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An Overview of Bacterial Isolates in a Tertiary Hospital in Guyana during a 1 Year Period (2023)

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Abstract

The emergence of antimicrobial resistance (AMR) leads to increased patient morbidity and mortality, along with prolonged hospital stay, decreased patient quality-of-life, and increased burden on healthcare infrastructure, as such, monitoring of AMR is very important. This research provides a first-time overview of bacterial isolates obtained at the Georgetown Public Hospital Corporation (GPHC) in 2023 along with their general resistance patterns which can be used to guide and monitor AMR programs. This was a descriptive retrospective cross-sectional study that consisted of extracting data on bacterial cultures from the VITEK 2 system at GPHC obtained from 1st January 2023 to 31st December 2023. WHONET 2023 was then used to analyze the data to obtain the prevalence of organisms in the hospital and access their antibiotic resistance patterns. A total of 6575 bacterial isolates were obtained, of which 1971 (30%) were gram-positive organisms which were 33.2%, 30.7%, and 28.8% resistant to trimethoprim/sulfamethoxazole, tetracycline, and clindamycin. 4604 (70%) were gram-negative organisms which were 61.1%, 18.4%, and 14.7% resistant to ceftazidime, piperacillin/tazobactam, and imipenem. The prevalence of extended spectrum beta-lactamase and carbapenem-resistant isolates was 66% and 15.6% respectively. Staphylococcus aureus (1122 or 59.6%) and Enterococcus species (402 or 20.4%) were the most prevalent gram-positive organisms while Klebsiella pneumonia and Escherichia coli were the most prevalent gram-negative isolates (1236 or 26.8% and 1120 or 24.3%). Better practices in antimicrobial use are needed to combat the high prevalence and resistance found, particularly of gram-negative bacteria, including ESBL and carbapenem-resistant isolates.

Keywords: *Antimicrobial Resistance, Carbapenem-Resistant, Extended Spectrum Beta-Lactamase, Gram-Negative, Gram-Positive.*

Introduction

In 2019, bacterial antimicrobial resistance (AMR) was estimated to have contributed to 4.95 million deaths globally and was directly responsible for 1.27 million global deaths [1]. This has led the World Health Organization to characterize AMR as a major global public health and developmental threat, and an integral part of attaining Sustainable Development Goal 3 (good health and well-being) [2]. In addition to increased patient morbidity and mortality, the emergence of AMR also leads to prolonged hospital stays, decreased patient quality of life, and increased burden on healthcare infrastructure [3]. Furthermore, AMR also carries with it a significant economic burden. The World Bank estimates that by 2030 AMR will result in gross domestic product losses ranging from

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US$ 1 trillion to US$ 3.4 trillion per year and by 2050 AMR is predicted to result in US$ 1 trillion additional healthcare costs [4].

There are multiple factors that contribute to the development of AMR and they vary in developing and developed nations. In the former, contributing factors include clinical misuse and overuse of antibiotics, ease of availability of antibiotics, poor quality of available antibiotics, and lack of surveillance of resistance development. On the other hand, in developed nations, excessive use of antibiotics in food-producing animals, poor hospital-level regulation of antibiotic use, and decline in the development of novel antibiotics due to the lack of economic incentives for antibiotic research are major contributing factors to AMR [5].

In Guyana, at its currently largest tertiary hospital, the Georgetown Public Hospital Corporation (GPHC) there are limited antimicrobial stewardship (AMS) interventions ongoing, and at the national level according to the Tracking AMR Country Self-Assessment Survey 2023 country report, Guyana is graded as having "limited" multisector and One Health collaboration, "limited" country progress with the development of a national action plan on AMR, "limited" national monitoring system for consumption and rational use of antimicrobials in human health, "limited" national surveillance system for AMR in humans, and "none" optimizing antimicrobial use in human health [6]. This research aimed to provide a first-time overview of bacterial isolates obtained at GPHC during the year 2023 along with their general resistance patterns which can later be compared with similar studies in the future to investigate for new emerging organisms or increase in the prevalence of known organisms along with changes in their resistance patterns. Such comparative data will be a valuable contribution to antimicrobial surveillance at GPHC and can later be used in part to access the progress and effectiveness of IPC and AMS programs at the institution. Hence, this study evaluated the prevalence of bacterial isolates obtained at GPHC during the year 2023 and investigated their general resistance patterns.

Materials and Methods

This was a descriptive retrospective cross-sectional study that consisted of extracting data on bacterial cultures and their respective antibiotic resistance from the laboratory information system of GPHC using a sample period of one year (1st January 2023 to 31st December 2023). This study included all GPHC inpatient and outpatient bacterial cultures that would have been lodged at the microbiology laboratory and isolated at least 1 organism that had antibiotic susceptibilities tested. Before commencing the research, approval was sought for and granted from the GPHC Research Committee and the Ministry of Health Institutional Review Board.

The microbiology laboratory at GPHC currently uses the VITEK 2 system which performs automated bacterial identification and antibiotic susceptibility testing in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines. In total, data on 6575 bacterial cultures that isolated at least one organism were electronically extracted from the VITEK 2 system and output in a Microsoft Excel spreadsheet document (Microsoft 365, version 2308, build 16.0.16731.20542).

The spreadsheet data was then cleaned to remove any irrelevant data then the software program BacLink 2023 (version 23.17.2) was used to convert and standardize the spreadsheet document into a format readable by WHONET 2023 (version 23.17.2). WHONET is a software developed by the WHO Collaborating Centre for Surveillance of Antimicrobial Resistance for the analysis and management of microbiology laboratory data. WHONET 2023 was then used to analyze the

data to obtain the prevalence of gram-positive and gram-negative organisms in the various wards of the hospital and to access their antibiotic resistance patterns.

Results

Prevalence of Bacterial Isolates

A total of 6575 bacterial isolates were obtained, of which 1971 (30%) were gram-positive organisms and 4604 (70%) were gram-negative organisms which are shown in figure 1. The prevalence of the most common gram-positive and gram-negative organisms are shown in tables 1 and 3 respectively. Table 2 shows the prevalence of staphylococcus aureus species isolated. Of the 1122 staphylococcus aureus identified, 538 (48%) were methicillin-susceptible staphylococcus aureus (MSSA), 514 (45.8%) were methicillin-resistant Staphylococcus aureus (MRSA) and 68 (6%) were not tested for methicillin or cefoxitin so they could not be characterized as MRSA or MSSA. Of 1052 staphylococcus aureus isolates identified as either MRSA or MSSA, 538 (51.1%) were MSSA, and 514 (48.9%) were MRSA. 402 enterococci were isolated, 282 (70.2%) of which were identified as enterococcus faecalis, 23 (5.7%) were identified as enterococcus faecium, and the species was not identified for 97 (24.1%) of them.

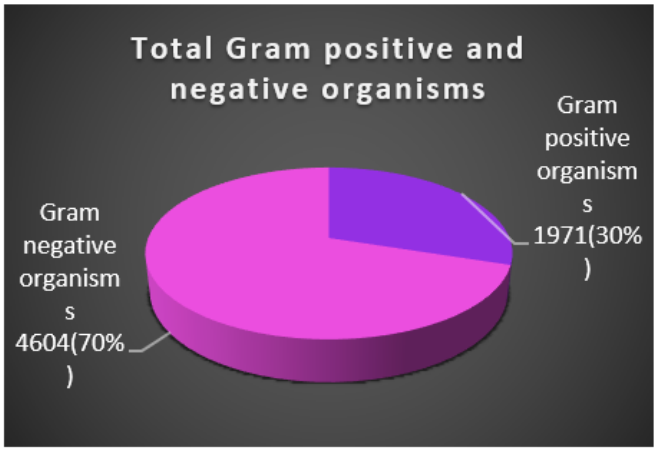

Figure 1. Showing Total Gram-Positive and Gram-Negative Organisms Isolated

Table 1. Showing the Most Common Gram-Positive Organisms Isolated

Gram-positive Organisms	**Number of isolates**	**% of gram-positive**	**% of total isolates**
Staphylococcus aureus	1122	56.9	17.1
Enterococcus sp.	402	20.4	6.1
Streptococcus sp.	216	11	3.3
Staphylococcus, coagulase-negative	195	9.9	3.0

Table 2. Showing the Prevalence of Staphylococcus Aureus Isolated

S. aureus characteristic	Number of isolates	% of S. aureus	% of gram-positive	% of total isolates
MSSA	538	48	27.3	8.2
MRSA	514	45.8	26.1	7.8
*undetermined	68	6	3.5	1.0
**VRSA	2	0.2	0.1	0.03

**Methicillin/cefoxitin was not tested so it was unable to determine whether these were MRSA or MSSA. ***Two Staphylococcus aureus isolates were reported by the VITEK as vancomycin-resistant, however, it is unclear whether any additional testing was done to confirm this.*

Table 3. Showing Most Common Gram-Negative Organisms Isolated

Gram-negative Organism	Number of isolates	% of gram-negative	% of total isolates
Klebsiella pneumoniae	1236	26.8	18.80
Escherichia coli	1120	24.3	17.03
Pseudomonas aeruginosa	492	10.2	7.48
Proteus sp.	351	7.6	5.34
Enterobacter sp.	316	6.9	4.81
Acinetobacter baumannii	287	6.2	4.37
Morganella morganii	101	2.2	1.49
Pantoea sp.	98	2.1	1.54
Serratia sp.	89	1.9	1.35
Providencia sp.	66	1.4	1.00
Burkholderia sp.	65	1.4	0.98
Stenotrophomonas sp.	60	1.3	0.91
Citrobacter sp.	57	1.2	0.87
Salmonella sp.	28	0.6	0.43

Isolates from cultures reported as “wound swabs”, “pus”, “tissue”, “aspirate”, “exudates”, “joint fluid” and “bone” collectively accounted for 1485 isolates or 22.6% of the total isolates. 540 (36.4%) of them were gram-positive organisms and 945 (63.6%) were gram-negative organisms. 1463 isolates (22.3%) were from urine cultures, of which 316 (21.6%) were gram-positive organisms and 1147 (78.4%) were gram-negative organisms. 1417 isolates (21.6%) were from blood cultures with 614 (43.3%) of them being gram-positive organisms and 803 (56.7%) being gram-negative organisms. Isolates from sputum totaled 684 (10.4%), 87 (12.7%) of which were gram-positive

organisms and 597 (87.3%) were gram-negative organisms. A collective total of 1526 (23.2%) isolates were from various other sources. The prevalence of the 10 most common organisms isolated from blood, urine, and wound cultures are shown in figures 2, 3, and 4 respectively.

The wards with the most isolated organisms included the male surgical ward (958 or 14.6%), female medical ward (717 or 10.9%), female surgical ward (506 or 7.7%), and male medical ward (492 or 7.5%), however, 511 (7.8%) isolates had no ward reported for them. Figure 5 shows the total number of organisms isolated per ward in wards that had at least 30 isolates.

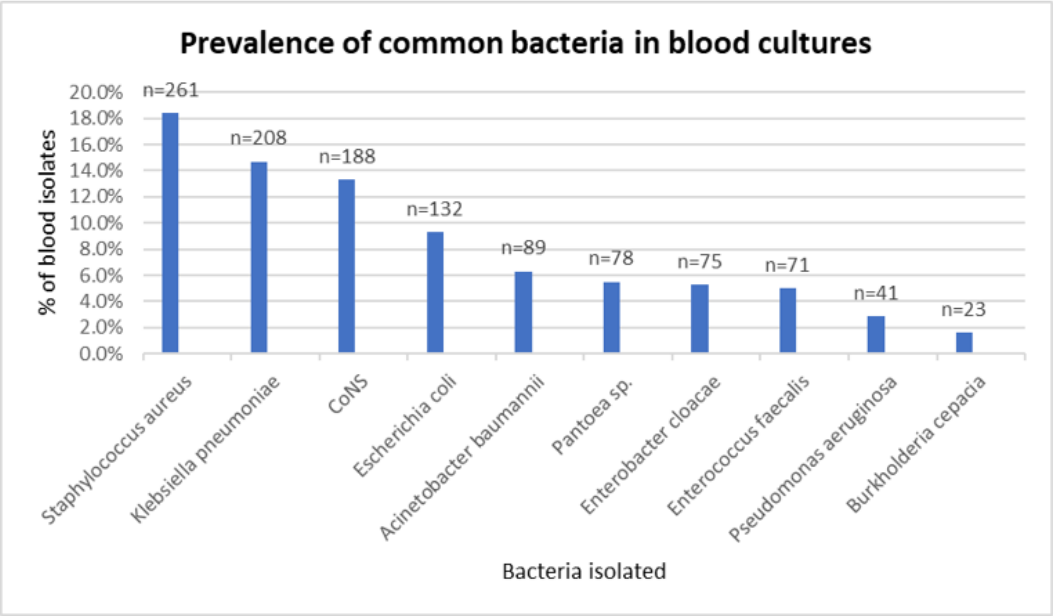

Figure 2. Showing the Prevalence of the 10 Most Common Organisms Isolated from Blood Cultures. n - Number of Isolates, CoNS – Coagulase-Negative Staphylococci

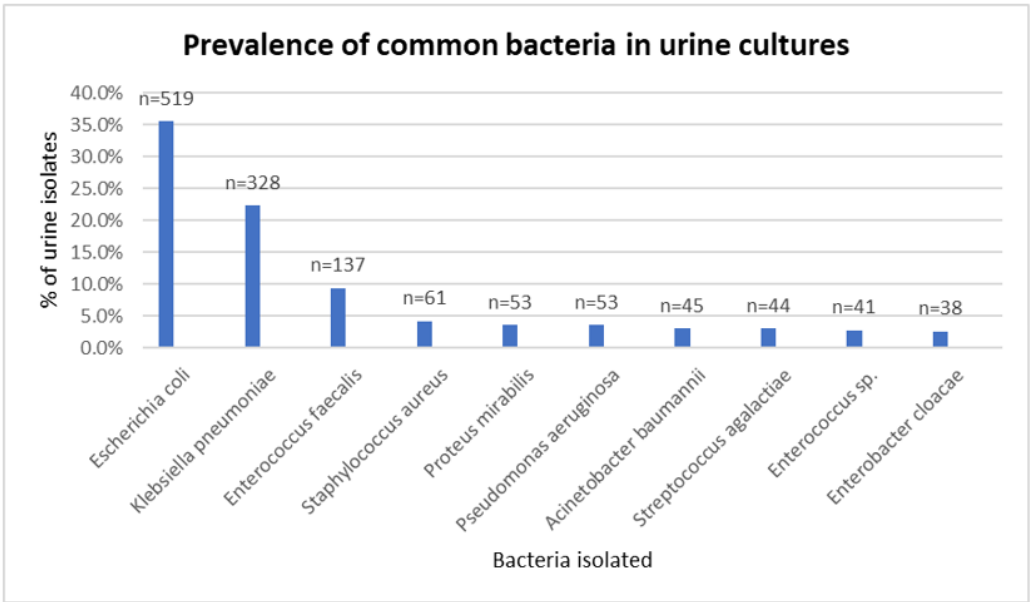

Figure 3. Showing the Prevalence of the 10 Most Common Organisms Isolated from Urine Cultures. n - Number of Isolates

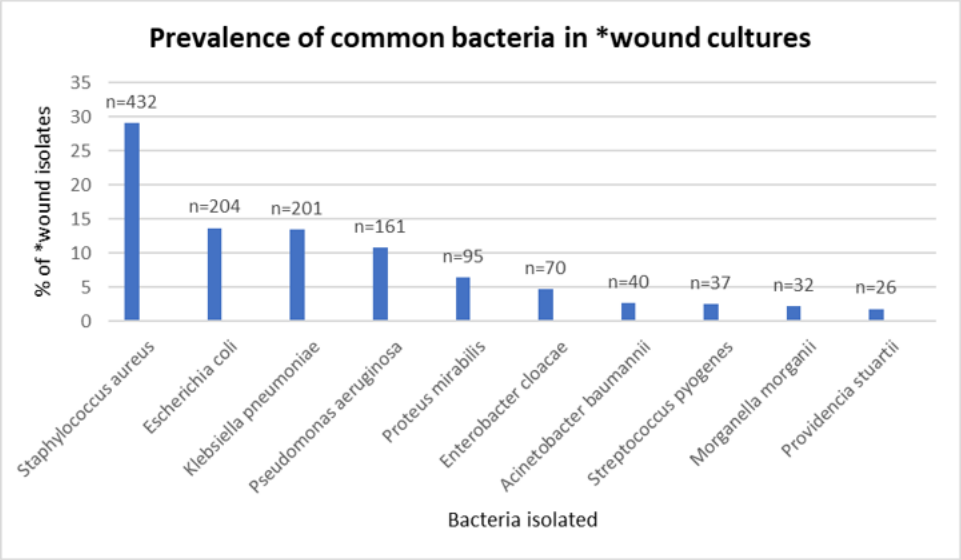

Figure 4. Showing the Prevalence of the 10 Most Common Organisms Isolated from Wound Cultures. *Wound Isolates Include all Cultures Reported as "wound Swabs", "Pus", "Tissue", "Aspirate", "Exudates", "Joint Fluid" and "Bone". n – Number of Isolates

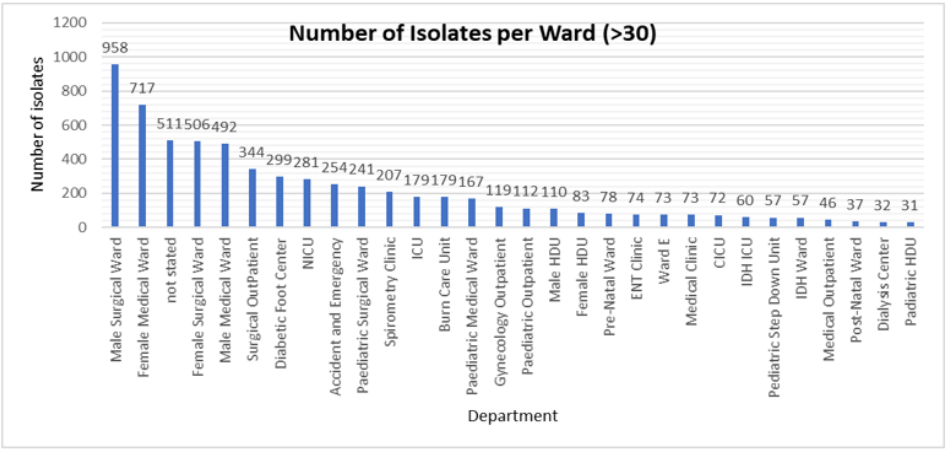

Figure 5. Showing the Total Number of Organisms Isolated per Ward in Wards that had at least 30 Isolates. NICU – Neonatal Intensive Care Unit, ICU – Intensive Care Unit, HDU – High Dependency Unit, Ent – Ears Nose And Throat, CICU – Cardiac Intensive Care Unit, IDH – Infectious Disease Hospital (An Extension of GPHC).

Resistance Characteristics of Isolates

The percentage of antibiotic resistance of gram-positive and gram-negative organisms to various antibiotics are shown below in tables 4 and 5 respectively. The percentage resistance is displayed as reported by the WHONET software after data analysis. Extended spectrum beta-lactamase (ESBL) organisms were not reported in the data set obtained from the VITEK so their prevalence was estimated by calculating the average resistance of gram-negative organisms to the third-generation cephalosporins cefotaxime and ceftazidime which was calculated to be 66%. Ceftriaxone was not used in this estimation because only 19 gram-negative isolates were tested for it while 2029 and 2924 gram-negative isolates were tested for cefotaxime and ceftazidime respectively. Similarly, the ESBL prevalence for K. pneumoniae, E. coli, P. aeruginosa, Proteus spp., and Enterobacter spp. was estimated to be 85.1%, 80.95%, 14.6%,

50.25%, and 71.4% respectively. From 2182 isolates tested for at least 1 carbapenem 340 (15.6%) were carbapenem-resistant, of which carbapenem-resistant Enterobacteriaceae (CRE), Pseudomonas aeruginosa, Acinetobacter baumannii and Burkholderia cepacia accounted for 63.2% (215), 12.1% (41), 10.6% (36) and 6.8% (23) respectively.

Table 4. Showing Percentage Resistance of Gram-Positive Isolates to the Various Antibiotics Tested Against Them.

Antibiotic name	**Number of isolates tested**	**% Resistance**
Meropenem	13	69.2
Ciprofloxacin	723	67.2
Erythromycin	1447	57.4
Methicillin	1258	50.0
Cefoxitin	409	49.4
Fosfomycin	52	48.1
Cefazolin	65	35.4
Trimethoprim /Sulfamethoxazole	1336	33.2
Tetracycline	931	30.7
Clindamycin	1444	28.7
Nitrofurantoin	272	26.8
Cefotaxime	54	20.4
Ceftriaxone	45	20.0
Amoxicillin/ Clavulanic acid	6	16.7
Chloramphenicol	54	13.0
Ampicillin	490	9.8
Gentamicin	161	8.1
Cefepime	31	3.2
Vancomycin	794	2.4
Minocycline	159	1.3
Linezolid	972	1.1

Table 5. Showing Percentage Resistance of Gram-Negative Isolates to the Various Antibiotics Tested against them.

Antibiotic name	**Number of isolates tested**	**% Resistant**
Ceftriaxone	19	89.5
Imipenem/Relebactam	37	89.2
Amoxicillin/ Clavulanic acid	1642	79.8
Ampicillin	924	74.7
Cefotaxime	2029	70.6
Ceftazidime	2924	61.1

Cefuroxime	3028	61.0
Cefazolin	231	59.7
Ampicillin/ Sulbactam	262	54.2
Trimethoprim/ Sulfamethoxazole	3744	52.4
Cefepime	147	50.3
Ciprofloxacin	3043	44.3
Tetracycline	75	34.7
Norfloxacin	63	33.3
Tobramycin	2968	30.9
Gentamicin	3607	27.3
Ertapenem	203	27.1
Nitrofurantoin	1036	20.7
Piperacillin/ Tazobactam	2805	18.4
Fosfomycin	1032	17.9
Imipenem	2100	14.7
Meropenem	1949	11.4
Amikacin	1137	10.3
Minocycline	123	9.8

Discussion

Published studies on the hospital-wide prevalence and resistance patterns of gram-positive and gram-negative organisms in the Caribbean are limited and most of the published studies focused only on specific organisms (such as staphylococcus aureus and ESBL organisms) or bacteria isolated from specific sites of infection (such as blood or wound). As such, the overall prevalence of organisms and their resistance patterns in hospitals of the Caribbean are not well characterized. To our knowledge, this is the first-ever hospital-wide study showing the prevalence and resistance characteristics of gram-positive and gram-negative bacteria in Guyana, and it adds to only a few such studies in the Caribbean region.

Prevalence of Gram-Positive Bacteria

The majority (56.9%) of the gram-positive bacteria isolated were staphylococcus aureus but 6% of the staphylococcus aureus isolated were not tested for susceptibility to methicillin or cefoxitin so it was not possible to determine whether those were MRSA or MSSA. However, of the 1052 staphylococcus aureus isolates that were tested for susceptibility to methicillin or cefoxitin, 51.1% were MSSA and 48.9% were MRSA. The staphylococcus aureus isolates accounted for 17.1% of the total isolates with MSSA making up 8.2% of all isolates and MRSA making up 7.8% of all isolates. A study previously done in Guyana in 2013 showed the prevalence of staphylococcus aureus to be 55% and that of MRSA to be 28%, however, this was specifically among skin and soft tissue infections in the emergency department and not a hospital-wide study [7].

The overall prevalence of MRSA in this study was found to be similar to that reported in Central America (7.8% vs 6%), however, in Barbados the same was found to be almost three times higher than this study (19.7% vs 7.8%) [8, 9]. The prevalence of MRSA among S. aureus isolates in Latin America in two separate studies was found to be 45% and

44.7% which is similar to that found in this study (48.9%) [9, 10]. But when compared to some countries in the Caribbean the prevalence of MRSA among S. aureus isolates in this study was much higher with similar studies showing the prevalence in Trinidad and Jamaica to be 18.6% and 23% respectively (Brown & Ngeno, 2007; Orrett & Land, 2006).

Coagulase-negative staphylococci were the third most prevalent bacteria (13.3%) isolated from blood cultures and since the isolation of this organism is used as a proxy for blood culture contamination this means that about 13.3% of blood cultures done at GPHC are contaminated which is more than four times higher than the recommended 3% target by the Clinical and Laboratory Standards Institute guidelines [13]. However, CoNS can cause true bloodstream infections but the data collected in this study is insufficient to differentiate true infections from contamination so this 13.3% contamination rate could be an overestimation.

Prevalence of Gram-Negative Bacteria

Gram-negative organisms were found to be the most common bacteria that caused infections at GPHC, more specifically, they were 2.3 times more likely to cause infections compared to gram-positive bacteria (70% vs 30%). This data coincides with some international studies, for example, one study of patients hospitalized in ICUs in the United States found that gram-negative pathogens were isolated from 67.1% of patients [14]. Another large study in a multi-hospital healthcare system in Saudia Arabia similarly found that hospital-acquired infections were 2.3 times more likely to be caused by gram-negative bacteria compared to gram-positive organisms [15]. However, the prevalence of gram-negative pathogens at GPHC was found to be above the regional findings with one study reporting gram-negative bacilli to make up 44.5% of bacterial organisms in Latin America and another study reporting gram-negative bacteria caused >50% of infections in ICUs of Latin America and the Caribbean [16, 17].

The most common gram-negative pathogens isolated in this study were Klebsiella pneumonia (26.8%), escherichia coli (24.3%), pseudomonas aeruginosa (10.2%), proteus species (7.6%), and Enterobacter species (6.9%). More specifically, escherichia coli and Klebsiella pneumonia were the first and second most prevalent organisms in urine cultures (35.5% and 22.4%), the second and third most prevalent in wound cultures (13.7% and 13.5%) and in blood cultures, klebsiella pneumonia was the second most prevalent (14.7%) while escherichia coli was the fourth most prevalent (9.3%). This data coincides with published common causes of gram-negative infections in urine, wounds, and blood both regionally and globally [13, 18, 19, 20].

Resistance Characteristics of Gram-Positive Organisms

Gram-positive bacteria had the highest resistance against meropenem, ciprofloxacin, and erythromycin (69%, 67%, and 57%), however, these are not antibiotics that are usually recommended to treat infections caused by gram-positive organisms so these are not of much concern. Additionally, the high resistance against meropenem is primarily due to MRSA which is known to be resistant to beta-lactam antibiotics like meropenem because of the 9 (69.2%) gram-positive isolates that were resistant to meropenem 7 were MRSA, however, it must be taken into consideration that only 13 gram-positive isolates in total were tested against meropenem. Methicillin and cefoxitin also had high resistance against them (50%, 49%) but these antibiotics are mainly used in vivo to differentiate MRSA and MSSA [21]. Trimethoprim/Sulfamethoxazole, tetracycline (doxycycline) and clindamycin are common

antibiotics that are used for empiric and culture-specific treatment of gram-positive organisms and they all had relatively high resistance against them (33%, 31%, and 29%). The resistance of MRSA isolates significantly differed from the collective resistance of all GPC against trimethoprim/sulfamethoxazole (54.2% vs 33%) and tetracycline (11.9% vs 29%) but was similar against clindamycin (33.4% vs 31%). These relatively high resistance rates are of great clinical concern because these are the most common oral agents used to treat infections caused by gram-positive organisms including MRSA so much intervention is needed in antimicrobial stewardship (AMS) and antimicrobial resistance (AMR) programs to prevent these high resistance rates from increasing further and better yet, to decrease them. The lowest resistance among gram-positive organisms was against cefepime (3.2%), vancomycin (2.4%), minocycline (1.3%), and linezolid (1.1%). Of the 2.4% that were resistant to vancomycin, 2 isolates were S. aureus, however, it is unknown whether further tests were done to confirm this resistance. These are promising results since minocycline and linezolid are among the first-line oral agents recommended for the treatment of MRSA skin and soft tissue infections while cefepime is commonly used as parental treatment for various gram-positive organisms (such as streptococci species and MSSA) and vancomycin is the first line treatment for MRSA bacteremia [22, 23].

Resistance Characteristics of Gram-Negative Organisms

Gram-negative bacteria were found to have the highest resistance rates against ceftriaxone (89.5%), imipenem/relebactam (89.2%), amoxicillin/clavulanic acid (79.8%), ampicillin (74.7%) and cefotaxime (70.6%). The high resistance rates against ceftriaxone and cefotaxime are likely attributable to the high prevalence of ESBL organisms estimated in this study (66%). Imipenem/relebactam had the second highest resistance against the gram-negative isolates (89.2%, n=33) and of the 33 that were resistant to it, 20 were Pseudomonas aeruginosa. This was found to be very surprising and alarming since this is a relatively new carbapenem β-lactamase inhibitor combination antibiotic which is currently not available in Guyana to our knowledge and is approved specifically for the treatment of multi-drug resistant (MDR) gram-negative infections including MDR Pseudomonas aeruginosa and carbapenem-resistant Enterobacteriaceae (CRE) such as Klebsiella pneumoniae carbapenemase [24]. One explanation for this could be that those were mostly from imported cases, but patient history was not collected in this study, so we are unable to confirm this. Further investigations are needed to assess why this novel combination antibiotic which is not available in Guyana currently has such a high resistance against it. Amoxicillin/clavulanic acid is usually used as an alternative treatment option for uncomplicated gram-negative infections so the high resistance to it is somewhat concerning because this means that if first-line treatment options become resistant and this alternative option is also resistant then treatment options might be very limited. Ampicillin was found to have one of the highest resistance levels (74.7%), but it is no longer routinely used to treat gram-negative infections due to high levels of resistance against it from beta-lactamase-producing organisms. Moreover, the high resistance to ampicillin in this study is mostly due to the high prevalence of ESBL organisms since 79.6% of gram-negatives that were resistant to ampicillin were estimated to be ESBL based on their resistance to ceftazidime, so novel combination antibiotics such as ampicillin/sulbactam are needed to aid clinicians overcome such high resistance caused by beta-lactamase-producing organisms [25].

The overall prevalence of ESBL organisms was estimated to be 66% based on their average resistance to ceftazidime and cefotaxime, however, this can be an overestimation since it's not based on confirmatory tests for ESBL. Among the 5 most prevalent gram-negative organisms in this study, namely K. pneumonia, E. coli, P. aeruginosa, Proteus species, and Enterobacter species, their ESBL prevalence was estimated to be 85.1%, 80.95%, 14.6%, 50.25%, and 71.4% respectively. This is significantly higher than ESBL prevalence reported in Latin America where overall, 52.7% of Klebsiella spp. and 24.7% of E. coli were found to have the ESBL phenotype [16]. In Trinidad, up to 63.2% of K. pneumonia and 32.4% of E. coli were reported as ESBL isolates, however, generally in the Caribbean 30% of K. pneumonia and 11% of E. coli were found to be ESBL producers [26, 27]. This data shows that Guyana has an alarmingly high prevalence of ESBL isolates when compared to Latin America and the Caribbean which can be a reflection of poor AMS and AMR strategies and programs in the country, however, further studies are needed to assess the prevalence of ESBL isolates based on confirmatory tests to compare them with the estimates that we calculated based on their resistance profiles.

Piperacillin/tazobactam, imipenem, and meropenem were among the antibiotics with the lowest resistance rates against gram-negative isolates (18.4%, 14.7% and 11.4% respectively) but even though they had the lowest resistance, these relatively high rates are concerning since they are the most potent antibiotics currently available for the treatment of gram-negative infections. Among carbapenem resistant isolates, 63.2% were carbapenem-resistant Enterobacteriaceae (CRE), 12.1% were Pseudomonas aeruginosa and 10.6% were Acinetobacter baumannii. These findings are of critical importance to clinicians and patient outcomes because if measures are not taken to reduce these resistance rates, then this can result in the increased prevalence of resistant infections with very limited or even no treatment options and it can lead to a heavy financial burden on the hospital because to treat such resistant infections novel combination antibiotics would have to be procured which are much more costly.

Limitations

Data extracted from the VITEK 2 system did not allow for de-duplication of culture results (that is, removal of repeated isolates of the same bacterial species from the same patient per analysis period), so the antimicrobial resistance rates may be overestimated in this study. Secondly, the laboratory usually tested susceptibilities for a standard list of first-line antibiotics against isolates and only did additional testing if there was resistance to the first-line agents, so the number of certain antibiotics tested against isolates is lower than ideal. Another limitation of this study was that infections were not reported as either community or hospital-acquired to the laboratory, so the authors were unable to do comparisons of prevalence and resistance between community and hospital-acquired isolates. Finally, this is the first such study done in Guyana and at GPHC, so the authors were unable to provide any comparison over time to access changes in AMR rates.

Conclusion

In conclusion, infections caused by gram-negative bacteria dominated at this tertiary hospital which were aggravated by high prevalences of resistant organisms including ESBL and carbapenem-resistant isolates. Poor practices in antimicrobial use both at this hospital and nationally coupled with lacking AMS programs and AMR strategies are likely the driving forces behind these high resistance rates. Better practices in antimicrobial use are needed to combat the high prevalence and

resistance, particularly of gram-negative bacteria including ESBL and carbapenem-resistant isolates.

Recommendations

We recommend the adoption and implementation of stricter infection prevention and control and AMS programs that provide guidance on minimizing inappropriate antimicrobial use, ensuring correct dosage and administration routes, and determining the optimal duration of therapy. These AMS programs should include strict monitoring of the use of reserve antibiotics such as carbapenems, for example, by having their orders co-verified by infectious disease physicians or clinical pharmacologists. When effectively executed, these programs can lead to notable reductions in the prevalence of antimicrobial resistance, as well as decreases in morbidity, mortality, and costs. Additionally, because of the relatively high resistance found against carbapenems, we recommend procurement of novel combination antibiotics which should be strictly reserved for carbapenem-resistant organisms when no other alternative agent can be used as deemed by an infectious disease physician. Lastly, we recommend similar surveillance studies to be repeated annually which would allow for tracking of AMR changes over time and assessment of effectiveness of AMS programs.

Conflict of Interest

The authors declare that there are no conflicts of interest.

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