# Bacterial Infections and Antimicrobial Susceptibility Test (AST) Patterns among Confirmed SARS COV-2 Individual in Southwestern Nigeria.

Bamigbola Florence Adenike[a,c], Raheem Toyosi Yekeen[b,c], Adesina Felicia[c], Adeniyi Akinbobola Ayokunle [a], Bamigbola Oreoluwa Elizabeth[d].

[a] bamifloadenike@gmail.com

a. Department of Medical Microbiology and Parasitology, University College Hospital, Oyo State, Ibadan, 200212, Nigeria.
b. Molecular Biology and Biotechnology Department, Nigerian Institute of Medical Research, Yaba, Lagos State, 101212, Nigeria.
c. Faculty of Basic Medical and Applied Science, Lead City University, Ibadan, Oyo State, 200255, Nigeria.
d. Department of Medicine and Surgery, AFE Babalola University, Ado-Ekiti, Ekiti State, 200212, Nigeria.

Abstract

Antimicrobial medications were given to patients with this illness without antimicrobial susceptibility since recent statistics on SARS-C0V-2 showed that bacterial infection increased mortality rate and lowered clearance rate of the virus. The goal of this study was to detect co-infecting pathogen(s) and analyze their antibiotic resistance profiles in confirmed SARS-CoV-2 cases in Oyo State, Nigeria. 400 symptomatic and asymptomatic infected individuals had their nasopharynx sampled, and structured questionnaires were administered to identify risk factors associated with the patients. Using API 20E and VITEK 2.0 ID cards, isolates were recognized after being collected using conventional microbiological techniques. Antimicrobial susceptibility testing was done using VITEK 2.0 AST card kits and Kirby Bauer disc diffusion techniques. The Enterobacteriaceae family had a large number of the observed bacteria. The COVID-19 cases treated with Azithromycin, which is more resistant to Gram positive bacteria, had a higher resistance rate (66.6%). However, bacterial isolates have significantly higher quinolone susceptibility (89.0%). Some of the microbiological isolates identified in individuals with SARS-CoV-2 infection were multidrug resistant, including Azithromycin. This discovery raises serious health concerns and requires additional investigation.

Keywords: SARS-CoV-2; Bacterial co-infection; API 20E; VITEK 2.0.

## 1.0 Introduction

The Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) that was initially discovered in December 2019 in Wuhan, China, and is currently circulating around the entire world is the infectious disease known as the novel Corona Virus Disease 2019 (COVID-19) (Wang et al., 2020). This virus is a member of the Nidovirales order's Coronaviridae family. Alpha, beta, gamma, and delta coronaviruses are the four subgroups of the coronavirus family. The four "common human coronaviruses" include the 229E coronavirus, NL63 coronavirus, OC43 coronavirus, and HKU1 (β coronavirus) (Zeng et al., 2018). SARS, MERS, and SARS-CoV-2 have all been reported to be susceptible of co-infecting in the context of community-acquired bacterial and fungal pneumonia (Edrada et al., 2020), according to a paper on the microorganisms that cause this form of pneumonia. Early in January 2020, the Chinese Health Authority identified a novel coronavirus as the disease's cause, and its whole genome was made public (Zhu et al., 2020). Because of how quickly it spread over the world, the illness was classified as a pandemic (WHO; 2020). The majority of COVID-19 patients with confirmed cases in China had mild or moderate infections, but a few others went on to have severe clinical infections or critically severe infections. Pneumonia and acute respiratory distress consequences such as an inflammatory storm, coagulation malfunction, septic shock, and multiple organ failure are characteristics of the severe clinical course (Huang et al., 2019). Age, hypertension, diabetes, and obesity are comorbid conditions that have been linked to higher COVID-19 severity and mortality. The COVID-19 pandemic resulted in a significant number of immunocompromised people to be hospitalized, and some studies claimed that some COVID-19 patients had secondary illnesses diagnosed (Rasmussen et al., 2019; Tetro et al., 2020). According to some research, COVID-19 patients frequently contract infections from other.

The first few days of January 2020 were marked by the Chinese Health respiratory viruses, including influenza virus (Kong et al., 2020). SARS-CoV, MERS-CoV, and other acute lung injury-causing coronaviruses are among the zoonotic coronaviruses .10 Patients with the SARS-CoV-2 infection have been documented to have co-infections with viruses, bacteria, and fungi (Lansbury et al., 2020). Nasopharyngeal swab samples were obtained for total RNA extraction, multiplex polymerase chain reaction, and mNext gene sequencing analysis during a multi-center investigation in Eastern China (Ai et al., 2020). The most frequent pathogens found were the influenza virus, adenovirus, acinetobacter baumannii, klebsiella pneumoniae, aspergillus flavus, candida glabrata, and candida albicans, and 11 of 20 co-infections were discovered in laboratory-confirmed COVID-19 cases (Lansbury et al., 2020). In addition, it is well known that bacteria take part in viral interactions with host cells (McCullers et al., 2014). Despite being secondary invaders in most influenza infections, bacteria nonetheless express virulence characteristics that support viral pathogenesis. The result is an increase in viral load and a decrease in clearance rates (McCullers et al., 2014. Co-infection with bacterial and fungal infections was one of the major problems seen, according to studies on confirmed SARS patients, particularly in those who required prolonged hospitalization and long-term mechanical ventilation (McCullers et al., 2014). Although the majority of conditional pathogens are found in the oral cavity, some including Enterococcus faecalis, Klebsiella pneumonia, Acinetobacter baumannii, Stenotrophomonas maltophilia, and Candida albicans, may be nosocomial in origin (Zheng et al.,2003; Li et al.,2015). 38 types of bacteria and 10 types

of viruses, with the exception of SARS-CoV-2, were detected in nasopharyngeal samples taken from individuals who were infected. They comprise bacteria like Dolosigaranulum spp., Megaphaera spp., Corynebacterium spp., Staphylococcus spp., Moraxella spp., Neisseria spp., Streptococcus spp., and Haemophilus spp. Similarly, viruses such as parainfluenza virus, respiratory syncytial virus, adenovirus, and human metapneumovirus (Zhou et al.,2020) were discovered, along with fungus such as Candida spp. and Aspergillus spp. Sputum, broncho-alveolar lavage fluid, oropharyngeal and nasopharyngeal swab specimens, and other bodily fluids are collected for the SARS-CoV-2 test (Huang et al.,2020). According to a study on 213 confirmed COVID-19 patients, sputum appeared to be a good clinical sample with a high positive rate (74.4-88.9%), followed by nasal swabs (53.6-73.3%) and throat swabs (50-61.3%). Viral ribonucleic acid could be detected in all Broncho Aleovelar Lavage Fluid samples of severe cases, but not from mild cases. 18 Sputum, nasopharyngeal swabs, and blood samples have been used by researchers to demonstrate the detection of bacterial or fungal infections in COVID-19 patients (Bhatraju et al.,2020). According to a study, Nasopharyngeal Swab samples from patients who had the SARS-CoV-2 virus were used. The swabs were also used to screen the patients for additional bacterial and fungal infections, and Bordetella pertussis, Chlamydophila pneumoniae, and Mycoplasma pneumonia were found (Wang et al., 2020).

Sputum and endotracheal aspirates were apparently employed for screening while looking for fungus and bacteria in people who had the SARS-CoV-2 virus, according to a record of several methods used (Chen et al., 2020). In a different study, it was noted that co-infections such bacterial and fungal infections may be found in SARS-CoV-2 patients by taking samples of their blood, urine, and respiratory tract (Paret et al., 2020). Folks with and without symptoms who are infected with. The clinical features of symptomatic and asymptomatic SARS-CoV-2 infected individuals may differ, with symptomatic patients always presenting with a greater number of symptoms than asymptomatic individuals (Fu et al., 2020). However, the asymptomatic group had a significantly longer duration of viral shedding than the symptomatic group. Also, viral-specific ImmunoglobulinG levels in the asymptomatic group were significantly lower and they exhibit lower levels of 18 pro and anti-inflammatory cytokines that are presented with less bacterial and fungal infections ((Fu et al., 2020).

The antibiogram, which is the overall profile of antimicrobial susceptibility data of a microbiological species to a battery of antimicrobial agents can be a valuable source of information for healthcare practitioners when appropriately created and understood (CLSI: 2017). When beginning empirical therapy and monitoring changes in antimicrobial resistance over time within a hospital or healthcare system, data from antibiograms are most helpful. Empirical antibiotic therapy is typically administered to SARS-CoV-2 infected patients, which may result in a rise in antimicrobial resistance. For instance, no bacterial or fungal co-infection was noted in a study of 102 patients receiving critical and non-critical care in China, where all (99%) patients received antibacterial therapy, 87/102 (85%) received quinolone therapy, 34/102 (33%) received cephalosporins, and 25/102 (25%) received carbapenems because it might be challenging to differentiate between pre-existing viral pneumonia and bacterial or fungal diseases based on clinical and radiological performance (Cao et al., 2020). This assertion is supported by an increase in reports on the co-occurrence of epidemic or pandemic respiratory viruses, such as the influenza virus, Severe Acute Respiratory Syndrome, Middle East Respiratory Syndrome, and Severe Acute Respiratory Syndrome Corona Virus-2, secondary

bacteria, and invasive fungal infection that led to poor patient outcomes and high mortality rates. This is a critical reality that calls for an urgent need for special attention (Huang et al., 2019).

1.1. Statement of the problem

According to epidemiological statistics on COVID-19, bacterial complications increased the morbidity and mortality of influenza infection. There are certain challenges in making the diagnosis of secondary coinfection in COVID-19 patients. Even though it could be difficult to distinguish between a bacterial or fungal disease and an already-existing viral pneumonia, microbiological investigation can significantly improve diagnoses (PCP: 2020). However, this strategy can pose substantial risks to bio-sample collectors and laboratory employees handling samples from COVID-19 patients because the virus is transferred via virus-laden aerosols in addition to respiratory droplets and direct contact. Traditional smears and cultures are frequently used in medical facilities to identify infections caused by bacterial and fungal pathogens, as well as to identify fungi. It is generally known that the culture technique takes a long time and that the sputum smear has a low positive rate (Loeffelholz et al., 2020). In addition, there is worry among individuals who are impacted regarding the growth in microbial resistance brought on by the prescription of antibiotics. A study found that the majority of infected individuals take antibiotics even when they are not at all tainted (Chan et al., 2020). Clinicians should be extremely concerned about the likelihood of co-infection with other respiratory diseases when managing COVID-19 in Nigeria and throughout Africa. Other difficulties include collecting sufficient clinical samples, the mode of transmission, the dynamics of viruses, and effective pharmaceutical treatments.

1.2. Justification of the study

Studies show that co-infection with bacteria is fatal in SARS-CoV-2 patients, is still poorly understood, and has severe consequences (Langford et al., 2020). Thorough diagnosis and treatment are critical to prevent death from co-infection-related causes and to provide information for providing the appropriate antibiotics for efficient management. The findings of this study will also aid in reducing and limiting unexpected consequences of antibiotic resistance among people with SARS-CoV-2 infection.

1.3. Materials and Methods

1.4. Study area

In Ibadan, Oyo State, Nigeria, several carefully selected public hospitals were the sites of the inquiry. This includes the Ade-Oyo General Hospital, University College Hospital, Olodo, Oyo State, Agbami Infectious Disease Center, and Infectious Disease Centre, Olodo. They were picked because they each represent a primary, secondary, or tertiary health institution, have sizable patient populations, or are isolation hospitals with specialist screening departments.

1.5. Sample Collection

The University College Hospital in Ibadan's Bio-respiratory Laboratory examined nasopharyngeal and oropharyngeal swab samples from all patients with suspected COVID-19. Oyo-state used real-time reverse transcriptase PCR to confirm the infection.

Then, at all the designated isolation and treatment facilities in Oyo-state, Nigeria, 400 Nasopharyngeal samples were collected from confirmed SARS-CoV-2 positive individuals, both symptomatic and asymptomatic, and placed in sterile Amie's Transport medium in cryo-vial plastic bottles labeled with the name, sex, and age of the clients for microbiological investigation.

1.6. Processing of samples

1.7. Culturing method

On Saboraud's Dextrose Biotech medium agar, all 400 samples were grown, inoculated, and incubated both aerobically and anaerobically at 37°C. Over the course of seven days, the Dextrose plates of Saboraud were regularly read. All growing organisms were stained with Gram's staining reagents to determine whether they were pollutants, bacteria, yeast, molds, or contaminants.

1.8. Confirmation of Bacterial Isolates using API 20E and VITEK 2.0

Is a standardized identification system for Gram positive cocci, Enterobacteriae and other non-fastidious gram negative rods which uses 21 miniaturized biochemical tests and a database?

The API 20E strip consists of 20 microtubes containing dehydrated substrates which are inoculated with a bacterial suspension that reconstitutes the media. During incubation metabolism produces color changes that are either spontaneous or revealed by the addition of the analytical profile index or using the identification software.

The microorganisms to be identified must first be isolated on a culture medium which is an 18-24 hours' pure culture of true organism to be identified was obtained from growth. Culture medium adapted to the culture of Enterobacteriacea and/or non-fastidious Gram negative rods according to standard microbiological techniques.

An 18-24 hours' pure culture of the organism to be identified were obtained from the agar media appropriate for the organism. Oxidase test was performed on the organism to be identified before carrying out the procedure.

2-3 colonies of the organism were emulsified in 5mls sterile normal saline. 4 drops of the suspension were dropped into each well with sterile pipette incubated at 35ºc±2ºc for 18-24 hours. Colour change was read and recorded after incubation. Additional tests such as Glucose, TDA, Indole and VP was done and color change was recorded

Reporting: The strip was removed from the incubator, peel back the sealing tape. The reactions were evaluated as positive or negative by comparing them with the color chart. The results were recorded under the appropriate heading on the report form. Identification is obtained with the numerical profile. By adding the values corresponding to positive reactions within each group, a 7-digits profile number is obtained for the 20 tests of the API 20E strip. The oxidase reaction constitutes the 21$^{st}$ test and has a value of 4 if it is positive. Identification is performed using the database version 5.0 with the analytical profile index. Enter the 7digits numerical profile manually into the computer package and the name of the organisms is revealed.

1.9. Identification and Antibiotic Susceptibility Testing for Bacteria Isolates using VITEK 2.0 System

All isolates are first sub-cultured in Nutrient agar and thereafter an appropriate differential and/or selective medium, MacConkey Agar was used. Pure isolated colonies are then piced for AST using the VITEK 2.0. Cards were selected based on Gram reactions of test isolates, For AST, 145ul or 280ul was transferred for Gram negative and Gram positive organisms respectively from adjusted organism suspension for identification(ID) into fresh tube containing 3mL saline. Capillary tube was inserted and attached to appropriate VITEK card into tube in the cassette. Load the suspension into the machine within 30 minutes of preparation of suspension. Then entered the test microbe and Ouality Control organism information in the application screen and double clicked the Manage Cassette View icon, circled below, then clicked on Maintain Virtual Cassette icon in the left view bar of the Setup Test Post Entry Window. Clicked again to Create New Virtual Cassette icon in the upper right view bar also called the Action Bar. The Maintain Virtual Cassette window appeared and Virtual Cassette stores the data scanned into the computer. Entered the cassette information by choosing the number from the drop down window labeled "cassette" and entered the card data by scanning the car code on the card. The Cursor must be in the Bar Code space to be entered. You may either hit ENTER and the cursor will move to the next line to be scanned or use the mouse button to move the cursor to the next Bar Code space. Verify that the slot in which the card is located in the cassette matches the corresponding slot in the Virtual Cassette.

1.10: Susceptibility Testing

Antibiotic susceptibility testing was done on all the confirmed bacteria isolates using Kirby Bauer disc diffusion method[4] and VITEK 2.0[4] while anti-fungal susceptibility testing of all fungi isolates were done using Kirby-bauer disc diffusion method[5]. All confirmed isolates were inoculated into sterile peptone water incubated for 2 hours to adjust turbidity of suspension to that of 0.5 McFarland standard ($1.5x10^8$ cfu/ml) inoculum. A sterile cotton swab, was dipped into the inoculums and drained by the side of the tube and was used to streak sterile Mueller-Hinton agar plate for confluent growth. After 5 minutes of streaking, the antibiotic disks were mounted, incubated at $37^0$C for 24 hours. Plates were examined for zones of inhibition and the diameter of positive plates was measured to the nearest millimeter (mm). The Antibiotic susceptibility testing results were compared with standard organisms Escherichia coli NCTC12241 and Staphylococcus aureus NCTC 12981 obtained from Department of Medical Microbiology and parasitology UCH, Ibadan. Oyo- State.

1.11. Ethical considerations

- Oyo State Ethical Review Committee, Ministry of Health, Ibadan, in Oyo State. Nigeria and

- UI/UCH Ethical Review Committee, Ibadan, Oyo- State. Nigeria.

1.12. Data analysis

Using SPSS version 20.0, the data collected from the questionnaires and other study-generated data were analyzed. The prevalence and frequency of the outcomes were presented using descriptive analysis. To find the relationship between two category variables, chi-square was applied. 95% confidence intervals and P values -0.05 were used to determine significance.

## 2.0 Results

2.1. Presentation of Data for Bacterial Isolates from SARS-CoV-2 Infected Individual

Also presented were the findings from experiments and characterisation studies on isolated pathogens from the isolation facilities. Additionally, given was the bacterial susceptibility pattern to antimicrobials.

After the appropriate normal incubation times and conditions, 240 (60.0%) of the 400 nasopharyngeal swab samples taken from the SARS-CoV-2 infected individuals and cultured on MacConkey agar medium, Chocolate agar medium, and Sabourauds Dextrose agar medium produced growth of bacteria, 63 (15.8%) produced growth of fungi, and 97 had either growth of a contaminant or no growth (Table 1).

Table 1: Nasopharyngeal Swab Culture Results of SARS-CoV-2 Infected Individual

| Variable | Frequency (n=400) | Percentage |
|---|---|---|
| Bacteria | 240 | 60.0 |
| Fungi | 63 | 15.8 |
| No growth/ Contaminant | 97 | 22.2 |
| **Total** | **400** | **100** |

Source: Author's Laboratory Analysis

According to Table 2, frequency and percentage distribution of Gram reactions among the different bacterial isolates, out of 240 (60.0%) bacteria, 124 (51.7%) were Gram negative bacilli, 86 (35.8%) were Gram positive cocci, and 30 (12.5%) were combined growths of Gram negative bacilli and Gram positive cocci.

26 (16.9%) of the 124 Gram negative bacteria isolates sub-cultured on CHROM Orientation agar medium for color speciation showed pinkish coloration, 97 (63.0%) showed bluish coloration, 21 (13.6%) showed creamy coloration, and 10 (6.5%) showed greenish coloration (Table 3).

Figure 1 shows the frequency and percentage of all isolated Gram-negative bacteria detected by API 20E. The isolates included Acinetobacter baumanii 7(4.5%), Citrobacter freundii 1(0.6%), Citrobacter koseri 3(1.9%), Cronobacter specie 1(0.6%), Enterobacter aerogenes 23(14.9%), Enterobacter cloacae 27(17.5%), Escherichia coli 8(5.1%), Klebsiella oxytoca 5(3.3%), Klebsiella pneumoniae 35 (22.7%), Kluyevera specie 3 (1.9%), Proteus mirabilis 4 (2.6%), Proteus vulgaris 1 (0.6%), Pseudomonas luteola 10 (6.5%), Raoultella ornithinolytica 6 (3.9%), Serratia ficaria 6 (3.9%), Serratia liquefaciens 2 (1.3%), Serratia rubidea 3 (1.9%) and Serratia marscensces 6 (3.9%), respectively.

Table 2: Gram Results of Bacteria Isolates from Samples of SARS-CoV-2 Infected Individual

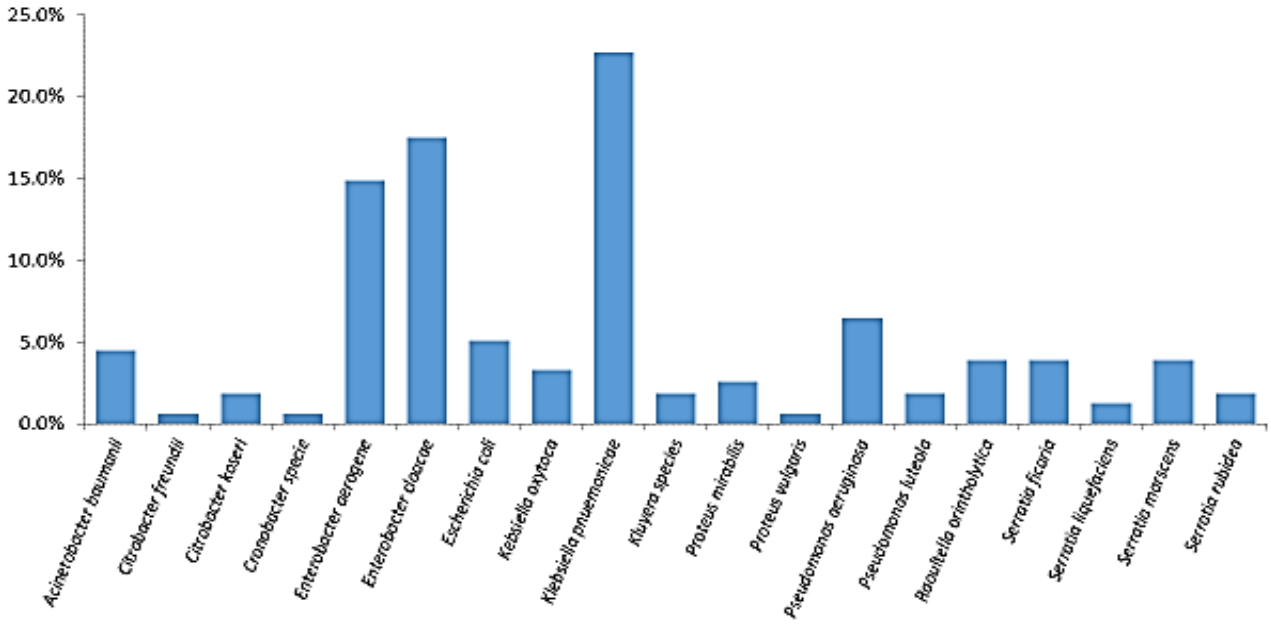
| Variable | Frequency (n=240) | Percentage |
|---|---|---|
| GRAM (n=240) | | |
| GNB | 124 | 51.7 |
| GPC | 86 | 35.8 |
| GNB + GPC | 30 | 12.5 |
| **Total** | **240** | **100** |

Source: Author's Laboratory Analysis

Table 3: Initial Identification of Gram Negative Bacteria on CHROM Orientation Agar

| Variable | Frequency (n=154) | Percentage |
|---|---|---|
| CHROM O (n=154) | | |
| Pinkish | 26 | 16.9 |
| Bluish | 97 | 63.0 |
| Creamy | 21 | 13.6 |
| Greenish | 10 | 6.5 |
| **Total** | **154** | **100** |

Source: Author's Laboratorty Analysis




Source: Author's Laboratory Analysis

Figure 1: API 20E Confirmatory Identification of all Gram Negative Bacilli

According to Table 4, of the 111 (35.8%) Gram positive cocci that were subcultured on Mannitol Salt Agar Medium from samples of SARS-CoV-2 infected people, 62 (54.7%) showed golden yellow coloration and 49 (45.3%) accounted for pinkish coloration.

Figure 2 shows the frequency and percentage distribution of all Gram-positive cocci organisms discovered by VITEK 2.0. The isolates are as follows: Enterococcus faecalis 4 (3.6%), Staphylococcus xylosus 1 (0.9%), Staphylococcus aureus 36 (32.4%), Methicillin Resistant Staphylococcus aureus 1 (0.9%), Staphylococcus equorum 4 (3.6%), Staphylococcus gallinarium 1 (0.9%), Staphylococcus lentus 16

Table 5 displays the frequency and percentage composition of all 37 Staphylococcus aureus identified with the VITEK 2.0 compact system, including 1 (2.7%) MRSA and 36 (97.3%) MSSA.

Table 4: Initial Identification of Gram Positive Cocci on Mannitol Salt Agar

| Variable | Frequency (n=111) | Percentage |
|---|---|---|
| GPC on MSA(n=111) | | |
| Golden Yellow | 62 | 54.7 |
| Pinkish | 49 | 45.3 |
| **Total** | **111** | **100** |

Source: Author's Laboratory Analysis

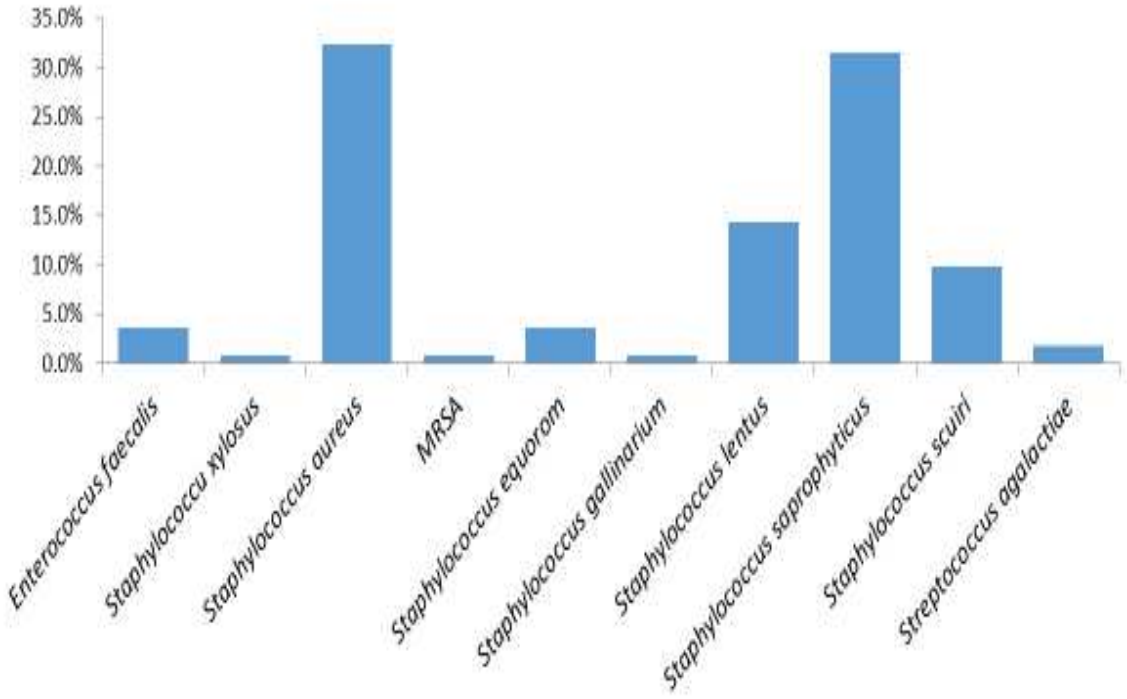
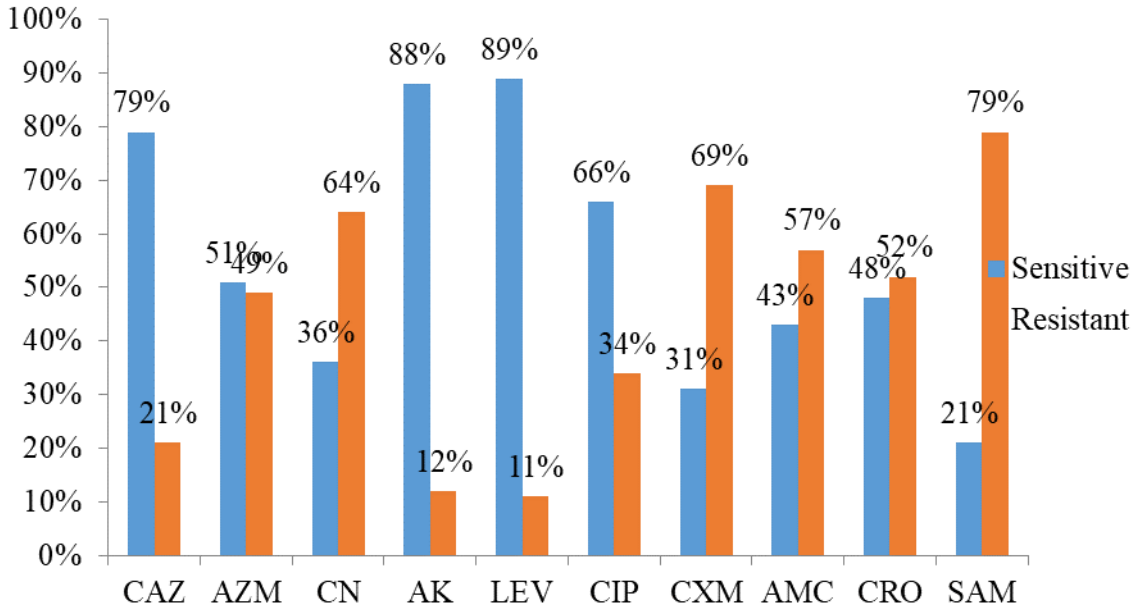



Figure 2: VITEK 2.0 Confirmatory Identification of all Gram Positive Cocci

Source: Author's Laboratory Analysis

The percentage distribution of antibiotics susceptibility pattern of Gram negative bacilli in Figure Figure 3 shows that the majority of Gram-negative bacilli isolates were mostly susceptible to the following antibiotics: Levofloxacin (89%), Amikacin (88%), Ceftazidime (79%), Ciprofloxacin (66%), Azithromycin (51%), Cefuroxime (11%), Sulbactam (11%), Ceftriaxone (8%), and Gentamycin (6%) respectively.

According to Figure 4's susceptibility pattern, the majority of Gram-positive cocci isolates were susceptible to the following antibiotics: Vancomycin (74.10 percent), Ciprofloxacin (71.30%), Levofloxacin (70.40 percent), Cefoxitin (69.40 percent), Gentamycin (45.40 percent), Erythromycin (42.60 percent), Azithromycin (33.30 percent), Clindamycin (29.60 percent), and Oxacillin (23.10%) respectively.




Source: Author's Laboratory Analysis

Figure 3: Antibiogram of Gram Negative Bacteria Isolates using Kirby Bauer Disc Diffusion and VITEK 2.0 System

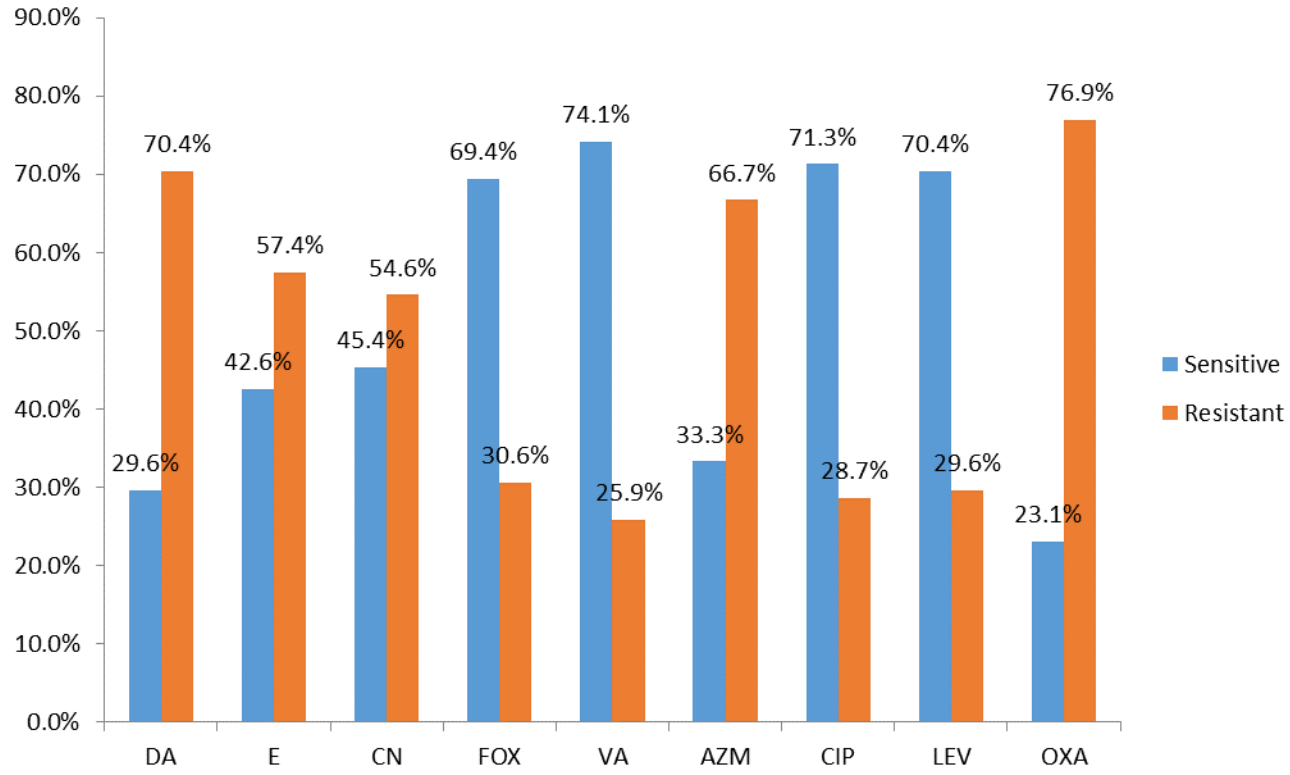



Figure 4: Antibiogram of Gram Positive Bacteria Isolates using Kirby Bauer and VITEK 2.0

Source: Author's Laboratory Analysis

## 3.0 DISCUSSION

From the on-going COVID-19 pandemic, viral and bacterial infection has been reported among the infected patient who is in concordance with the results of various pathogens recorded in this research study (Lansbury et al., 2020). Also, in this study out of 400 SARS-CoV-2 infected individual samples collected, mixed growth of bacterial and fungal pathogen co-infected with SARS-CoV-2 was 7.3% in agreement with 8% reported by some researchers[4]. The rates of bacterial coinfection reported in this study appeared to be a little above the percentage reported by some researcher 240(60%) compared with 62(8%) reported (Rawson et al., 2020), which might be due to climatic changes, adaptation measures, environmental condition and immune status in this part of the continent.

Early detection of bacterial infection in 3.2% of all hospitalized patients, 13.5% of those requiring critical care supports the isolation of most pathogen from symptomatic individual in this study population ((Hughes et al., 2020). A report of bacterial co-infection within 48 hours of admission to ICU in 8% of patients with SARS-CoV-2 is also in agreement with outcome results in this study that most of bacteria isolates were recorded from symptomatic individuals. In the US, higher early bacterial co-infection rates (16.6%) were identified by a researcher (Young et al., 2020) isolated from respiratory cultures for oral bacteria flora which constituted 15/25 of these cases and is in agreement to this research study that relied predominantly on culture-based techniques (He et al., 2018). Bacterial co-infection within 48 hours of hospital admission for COVID-19 infection in adults was common and this confirm that bacterial are secondary invader, able to participate in interactions between host cells and viruses by expressing virulence factors that promote viral pathogenesis which helps viral load to increase and clearance rates to decline (Kim et al., 2019). The proportion of pathogens detected were noted to increase with duration of ICU stay and symptoms exhibited which consisted largely of Gram negative bacteria, where most of the bacterial pathogens isolated were majorly classes of Enterobacteriacea such as Klebsiella pneumonia, Enterobacter cloacae, Enterbacter aerogenes, Pseudomonas aerogenes, Pseudomonas luteola, Acinetobacter baumanni, Escherichia coli and this is in agreement with the isolated pathogen reported by a researcher (McCullers et al., 2014; Wang et al., 2020; Phua et al., 2020).

However, the rate of co-infection is markedly higher than what was observed during the pandemic of influenza, suggesting that, it is more of a significant issue with SARS-CoV-2 infection having coinfection with bacterial and this is relatively agreed with outcome result from this study of 32.4% Staphylococcus aureus and predominant pathogens observed among Gram-negative bacteria, particularly K. pneumonia 22.7%, E. cloacae 17.5% and E aerogenes 14.9%, but in contrast to wide range of bacterial pathogen that includes Heamophilus, Lautrlopia, Prevotella been detected as coinfection in Brazil, China and USA (Phua et al., 2020).

Also, isolation of some pathogen like Klebsiella pneumonia, Pseudomonas aeruginosa, Enterococcus, Acinetobacter baumanii, which were all in conformity with some of the isolates identified in this research work (McCullers et al., 2014). From this study Gram negative bacteria had 49% resistant while Gram positive bacteria has 66.7% phenotypical

resistant to Azithromycin drug of choice for empirical management of COVID-19 disease which corroborate highest detection of mefA and ermB macrolides resistance genes among Gram positive bacteria isolates.

3.1. Conclusion

In the ongoing COVID-19 pandemic, the rising frequency of coinfection of bacterial and fungal (data published in another paper) with SAR-CoV-2 infected individual as well as increasing reports of resistance to some antimicrobial agents is imperative.

In summary, report from this research study confirms the presence of bacterial co-infecting agents (data published in another paper) among individual with COVID-19 infection in our setting. Meanwhile, the occurrence of these coinfections was high when compared to reports from other researchers in other countries setting. Also the predominance of Gram-negative pathogens, presence of methicillin resistance Staphylococcus aureus and incidence of bacterial l isolates harboring macrolide resistant strain are of great alertment and concern (data published in another paper).

In conclusion this study recorded:

Bacterial isolates as co-infecting pathogen among SARS-CoV-2 infected individual.

Declearation of conflict of interest:

I declare there is no conflict of interest.

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