viewed under microscope using the 10X and 40X lenses[16].

2.4 Molecular Identification.

2.41. Fungal and Bacterial Genomic DNA Extraction

The extraction was carried out using an Inqaba South Africa ZR fungal/bacterial DNA micro prep extraction kit. After a vigorous growth of the isolates' pure culture was suspended in 200 microliters of isotonic buffer, 750 microliters of lysis solution were added to a ZR Bashing Bead Lysis tube. The tubes were subjected to a bead beater treatment for 5 minutes at full speed with a 2 ml tube holder assembly attached. The ZR bashing bead lysis tubes were centrifuged for one minute at 10,000 x g.

The supernatant was divided into 400 microliters, added to an orange-topped Zymo-Spin IV spin filter, and centrifuged at 7000 x g for one minute. A fungal/bacterial DNA binding buffer containing 1,200 microliters was added to the filtrate in the collecting tubes, bringing the total volume to 1600 microliters. After that, 800 microliters were put into a collecting tube and spun at 10,000 x g for one minute using a Zymo-Spin IIC column. The collection tube's flow through was thereafter empty. The remaining volume was combined with the original Zymo-spin. The Zymo-spin IIC was centrifuged at 10,000 x g for 1 minute after receiving 200 microliters each of the DNA Pre-Was buffer and the fungal/bacterial DNA Wash Buffer, followed by the addition of 500 microliters of each.

The Zymo-spin IIC column was transferred into a clean 1.5 microliter centrifuge tube, and the column matrix was then given 100 microliters of DNA elution buffer. The DNA was then removed from the column by spinning it at 10,000 x g for 30 seconds. The ultrapure DNA was then stored at -20 degrees for the following process [17].

2.4.2DNA Quantification

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To ascertain the DNA's content and purity, DNA quantification was done. The isolated genomic DNA was quantified using the Nanodrop 1000 spectrophotometer. The Nanodrop icon was double-clicked to launch the equipment's application. 2 l of sterile, distilled water was used to start the device after it had been blanked with ordinary saline. Two microliters of the extracted DNA were placed onto the bottom pedestal and the top pedestal was lowered to establish contact with the extracted DNA. The DNA concentration was calculated by pressing the "measure" button [18].

2.4.3 16S rRNA Amplification

The 16s RRNA region of the rRNA genes of the isolates was amplified using the 27F: 5'-AGAGTTTGATCMTGGCTCAG-3 and 1492R: 5'-CGGTTACCTTGTTACGACTT-3 primers on an Applied Biosystems ABI 9700 thermal cycler with a final volume of 50 microliters for 35 cycles. The PCR mix included primers at a concentration of 0.4M, the extracted DNA as a template, the X2 Dream taq Master mix from Inqaba, South Africa, taq polymerase, DNTPs, and MgCl. The PCR was carried out under the following conditions: initial denaturation at 95°C for 5 minutes, further denaturations at 95°C for 30 seconds, 52°C for 30 seconds, extension for 35 cycles, and final extension at 72°C for 5 minutes. After being resolved on a 1% agarose gel at 120V for 15 minutes, the material was visible on a UV transilluminator [17].

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2.5.4 Internal Transcribed Spacer (ITS) Amplification

The ITS region of the isolate's rRNA genes was amplified using the primers ITS1F: 5'-CTTGGTCATTTAGGAAGTAA-3' and ITS4: 5'-TCCTCCGCTTATTGATATGC-3' using an ABI 9700 Applied Biosystems thermal cycler at a final volume of 50 microliters for 35 cycles. The PCR mixture contained the X2 Dream Taq Master mix from Inqaba, South Africa (Taq polymerase, DNTPs, MgCl), primers at a concentration of 0.4M, and the extracted DNA as a template. The PCR conditions were as follows: denaturation at 95 °C for 5 minutes, denaturation at 95 °C for 30 seconds, annealing at 53 °C, extension at 72 °C for 35 cycles, and extension at 72 °C for a total of 5 minutes. After being resolved on a 1% agarose gel at 120V for 15 minutes, the outcome was seen on a UV transilluminator.

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2.4.5 Sequencing of 16SRNA and ITS

Inqaba Biotechnological, Pretoria, South Africa, used a 3510 ABI sequencer to perform the sequencing using the BigDye Terminator kit. The BigDye® terminator v1.1/v3.1, 2.25 l of 5 x BigDye sequencing buffer, 10 mM Primer PCR primer, and 2–10 ng of PCR template per 100 bp were used in the sequencing, which was done at a final volume of 10 l. The following were the sequencing requirements: 32 times at 96°C for 10s, 55°C for 5s, and 60°C for 4 minutes. [17].

2.4.6 Phylogenetic Analysis

The retrieved sequences were modified using the bioinformatics technique Trace edit, and related sequences were found using the BLASTN method by searching the National Center for Biotechnology Information (NCBI) database. These sequences were aligned using ClustalX. Using MEGA 6.0's Neighbor-Joining method, the evolutionary history was inferred [19]. The bootstrap consensus tree created from 500 replications is supposed to represent the evolutionary history of the species under study [20]. The evolutionary distances were calculated utilizing the Jukes-Cantor method[21].

2.5 Susceptibility Testing

2.5.1. Preparation of Standard Bacterial Suspension

Pure cultures (24 hours old) of the various investigated microorganisms were emulsified inside test tubes which contain sterile normal saline. The turbidity of the tubes was continuously adjusted to the 0.5 McFarland Turbidity Standards. The suspensions were used for the susceptibility test[22].

2.5.2. Mueller-Hinton Agar Preparation

To make the Mueller-Hinton agar, 38g were dissolved in 1 liter of distilled water. The mixture was autoclaved for 15 minutes at 121°C and 15 pressure to sterilize it. A cooling period of 50 to 45°C was allowed. Each petri plate received about 20 ml, which were then flamed and given time to set.

2.5.3 Antimicrobial effect of Honey and Aloe Vera Gel on the Bacterial Isolates.

The agar well diffusion method was used to evaluate the effect of Honey and Aloe Vera on the bacterial isolates. Fresh Aloe Vera plant was bought from mile 3 market.

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It was thoroughly washed and decontaminated using 95% ethanol. Following standard procedure, the gel was aseptically extracted and stored in the fridge using sterile universal container for usage[23].Locally harvested, 100% undiluted honey was used for this study.

Each tube containing the bacterial suspension had its turbidity adjusted to meet the McFarland Turbidity standard before a sterile swab stick was inserted. The inoculums were dispersed on the surface of a comparable petri dish containing solidified Mueller-Hinton agar using swab sticks. By rotating the plates to around 600, the surface area of the plates was evenly swabbed. To ensure that the medium properly absorbed the inoculum, the plates were allowed to dry for three to five minutes. Using a sterile cork borer, holes or wells with a diameter of 6 to 8 mm were punched into the plates aseptically. Each of the wells received a 100-L introduction of honey and Aloe Vera gel extract. After incubation, the zone of inhibition around the wells was assessed[24].

2.5.4 Tests for Antibiotic Susceptibility (Kirby-Bauer Disc Diffusion)

Each tube containing the bacterial suspension had its turbidity adjusted to meet the McFarland Turbidity standard before a sterile swab stick was inserted. The inoculums were dispersed on the surface of a comparable petri dish containing solidified Mueller-Hinton agar using swab sticks. By rotating the plates to roughly 600, the surface area of the plates was uniformly swabbed. To ensure that the medium properly absorbed the inoculum, the plates were allowed to dry for three to five minutes. The antibiotic discs were picked up with sterile forceps and set 15 mm from the edge of the surface of the dry inoculated plates. Each disc was pressed into contact with the agar using the forceps' head. For 16 to 18 hours, the plates were incubated aerobically at 350°C. After incubation, the diameter of the zone of inhibition was measured from edge to edge from the underside of the plates using a metric ruler.

The results were compared with CLSI guidelines and reported as Susceptible (S), Intermediate (I), or Resistant (R) [25].

3.0 RESULTS

3.1. Molecular Characterization of the Bacterial and Fungal Species

The molecular characterization of the 16S rRNA and ITS sequence of the isolates showed that the evolutionary distances computed using the Jukes-Cantor method were in agreement with the phylogenetic placement of the ITS of the isolates within the *Aspergillus* sp and revealed a closely relatedness to *Aspergillus niger*while the 16S rRNA of the isolates were within the *Bacillus, Enterococcus, Klebsiella, Staphylococcus* and *Escherichia coli* spp and revealed a closely relatedness to *Bacillus flexus, Enterococcus feacalis, Klebsiella pneumoniae, Serretialiquefaciens,*and *Kocuria palustris*.

The agarose gel electrophoresis of the amplified 16SrRNA gene of bacterial isolates before sequencing showed that Lanes O1-05 demenstrated the 16SrRNA gene bands (1500bp) while the k represented the 100bp molecular ladder (plate 1).
The agarose gel electrophoresis of the ITS gene of Fungal isolate before sequencing showed that Lanes 06 represented the ITS gene bands (550bp) while the k represented the 100bp molecular ladder (plate 2).
The obtained ITS sequence from the isolates produced an exact match during the megablast search for highly similar sequences from the NCBI non-redundant nucleotide (nr/nt) database. The ITS of the isolates showed a percentage similarity to other species at 100%. The evolutionary distances computed using the Jukes-Cantor method were in agreement with the phylogenetic placement of the ITS of the isolates within the *Aspergillus* spp and revealed a closely relatedness to *Aspergillus niger.*

During the megablast search for extremely similar sequences from the NCBI non-redundant nucleotide (nr/nt) database, the 16s rRNA sequence retrieved from the isolate gave a perfect match. The isolates' 16S rRNA gene displayed 100% similarity to other species.The Jukes-Cantor method was used to calculate evolutionary distances, which were consistent with the isolates' phylogenetic placement within the Bacillus, Enterococcus, Klebsiella, Serretia, and Kocuriagenera. They also revealed a close relationship to *Bacillus flexus*, *Enterococcus feacalis*, *Klebsiella pneumoniae*, *Serretia liquefaciens*, (Fig 1).

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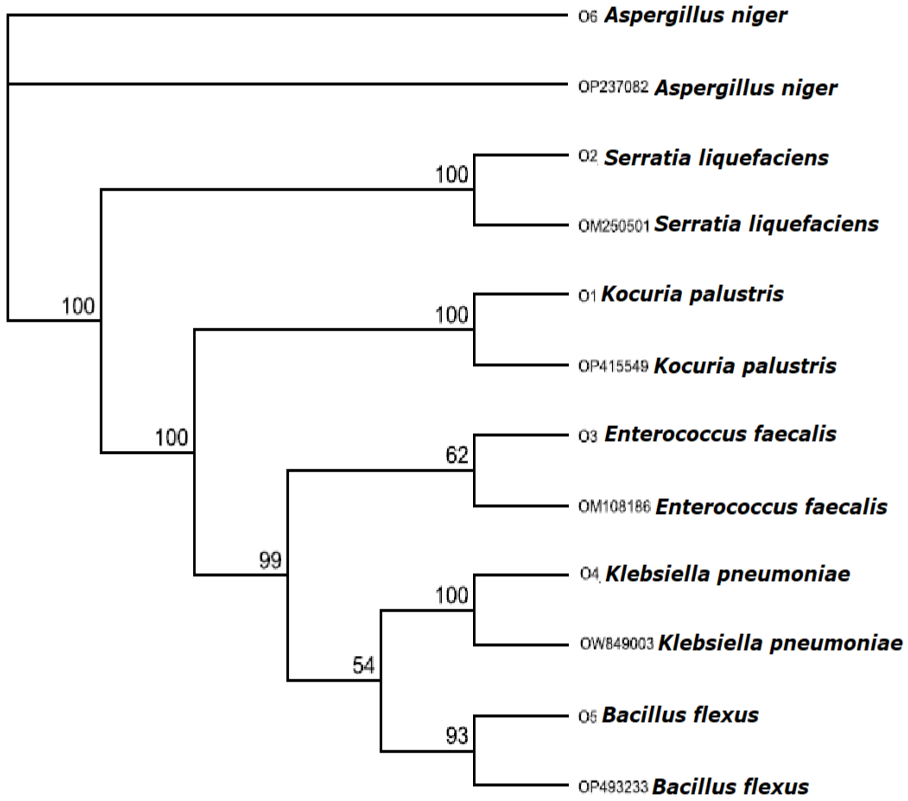

Figure 1. Evolutionary Distance between the Microbial Isolates.

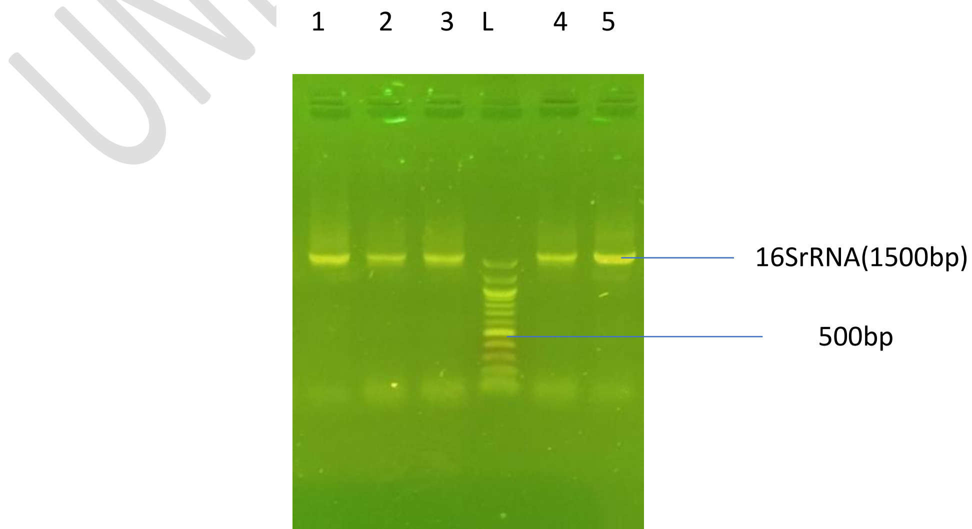

Plate 1: Amplified 16S rRNA Fragment. Lanes 1-5 represent the amplified 16SrRNAbands at 1500bp while L represents the 100bp molecular ladder.

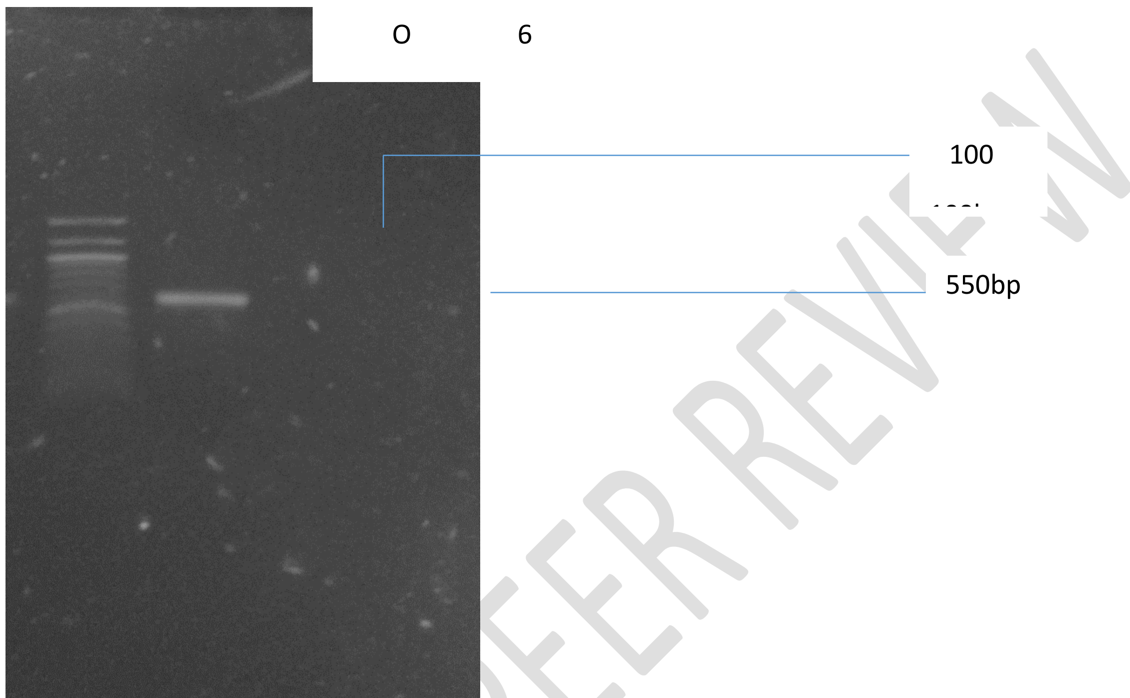

Plate 2: ITS gene of the fungi isolate. Lane 6 represent the ITS gene (550bp). Lane O represents 100bp DNA ladder of 1500bp.

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3.2 Antibiotic Sensitivity Pattern of the Isolates

As shown in figure 2, 100% of the Gram negative bacterial isolates from the skin were resistant to Vancomycin and Meropenem. Also, 81%, 71%, and 90% of the isolates were resistant to Cefuroxime, Tetracycline and Ciprofloxacin, repectively.

As shown in figure 3, 93% of the Gram positive isolates from the skin were resistant to Ampicillin, 96% to Meropenem, 62% to Augmentin, 82% to Cephalexin, and 89% of the isolates were resistant to Ceflazidine.

Data obtained showed that the prison wall isolates (Gram negative) were resistant to 100% of Vancomycin and Meropenem. Also, 78% of the isolates were resistant to Cefuroxime and Tetracyclin, and 57% toCeftazidine and Ciprofloxacin (Figure 4).

As reported in Figure 5, 100% of the isolates were resistant to Meropenem, cefuroxime, and Ceftazidine. Data further indicated that 66% of the isolates were also resistant to of Cephlexin, 85% to Augmentin, and 95% to Ampicillin.

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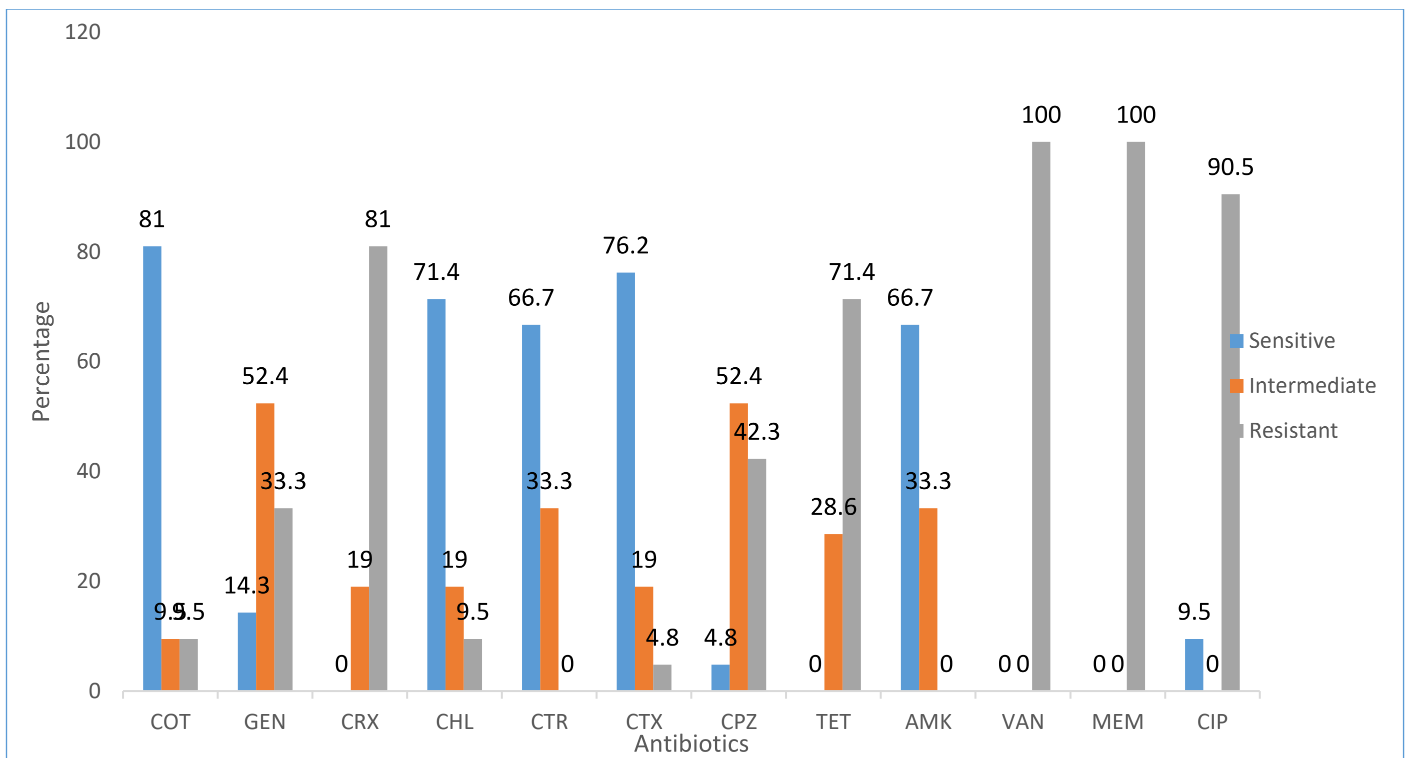

Figure 2 Antibiotic Sensitivity Pattern of the Gram negative Isolates from the Prison Inmate

Key:

COT= Cotrimazole
GEN= Gentamicin
CRX= Cefuroxme
CHL= Chloramohenicol
CTR= Ceftriaxone
CTX= Cefotazime
CPZ= Cectazidine
TET= Tetracyclin
AMK= Amikacin
VAN= Vancomycin
MEM= Meropenem
CIP= Ciprofloxaci

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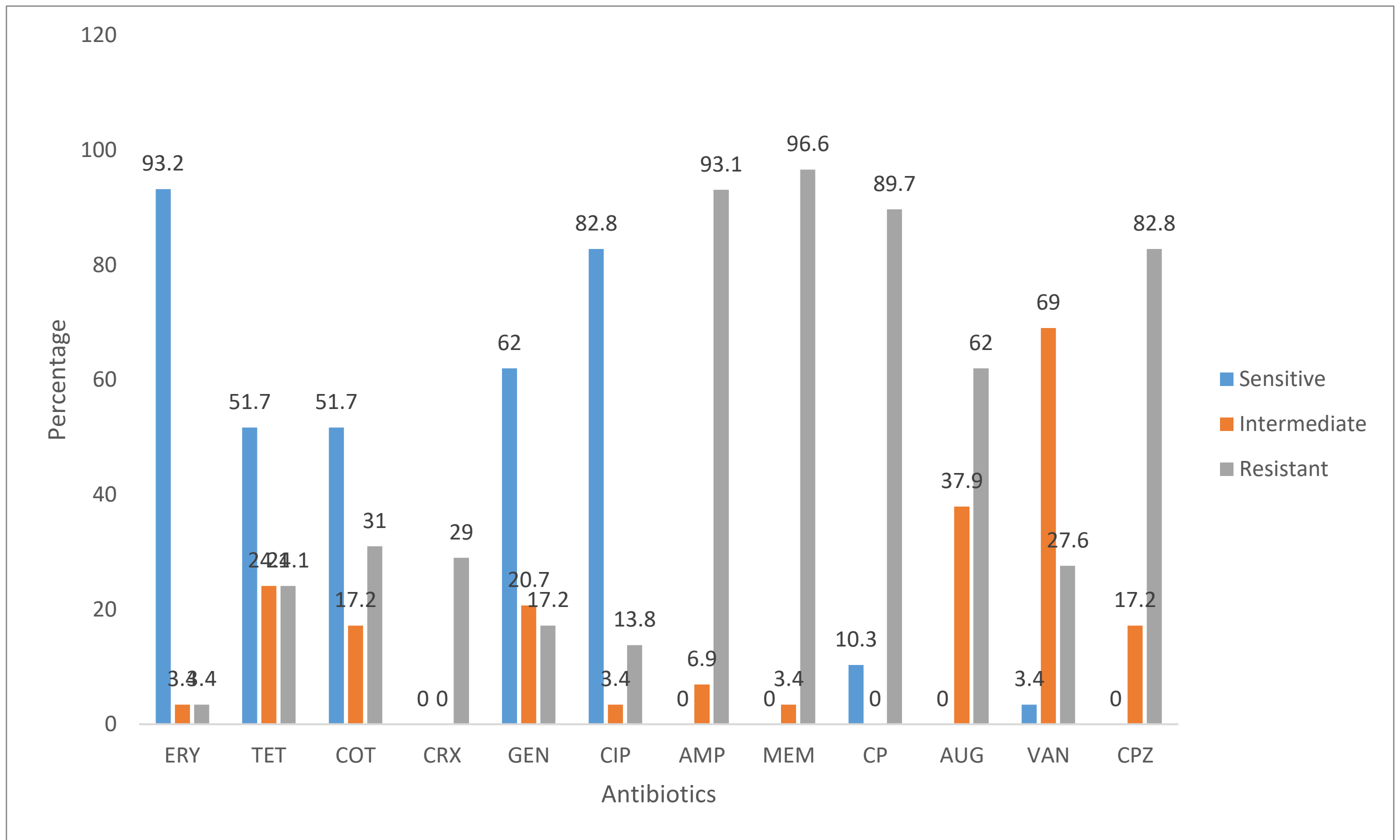

Figure 3 Antibiotic Sensitivity Patterns of the Gram-positive Isolates from the Prison Inmates

Keys:

ERY= Erythromycin
TET= Tetracyclin
COT= Cotrimozazole
CRX= Cefuroxime
GEN= Gentamicin
CIP= Ciprofloxacin
AMP= Ampicillin
MEM= Meropenem
CP= Cephalexin
AUG= Augmentin
VAN= Vancomycin
CPZ= Ceflaxidime

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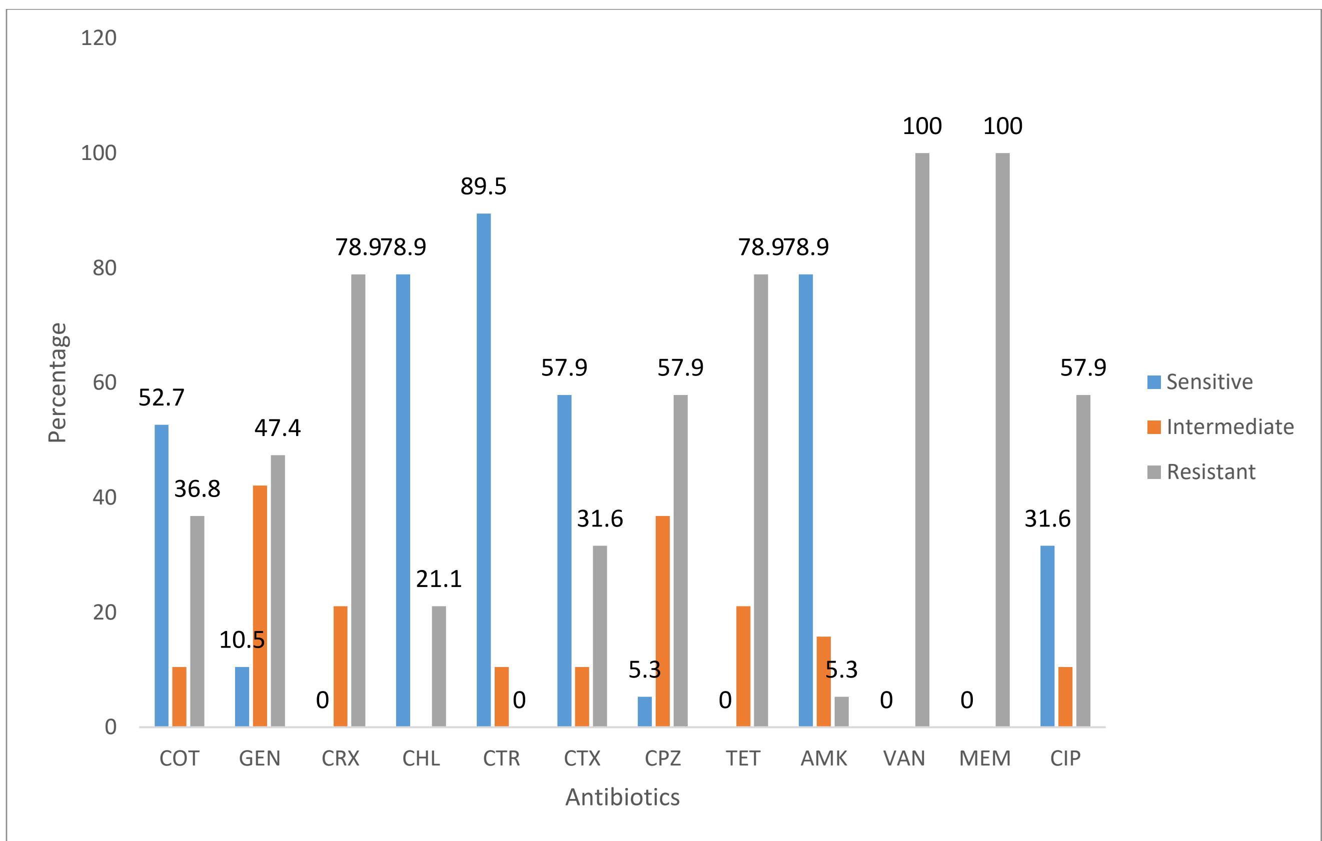

Figure 4 Antibiotic Sensitivity Pattern of the Gram negative Isolates from the Prison Cells

Key:

COT= Cotrimazole
GEN= Gentamicin
CRX= Cefuroxme
CHL= Chloramohenicol
CTR= Ceftriaxone
CTX= Cefotazime

CPZ= Cectazidine
TET= Tetracyclin
AMK= Amikacin
VAN= Vancomycin
MEM= Meropenem
CIP= Ciprofloxacin

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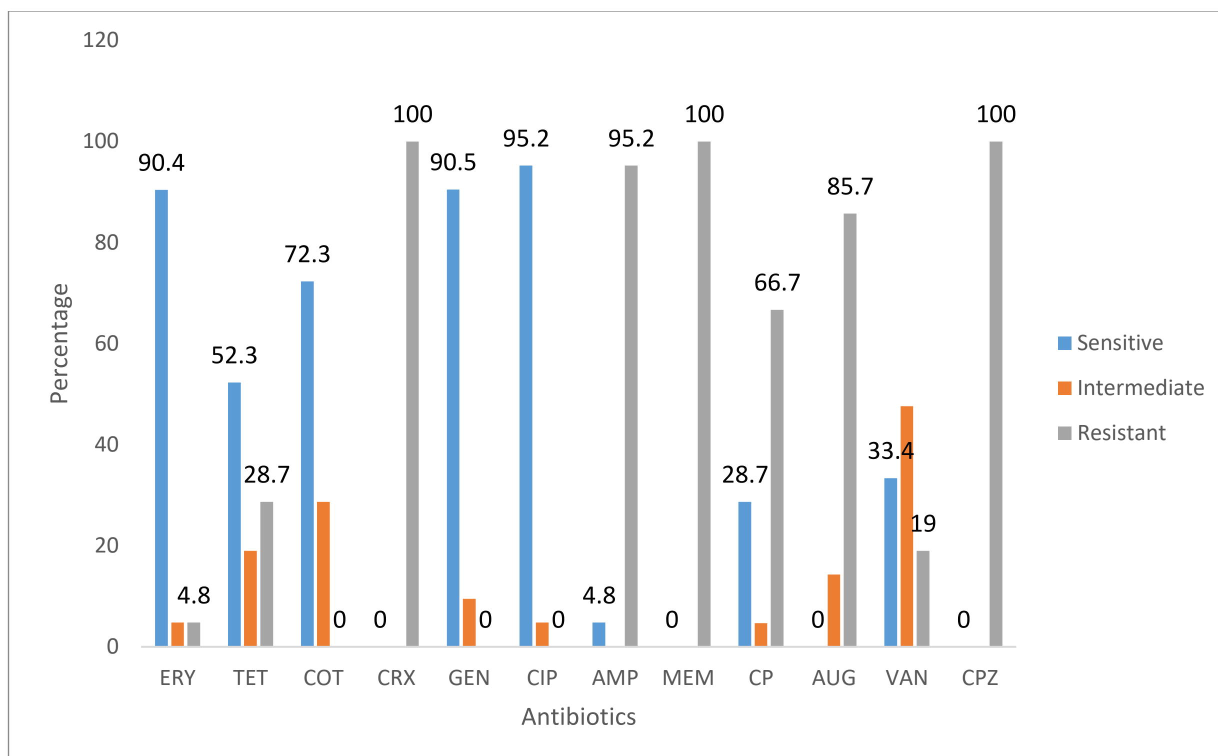

Figure 5 Antibiotic Sensitivity Pattern of the Gram positive Isolates from the Prison Cells

Keys:

ERY= Erythromycin
TET= Tetracyclin
COT= Cotrimozazole
CRX= Cefuroxime
GEN= Gentamicin
CIP= Ciprofloxacin
AMP= Ampicillin
MEM= Meropenem
CP= Cephalexin
AUG= Augmentin
VAN= Vancomycin
CPZ= Ceflaxidime

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3.3 Occurrence of Multiple Antibiotic Resistance Bacterial Species in the Study Groups

Data showed that the MAR index ranged from 0.3 to 0.8 (Table 1). The study showed that 100% of the streptococcal isolates from the cell walls had MAR index of 0.4, while 100% of the *Klebsiella*spp had MAR index of 0.8. The study further showed that higher percentage of MAR index was associated with isolates from the prison cell wall surfaces compared to those from the skin swabs, except for MAR index 0.6 and 0.8, where skin had the highest percentage of isolates. Statistical analysis showed no significant differences in the MAR indices of isolates from the skin and wall samples ($p > 0.05$).

Table 1MAR indices of the Bacteria from the Inmates and Wall Surfaces (%)

	0.3		0.4		0.5		0.6		0.7		0.8	
	Skin	**Cell**	**Skin**	**Cell**	**Ski n**	**Cell**	**Skin**	**Cell**	**Skin**	**Cell**	**Skin**	**Cell**
Staphylococcus spp	5.6	11.8	22.2	0	11.1	52.9	27.8	29.4	16.7	5.9	16.7	0
Streptococcus spp	9.1	0	27.3	100	36.4	0	27.3	0	0	0	0	0
E. coli	25	38.5	35	23.1	20	15.4	20	23.1	0	0	0	0
*Klebsiella*spp	0	0	0	0	0	0	0	16.7	0	50	100	33.3
Mean	9.9	12.6	21.1	30.8	16.9	17.1	18.8	17.3	4.2	14.0	29.2	8.3
P –value	0.8099		0.7114		0.9896		0.8762		0.4762		0.4421	

3.4. Response of the Bacterial Isolates to Honey and Aloe Vera gel

The effect of honey on the isolates is displayed in Table 2. The outcome demonstrated that all of the examined isolates of *Staphylococcus* spp. and *Kebsiella* spp. were completely inhibited by honey. Honey inhibited 71.4% of *Escherichia coli* isolates. Also, it inhibited 33.3% of the *Streptococcus* spp. The result further reviewed that the highest zone of inhibition with the range of 12-32mm*was* against*Escherichia coli.*

Aloe Vera showed 18mm zone of inhibition on only one of the isolates, *Escherichia* coli, with no effect on the rest of the tested isolates.

Table 2. Antimicrobial Effect of Honey on the Isolates

SN	Isolates			
	Staphylococcus spp	*E.coli*	*Klebsiella*spp	*Streptococcus*spp
No. of Isolates	10	7	5	6
Total inhibited (%)	10 (100)	5(71.4)	5(100)	2(33.3)
Zone of inhibition (range)	12 - 19	12-32	14-16	12-20

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4.0 DISCUSSION

The molecular characterization of the 16S rRNA and ITS sequence of the isolates showed that the evolutionary distances computed using the Jukes-Cantor method were in agreement with the phylogenetic placement of the ITS of the isolates within the *Aspergillus* sp and revealed a closely relatedness to *Aspergillus niger*while 16S rRNA of the isolates within the *Bacillus, Enterococcus, Klebsiella, Staphylococcus* and *Escherichia coli* spp and revealed a closely relatedness to *Bacillus flexus, Enterococcus feacalis, Klebsiella pneumoniae, Serretia liquefaciens,*and *Kocuria palustris*. This is similar to the report of[26], who recovered all the organisms mentioned above apart from *Aspergillus niger* and *Bacillus* flexus.

As shown in the data, the tested Gram negative isolates were resistant to Vancomycin and Meropenem. The pattern of antibiotic resistance is in agreement with the work ofSelim, 2021[27].The findings from this study are also in agreement with the report by a previous researcher [28], who also stated that in medicine and public health, vancomycin-resistant bacteria (VRB) are a crucial factor because they can result in infections that are fatal, seem resistant to treatment, and linger in the body even after treatment.

All the isolates (100%) had MAR index of 0.3 to 0.8. The study therefore showed that higher percentage of MAR index was associated with isolates from the prison cell wall surfaces compared to those from the skin swabs, except for MAR index 0.6 and 0.8, where skin had the highest percentage of isolates. This implies that the correctional center being the source, is highly polluted or the inmates are heavy antibiotic users.

The result of the susceptibility pattern of the isolates to honey and Aloe Vera extract revealed that honey had more effect on the isolates (100%) than the Aloe Vera extract. All the 6 genera of the isolates were significantly inhibited by honey. This is in agreement with the finding of a previous researcher [13], who attributed the effect of honey on bacterial isolates to its low water content (low water activity), high viscosity, acidity, and H_2O_2 content.

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Aloe Vera extract was observed to be effective on only one isolate (*E. coli*) with 18mm zone of inhibition. This is however contrary to the report byMbajiuka, 2014[29], who reported that Aloe Vera extract was effective against both Gram negative and Gram positive isolates. This difference in the result might be as a result of difference in extraction methods or concentration.

5.0 CONCLUSION

This study has shown that that both Gram positive and Gram negative bacterial isolates were resistant to Vancomycin, Ceflazidine, and Meropenem. The bacterial isolates (Gram negative) were susceptible to Ceftriaxone, Chloramphenicol, Cefotaxime, and Amikacin while Gram positive organisms were susceptible to Cotrimozazole, Ceftriaxone, Cefotaxime, and Ciprofloxacin. This implies that these drugs may have therapeutic value because the tested organisms showed no resistance to them. Therefore, they can be used to treat infections caused by these mentioned bacterial species.

The study further showed that higher percentage of MAR index was associated with isolates from the prison cell wall surfaces compared to those from the skin swabs, except for MAR index 0.6 and 0.8, where skin had the highest percentage of isolates. This implies that the correctional center being the source, is highly polluted or the inmates are heavy antibiotic users.

Also, the study reported several pathogens of concern with MAR indices ranging from 0.3 – 0.9 in the correctional facility. This is of epidemiological importance for health planning and interventions. This study further showed that honey can be used in the correctional centre to control skin related bacterial infections.

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