Antimicrobial Resistance in the Caribbean

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DOI:
DOAJ: ecc9f1ed3e3944168ac7f5893bc6bc80

ABSTRACT

Objectives

Antimicrobial resistance is a global problem. The extent of this problem in the Caribbean sub-region is not well characterised. Most reports are from a few countries within the Caribbean sub-region. The aim was to develop and refine an antimicrobial resistance surveillance system at the Caribbean Public Health Agency (CARPHA) for member states. The objectives were to: 1. establish and test a surveillance system for antimicrobial resistance (AMR) starting with key bacterial isolates such as *Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, Enterococcus* spp. and *Streptococcus pneumoniae* from key specimens such as blood, in line with the Global Antimicrobial Resistance and Use Surveillance System (GLASS), 2. to expand this surveillance to other organisms and specimens, 3. to share data with CARPHA member states (CMS) for quality improvement.

Methods

Isolates were submitted by hospitals from 13 (50%) CMS. The CMS laboratories sent clinically relevant isolates of five key species: *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae*, *Streptococcus pneumoniae* and *Enterococcus faecium*. The isolates were mainly from urine, blood, and wound samples. Phenotypes and antimicrobial susceptibilities were determined using the VITEK 2 Compact (VITEK) system. The VITEK identification and susceptibilities were emailed back to the laboratories.

Results

The laboratory received 1013 isolates from April 2017 through July 2018. Most of the bacteria received were *Escherichia coli*, *Klebsiella pneumoniae* and *Staphylococcus aureus*. Three hundred and sixteen isolates were identified as *S. aureus* from 323 *Staphylococcus* spp. and 38% of the *S. aureus* isolates received were Methicillin Resistant *Staphylococcus aureus* (MRSA). Two hundred and seventy-eight isolates of *E. coli* were tested and identified; 11% were extended spectrum beta-lactamase (ESBL) producers. Two hundred and eighty-three isolates

of *K. pneumoniae* were identified from 291 *Klebsiella* spp.; 30% were ESBL producers. The samples were received from multiple specimen types. Three carbapenem resistant isolates of *K. pneumoniae*, confirmed on subculture and repeat testing, were obtained from 3 CMS, widely distributed in the Caribbean region.

Conclusions
Antimicrobial resistance within the Caribbean is widespread. There is need for continued antimicrobial stewardship and infection control efforts. Surveillance should be started with *Escherichia coli*, *Klebsiella pneumoniae* and *Staphylococcus aureus*, from blood specimens.

Key Words: antibiotic, antimicrobial, resistance, Caribbean, Staphylococcus, Klebsiella, Escherichia, Yeast

BACKGROUND

Antimicrobial resistance (AMR) has become recognized as a global problem. Following a United Nations (UN) resolution in 2015 (Resolution: WHA A68/20 - Antimicrobial resistance. Draft global action plan on antimicrobial resistance), countries were asked to produce country plans. Surveillance of antimicrobial resistance is an essential component of the action plans, alongside antibiotic stewardship and infection prevention and control.[1,2]

The extent of AMR within the Caribbean is poorly documented. A Caribbean regional AMR working group concluded there was a lack of local AMR information, as well as limited laboratory capacity for antimicrobial susceptibility testing. An online survey of Caribbean Public Health Agency's (CARPHA) member states (CMS) confirmed this conclusion and led CARPHA to establish a regional reference service for antimicrobial susceptibly testing (AST). Details of the antimicrobial stewardship activities associated with this survey of antimicrobial resistance are available from a paper on the genetics of *Klebsiella pneumoniae* from the Caribbean.[3]

We aligned the call for isolates and thus the surveillance with World Health Organization's (WHO) Global Antimicrobial Resistance and Use Surveillance System [GLASS].[4] We therefore focused on *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae* and to a lesser extent, *Streptococcus pneumoniae*. We also included yeast, *Enterococcus* spp., and other multi-drug resistant bacteria which were submitted. As noted by Sparo *et al*, the impact of resistance in *Enterococcus* spp. is of concern globally.[5] In addition, according to the Centres for Disease Control (CDC), Atlanta in the United States of America (USA), certain yeasts are of concern globally.[6] Thus, although our study and surveillance methodology are aligned to WHO GLASS, it also deals with other microorganisms of global concern. The aim includes investigating the implications for CMS and developing a comprehensive, region specific (CMS) surveillance system. The use of multiple organisms allowed us to arrive at a more focused list of the most relevant organisms, as we illustrated in this study.

The aim was to develop an antimicrobial resistance surveillance system in the Caribbean Public Health Agency (CARPHA) member states. The objectives were to: 1. establish and test a surveillance system for antimicrobial resistance (AMR) starting with key bacterial isolates such as *Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, Enterococcus* spp. and *Streptococcus pneumoniae* from key specimens such as blood, in line with WHO GLASS, 2. to expand this surveillance to other organisms and specimens, 3. to share data with CARPHA member states (CMS) for quality improvement.

METHODS

Isolates were submitted by hospitals and not community institutions, from CMS: Antigua, Barbados, Belize, Bermuda, Cayman Islands, Dominica, Grenada, Haiti, Jamaica, Saint Kitts, Saint Lucia, Saint Vincent and the Grenadines and Trinidad and Tobago. This represented 13 of the 26 CMS (50%). Further, isolates were de-duplicated at the submitting hospital and at CARPHA. Contributing CMS were anonymised, and no patient details accompanied the isolates. No clinical information was sought other than the specimen type. The laboratories were asked to send clinically relevant isolates of five key species: *Staphylococcus aureus, Escherichia coli, Klebsiella pneumoniae, Streptococcus pneumoniae* and *Enterococcus faecium*. Clinically relevant isolates were defined as significant growth or 10^5 or 10^4 for urine,

any growth for swabs, cerebrospinal fluid (CSF), blood, respiratory specimens, wound swabs, and any other relevant specimens. When yeast identification and susceptibility testing became available, participating laboratories were asked to send clinically relevant isolates. The isolates were not selected for submission in a structured fashion, and submission was dependent on the availability of transport media, specimen transport and laboratory staff. The isolates were sent in batches, generally grouped by bacterial species. Phenotypes and antimicrobial susceptibilities were determined using the VITEK 2 Compact (VITEK) System (bioMérieux Inc., Durham, NC) within the CARPHA Laboratory, Port of Spain, Trinidad. The VITEK is an automated machine which utilized predefined panels for identification and antibiotic testing. The VITEK contains software which aids with identification of resistance patterns and resistance mechanisms.[7] There were no facilities for onward referral or confirmatory testing except by disc diffusion and E-Test. All isolates received from CMS were not necessarily reported and tested. This would have occurred if quality control tests failed in data validation. Quality control included de-duplication, analysing submitted results versus actual results obtained from the automated identification and susceptibility machine at the CARPHA laboratory. Table 1 shows the isolates received. The susceptibility results reported, are those without any modification by the VITEK rules base. The VITEK identification and susceptibilities were emailed back to the laboratories as soon as testing was complete. These antibiotics were selected as they met Clinical Laboratory Standards criteria (CLSI). The antibiotics tested for *Staphylococcus aureus* were clindamycin, erythromycin, gentamicin, levofloxacin, rifampicin, cotrimoxazole and tetracycline. In addition, cefoxitin was utilized as the indicator of methicillin resistance. *Escherichia coli* and *Klebsiella pneumoniae* were tested with amikacin, gentamicin, ciprofloxacin, ampicillin, ceftriaxone, meropenem, aztreonam, nitrofurantoin, ampicillin-sulbactam, tazobactam-piperacillin, cotrimoxazole and tigecycline.

Ethical exemption was obtained for the ethics committee of the Eastern Regional Health Authority, Trinidad and Tobago, for this study, as it simply dealt with isolates and no human subjects or specimens were directly involved.

RESULTS

The laboratory received 1013 isolates from April 2017 through July 2018. Most of the bacteria received were *Escherichia coli:* Two hundred and seventy-eight (27.4%), *Klebsiella pneumoniae*: 283 (28%) and *Staphylococcus aureus*: 316 (31.2%). The isolates were mainly from urine, blood, and wounds samples, but also from a wide range of other sources; details on the specimens and the bacterial genera received are given in the Table 1. The laboratory received 71 isolates from blood cultures and two isolates from cerebrospinal fluids: one an *Enterococcus faecalis* and one *Klebsiella pneumoniae*. Isolates other than those requested were either sent because they were found to be multi-resistant or were thought to be misidentified. Fourteen (1.34%) yeast isolates were received, and no significant antifungal resistance was detected.

Table 1: Genera and specimen types received and de-duplicated by CARPHA

	Blood	Respiratory	Urine	Wound	CSF*	Unrecorded	Total
Escherichia coli	14	9	205	48	0	44	320[2]
***Klebsiella* spp.**	17	29	146	86	1	12	291
***Staphylococcus* spp.**	25	35	21	226	0	16	323
Other Enterobacteria[1]	11	3	18	7	0	2	41
***Enterococcus* spp.**	1	1	15	15	1	0	33
Streptococcus pneumoniae	3	1	0	0	0	1	5
Total	71	78	405	382	2	75	**1013**[2]

CARPHA – The Caribbean Public Health Agency. Eye, ear, throat, nose specimens are included in respiratory. Genital, skin, and fluid specimens are included in wound. *Acinetobacter spp.* (8), *Burkholderia cepacia* (1), *Pseudomonas spp.* (9) and *Candida spp.* (14); total 32 isolates, are not included in the table. This table includes received isolates. Note that not all isolates received were tested or failed quality checks e.g., 320 *E. coli* were received but 278 were tested as shown in supplementary table 2 (S2).

*CSF – Cerebrospinal Fluid

[1]Other Enterobacteria included *Citrobacter* spp. (4), *Enterobacter* spp. (28), *Morganella* spp. (5) and *Proteus* spp. (4).

[2]Specimens were further de-duplicated at CARPHA.

Susceptibility patterns for each key bacterium

The percentages of antibiotic susceptibilities, for each of the three major bacteria, are shown below in supplementary tables 1 to 3. The susceptibilities were displayed, as reported by the VITEK software. *Staphylococcus aureus* showed 62% cefoxitin susceptibility and 100% vancomycin susceptibility. *E. coli* and *K. pneumoniae* showed 11% and 30% extended spectrum beta-lactamase (ESBL) production, respectively. Additionally, the resistance rates to key antibiotics tested are displayed in tables S1 to S3. These rates are not those of community acquired infections but of laboratory isolates of strains obtained from hospitals. Supplementary tables S1 to S4 also display antibiotics that were available on the VITEK antibiotic susceptibility panels.

Table S1. Susceptibilities of all isolates of *Staphylococcus aureus* tested

Antibiotic	**Number susceptible**	**Percent-age****
Ciprofloxacin	218	69%
Clindamycin	300	95%
Erythromycin	181	57%
Nitrofurantoin	284	90%
Gentamicin	310	98%
Non-Inducible Clindamycin	308	97%
Levofloxacin	221	70%
Linezolid	313	99%
Moxifloxacin	259	82%
Oxacillin	188	59%
MSSA (Cefoxitin)	197	62%
Penicillin	52	16%
Quinupristin-dalfopristin	312	99%
Rifampicin	314	99%
Trimethoprim-Sulfamethoxazole	273	86%
Tetracycline	305	97%
Tigecycline	314	99%
Vancomycin	315*	100%
Total tested	**316**	**100%**

*A Methicillin Resistant *Staphylococcus aureus* (MRSA) isolate was reported by VITEK as Vancomycin resistant, but this was not confirmed on disc testing or by E-Test. ** All percentages are rounded to the nearest whole number.

Table S2. Susceptibilities of all isolates of *Escherichia coli* tested

Antibiotic	Number susceptible	Percentage*
Ampicillin	142	51%
Amikacin	278	100%
Aztreonam	262	94%
Ceftazidime	278	100%
Ciprofloxacin	181	65%
Ceftriaxone	250	90%
Cefazolin	247	89%
ESBL Negative	247	89%
Ertapenem	278	100%
Cefepime	275	99%
Nitrofurantoin	264	95%
Gentamicin	251	90%
Meropenem	278	100%
Ampicillin-Sulbactam	165	59%
Trimethoprim-Sulfamethoxazole	195	70%
Tigecycline	278	100%
Piperacillin-Tazobactam	273	98%
Total tested	**278**	**100%**

* All percentages are rounded to the nearest whole number.

Table S3. Susceptibilities of all isolates of *Klebsiella pneumoniae* tested.

Antibiotic	Number susceptible	Percentage*
Ampicillin	5	2%
Amikacin	279	99%
Aztreonam	200	71%
Ceftazidime	205	72%
Ciprofloxacin	208	73%
Ceftriaxone	196	69%
Cefazolin	195	69%
ESBL Negative	198	70%
Ertapenem	279	99%
Cefepime	258	91%
Nitrofurantoin	118	42%
Gentamicin	208	73%
Meropenem	280	99%
Ampicillin-Sulbactam	168	59%
Trimethoprim-Sulfamethoxazole	183	65%
Tigecycline	275	97%
Piperacillin-Tazobactam	234	83%
Total tested	**283**	**100%**

Table S4. Susceptibilities of all isolates of *Enterobacter cloacae* tested.

Antibiotic	Number susceptible	Percentage*
Ampicillin	2	8%
Amikacin	24	100%
Aztreonam	24	100%
Ceftazidime	24	100%
Ciprofloxacin	24	100%
Ceftriaxone	24	100%
Cefazolin	0	0%
ESBL Negative	0	0%
Ertapenem	24	100%
Cefepime	24	100%
Nitrofurantoin	6	25%
Gentamicin	24	100%
Meropenem	24	100%
Ampicillin-Sulbactam	20	83%
Trimethoprim-Sulfamethoxazole	24	100%
Tigecycline	24	100%
Piperacillin-Tazobactam	24	100%
Total tested	**24**	**100%**

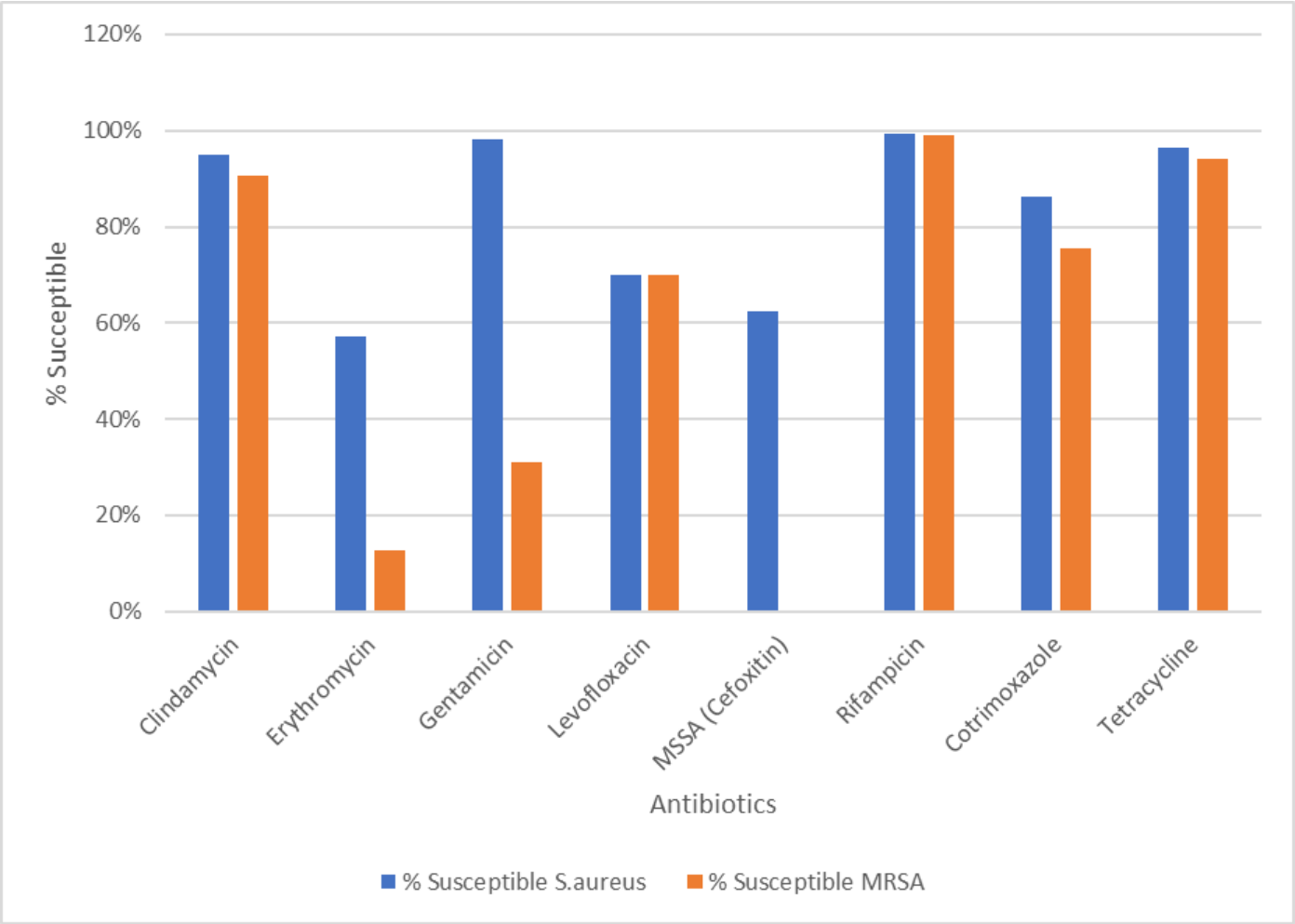
* All percentages are rounded to the nearest whole number.

Staphylococcus aureus

Three hundred and sixteen (31.2%) isolates were identified as *S. aureus* from 323 *Staphylococcus* spp. Cefoxitin was used to determine methicillin resistance (MRSA). Thirty eight percent of the *S. aureus* isolates received were MRSA. Figure 1 shows the overall susceptibility pattern of methicillin susceptible *Staphylococcus aureus* (MSSA) and the susceptibilities of the MRSA isolates. The MSSA and MRSA both showed sensitivity to clindamycin, rifampicin and tetracyclines. Additionally, MSSA and MRSA both showed resistance to the fluoroquinolone, levofloxacin.

Figure 1: The overall susceptibility pattern of *S. aureus* and the susceptibilities of the MRSA isolates.

(a).



These antibiotics were selected as they met Clinical Laboratory Standards Criteria (CLSI).

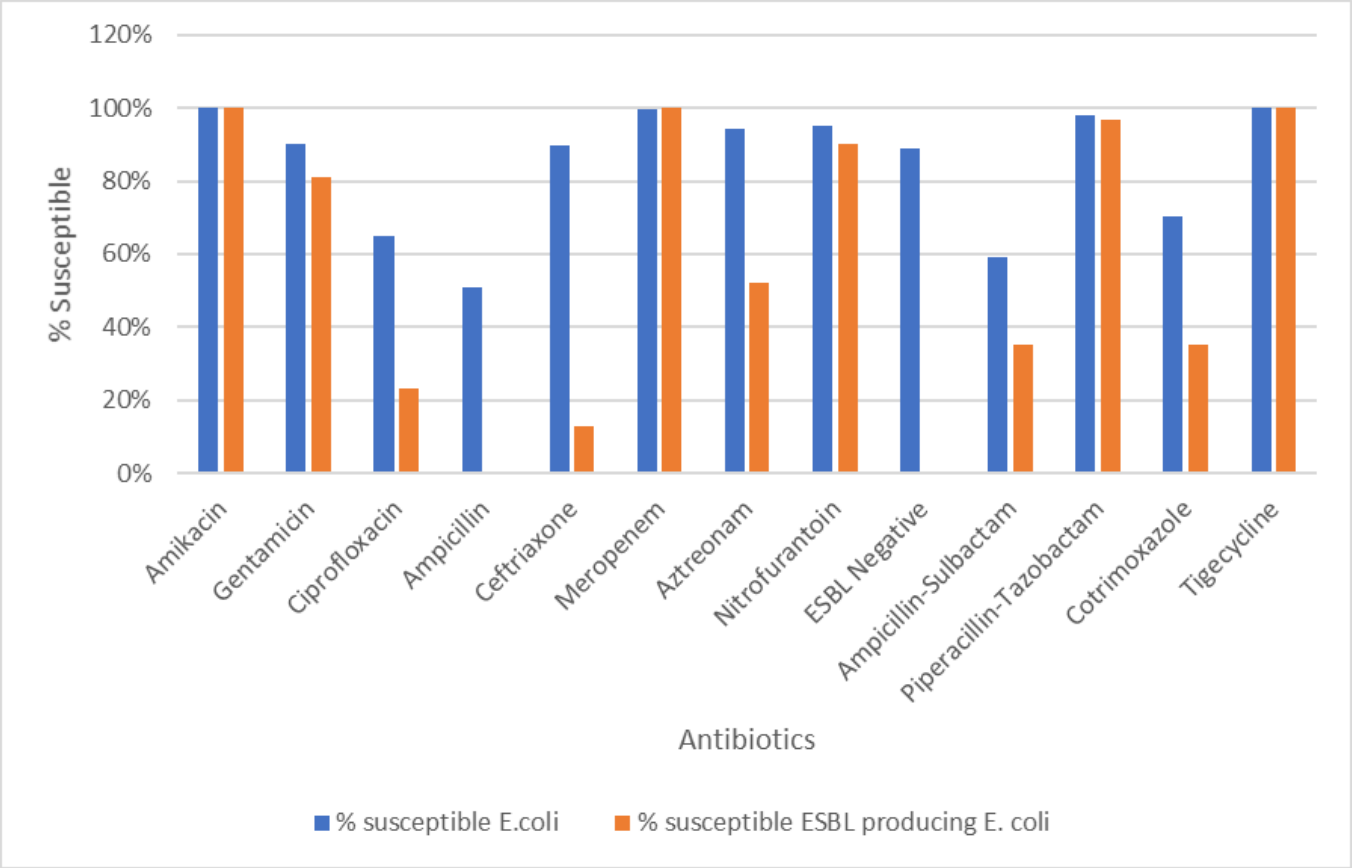
This diagram represents susceptibility percent in Methicillin Susceptible *Staphylococcus aureus* (MSSA) [BLUE] and Methicillin Resistant *Staphylococcus aureus (*MRSA)[ORANGE].

Escherichia coli

Two hundred and seventy-eight (27.4%) isolates of *E. coli* were tested and identified; 11% were extended spectrum beta-lactamase (ESBL) producers. Three *E. coli* isolates were initially found to be carbapenem resistant from two CMS, but this was not confirmed after repeated subculture and retesting. The ESBL producing *E. coli* were sensitive to amikacin, meropenem and tigecycline. Figure 2 shows the overall susceptibilities of *E. coli* and the susceptibilities of the ESBL producing *E. coli* isolates.

Figure 2: The overall susceptibility pattern of *E. coli* and of the ESBL *E. coli* isolates.

(a).



These antibiotics were selected as they met Clinical Laboratory Standards Criteria (CLSI).

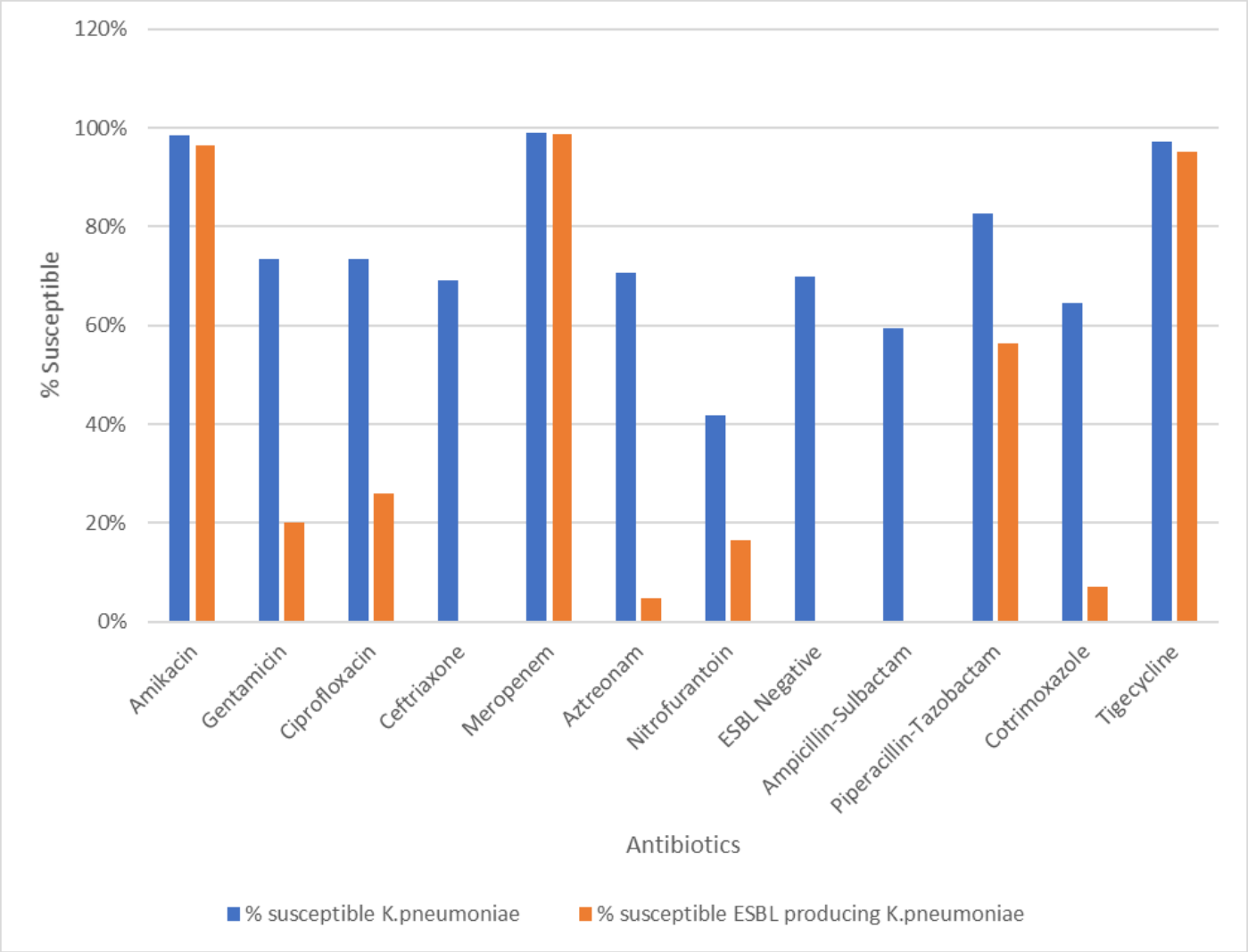
This diagram represents susceptibility percent in Susceptible *Escherichia coli* [BLUE] and extended spectrum producing beta-lactamase producing *Escherichia coli* (ESBL)[ORANGE].

Klebsiella pneumoniae

Two hundred and eighty-three (28%) isolates of *K. pneumoniae* were identified from 291 *Klebsiella* spp.; 30% were ESBL producers. Three (3) carbapenem resistant isolates of *K. pneumoniae*, confirmed on subculture and repeat testing, were obtained from 3 CMS, distributed in the Caribbean region. In addition, the ESBL producing *K. pneumoniae* showed sensitivity to meropenem, amikacin and tigecycline. Figure 3 shows the overall susceptibilities of *K. pneumoniae* and the susceptibilities of the ESBL producing *K. pneumoniae* isolates.

Figure 3: The overall susceptibility pattern of *K. pneumoniae* and the susceptibilities of the ESBL *K. pneumoniae* isolates.

(a).



These antibiotics were selected as they met Clinical Laboratory Standards Criteria (CLSI).

This diagram represents susceptibility percent in Susceptible *Klebsiella pneumoniae* [BLUE] and extended spectrum producing beta-lactamase producing *Klebsiella pneumoniae* (ESBL)[ORANGE].

Other Gram-positive bacteria

Streptococcus pneumoniae: 5 isolates were received, all from the same CMS. Four were erythromycin resistant but otherwise fully susceptible. *Enterococcus faecalis*: 31 isolates from 5 CMS. *Enterococcus faecium*: 2 isolates from 2 CMS. No vancomycin resistance was detected.

Other Gram-negative bacteria

Pseudomonas aeruginosa: 8 isolates were received, from 4 CMS. Two were resistant to all antibiotics available for testing. *Enterobacter cloacae*: 24 isolates were received, from 5 CMS. They were all ampicillin-sulbactam and cefazolin resistant. *Morganella morganii*: 5 isolates were received from 3 CMS. *Proteus* spp.: 4 isolates were received from 4 CMS. *Acinetobacter baumannii*: 7 isolates were received, from 4 CMS, 5 were beta-lactam, carbapenem, gentamicin and ciprofloxacin resistant.

DISCUSSION

Only three of the five pathogens requested, were supplied in significant numbers for analysis. This allowed us to narrow, revise and focus our surveillance strategy. These were *Escherichia coli*, *Klebsiella pneumoniae* and *Staphylococcus aureus*. The prevalence was high among these organisms, with *E. coli* at 27.4%, *K. pneumoniae* at 28% and *S. aureus* at 31.2%. This would have aligned well with the pathogens identified for surveillance by WHO GLASS.[4] It is well known that *K. pneumoniae* and *E. coli* are global threats with regards to established and emerging resistance in ESBLs and carbapenem resistance.[8-12] The study by Munoz-Price *et al* shows the distribution of carbapenemases in neighbouring Latin America and North America.[8] Munoz-Price has also shown that carbapenem resistance was identified in the 1990's and has spread within the Americas and around the world, across continents, especially among Gram negative bacilli.[8] In addition, the study shows that there is increased mortality and limited antibiotic options associated with these carbapenemases.[8] Some of the last options for treatment include colistin and tigecycline.[8] The prevalence of antibiotic resistance seen in the CMS, are also congruent with that seen globally.[3, 4, 8-22]

Extended Spectrum Beta-Lactamases

There was more ESBL production, among the *K. pneumoniae* tested, compared to the *E. coli*. The resistance in ESBL producing *E. coli* and ESBL producing *K. pneumoniae* were higher than non ESBL producing strains, to the antibiotics tested. There was resistance to other classes of antibiotics, other than beta-lactams, such as the fluoroquinolones, sulphur drugs such as co-trimoxazole and aminoglycosides such as gentamicin. Among ESBL producing bacteria, the last line antibiotics such as meropenem, tigecycline and amikacin still appeared useful. Carbapenem resistance appeared more prevalent in *K. pneumoniae* than *E. coli* .[3, 9, 11, 24] In contrast to this study, Stanley *et al*, found more carbapenem resistance in *E. coli* compared to *K. pneumoniae*.[9] This study was however, done in Uganda.[10] Navon-Venezia *et al* in their review of *K. pneumoniae* resistance have described plasmid encoded ESBL and carbapenem resistance genes and other resistance genes and mechanisms. They have also noted that resistance genes to multiple antibiotic classes are found in *K. pneumoniae*. This may account for the multiple antibiotic class resistance seen within ESBL producing strains in our study.[10]

Extended Spectrum Beta-Lactamases in the Caribbean

ESBLS have been detected in the Caribbean, however most of this research has been carried out in Trinidad and Tobago, and Jamaica.[23-26] A publication by Heinz *et al* gives an overview of ESBL and carbapenem resistance in *K. pneumomiae* in the Caribbean. This study revealed that carbapenem resistance was widely distributed and that molecular ESBL types and sub-types were found.[3] ESBL producing *E. coli* and *K. pneumoniae* have been noted to be susceptible to carbapenems and amikacin in our study, which is congruent with other studies.[3, 26] Generally, there was reduced susceptibility to fluoroquinolones, as seen in other studies.[3, 11] Our study highlighted a reduced susceptibility to co-trimoxazole, in ESBL producing isolates compared to the study by Wiener *et al*.[11] This study also shows susceptibility to tigecycline, among ESBL producing isolates in CMS.

Staphylococcus aureus

S. aureus is also spread extensively, globally.[13-22] There was a high percentage of MRSA isolated from CMS. The MRSA displayed increased resistance to the antibiotics reported compared to susceptible *Staphylococcus aureus*. There was resistance to macrolides such as erythromycin, fluoroquinolones such as levofloxacin, co-trimoxazole and gentamicin in the MRSA tested. There was no resistance, displayed by MRSA, to the last line antibiotic vancomycin. However, minimal resistance to linezolid and tigecycline were detected. There was also minimal resistance of MRSA to clindamycin and rifampicin across CMS. *S. aureus* is of major concern for multiple antibiotic class resistance, particularly MRSA.[16-22, 33]

Staphylococcus aureus in the Caribbean

Studies have been done across the Caribbean for *Staphylococcus aureus* and MRSA. This includes St Kitts and Nevis, Barbados, Jamaica, Anguilla, Trinidad and Tobago, Guadeloupe, and Martinique.[23-34] A study by Brown *et al* showed that multidrug resistance was common among MRSA, similar to this study.[32] Most studies found no resistance to vancomycin and very little resistance to linezolid.[31, 32] In addition, Gittens *et al* found a low level of resistance to rifampicin in MRSA, similar to

this study.[31] Akpaka *et al*, in their study in Trinidad and Tobago, found low levels of resistance to rifampicin but alarming levels of resistance to vancomycin, linezolid and clindamycin.[26] The studies are also congruent with the increased susceptibility seen in methicillin susceptible *Staphylococcus aureus* [MSSA].[16-22, 28-34]

Other Bacteria

There was a small amount of resistance detected in *S. pneumoniae* to erythromycin and no vancomycin resistance was detected in the *Enterococcus* spp. tested. A study by Jaocobs *et al* is congruent with our study, showing a small amount of resistance in *S. pneumoniae* to the antibiotics tested. Another study done by Hawkins *et al* showed only a small amount of resistance, in a limited number of isolates tested, in Trinidad and Tobago.[37,38] Unlike the Caribbean wide study done on *Enterococcus*, our study showed no resistance while their study showed vancomycin resistance and resistance to other antibiotic classes such as fluoroquinolones.[39] The *Pseudomonas aeruginosa* and *Acinetobacter baumannii* tested were resistant to multiple antibiotics in our study. This multidrug resistance has been seen in other studies and is noted to be common for these bacteria.[40, 41]

Yeast

In addition, only a small amount of yeast were tested. These yeast isolates were susceptible.[37] The resistance in yeast was small however, in the Caribbean, there should be vigilance for the emergence of resistant yeast such as *Candida auris*.[42] *Candida auris* has already been detected in nearby Latin American countries. [6, 42]

Limitations

The laboratories found it difficult to determine the difference between the *Enterococcus* spp. They also had difficulties in isolating *Streptococcus pneumoniae.* This may have occurred because many patients were already reported to be on antibiotics prior to sampling. In addition, because of limited resources, the CMS laboratories did not have more sophisticated equipment to identify these bacteria to the species level. This would have reduced the number of isolates provided and showed greater resistance. This is because susceptible isolates would not have grown, and resistant isolates would not have been identified due to limited capabilities. Thus, we should find ways to help build technical capacity and provide resources for some of the CMS laboratories. A great deal of effort was required to obtain the isolates from the laboratories; communication directly to the technologist staff succeeded where more formal routes had failed, and there were difficulties with intra-Caribbean transport.

Refinement of Organisms under Surveillance

Interestingly, the inclusion of multiple organisms allowed us to reach a consensus on the most appropriate organisms on which to build the resistance surveillance system. Hence, we were able to narrow our surveillance strategy to 3 main organisms, *Escherichia coli*, *Klebsiella pneumoniae* and *Staphylococcus aureus*. The original plan was that antimicrobial resistance monitoring and reporting would become a continuous process with data taken directly from the CMS with confirmation and extending testing performed by the CARPHA laboratory. Unfortunately, funding for this project ceased during 2018. The project has not been re-established since discontinuation. However, we have been able to demonstrate that antimicrobial resistance is widespread with a consequent reduction in the availability of effective antimicrobials. Additionally, we were only able to obtain isolates from only 50% of CMS. In alignment with objective 3, we gave each CMS feedback via an emailed report, for all laboratories and a spreadsheet, for individual laboratories.

Benefits of the Current Study

Overall, there appears to be more published data on MRSA than ESBL resistance in the Caribbean and globally.[23-34] This study will add to the existing knowledge about ESBLs, other organisms highlighted and resistance surveillance methodology refinement within the context of the Caribbean. This has provided us with a snapshot of the prevalence of antimicrobial resistance and demonstrates that the range of resistance is similar to that observed in the Americas, Europe and across the world.[4, 6, 35-36] Notably, one CMS state is enrolled in WHO GLASS, and we hope that we can encourage other CMS to contribute to international antimicrobial resistance surveillance data.[43]

Conclusion

An antimicrobial surveillance system is suggested for the CMS located at the CARPHA laboratory in Port of Spain,

Trinidad and Tobago. This is due to the widespread resistance in the Caribbean and the fact that this problem can impact on the economies of small island developing states. This also leads to increases morbidity, mortality and increased economic burden inclusive of increased hospital related costs. *Escherichia coli, Klebsiella pneumoniae* and *Staphylococcus aureus* are suggested as the first organisms under surveillance using blood specimens. This will be in line with WHO GLASS and based on the findings of this study. We believe that continued surveillance, infection control and antimicrobial stewardship are needed to limit the spread of resistance. We hope that this limited survey of antimicrobial resistance has provided evidence that it is prevalent within the Caribbean and that action is needed to control it.

Ethical Approval statement: Ethical exemption was obtained for the ethics committee of the Eastern Regional Health Authority, Trinidad and Tobago.

Conflict of Interest statement: The authors have no conflict of interest to declare.

Informed Consent statement: Not applicable.

Funding: This work was supported by The United States Centres for Disease Control (CDC), Atlanta.

Author Contributions: Richard J Brindle conceptualised, analysed, and approved the final study. Avery QJ Hinds reviewed the data and reviewed the final manuscript. Keisha Peters and Andrina Morgan-Mc Calla analysed specimens, worked on the data, and approved the final manuscript. Rajeev P. Nagassar and Keston Daniel analysed the data, wrote the manuscript, and reviewed for final publication.

Acknowledgements: We the authors would like to thank all the CARPHA member states for submitting isolates for this study. We would also like to thank the Eastern Regional Health Authority in Trinidad and Tobago, for supporting this Publication.

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