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Implementation of a Modified AWaRe Guideline and Its Association with Antimicrobial Resistance Patterns in a Tertiary-Care Hospital

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Abstract

Objective

To evaluate the implementation of a modified AWaRe guideline and its association with antibiotic use and antimicrobial resistance patterns in a tertiary-care hospital.

Methods

A retrospective comparative study was conducted. A modified AWaRe guideline, adapted according to previously reported antimicrobial resistance patterns, was implemented. To assess its association with antimicrobial resistance, microbiological culture and antimicrobial susceptibility test results recorded before implementation were reviewed and compared with those obtained after implementation. Statistical analysis was performed using the chi-square test to identify significant differences between both periods.

Results

The number of bacterial isolates was higher in 2022 than in 2023. Regarding microorganisms' prevalence, the most frequently identified bacterial species remained consistent across both years. Analysis of antimicrobial susceptibility profiles showed a reduction in resistance rates for most antimicrobial agents following implementation of the modified AWaRe guideline.

Conclusions

Implementation of the modified AWaRe guideline was associated with changes in antimicrobial susceptibility patterns and a trend toward lower levels of antimicrobial resistance.

Introduction

Antimicrobial resistance (AMR) represents an immediate global health threat that requires urgent and coordinated action. Although resistance has been documented since the discovery of penicillin in 1928, the inappropriate and excessive use of antibiotics has accelerated the emergence and spread of resistant microorganisms, progressively limiting available treatment options. Antibiotic-resistant infections are currently associated with a substantial burden of morbidity and mortality worldwide (1). This phenomenon has been driven by multiple factors, including the indiscriminate use of antibiotics, inappropriate prescribing and dispensing practices, and the extensive use of antimicrobial agents outside healthcare settings, particularly in agriculture and animal production (2). Furthermore, the interconnected nature of human, animal and environmental health facilitates the dissemination of bacterial communities, resistant clones, mobile genetic elements, and resistance genes across different settings, contributing to the global spread of AMR (3).

Despite the prominent position of AMR on the international public health agenda, the implementation of effective control strategies remains uneven across countries. Significant disparities in resources, infrastructure, and surveillance capacities persist, particularly in low- and middle-income settings. In addition, global coordination among governments, healthcare systems, industries, and international organizations remains fragmented. Addressing AMR requires sustained investments in research, surveillance systems,

healthcare infrastructure, and the development of innovative approaches to optimize antimicrobial use. Overcoming existing human and structural barriers will require coordinated efforts, public policies, financial incentives, and the adoption of evidence-based interventions (4).

A comprehensive understanding of bacterial susceptibility and resistance patterns is essential for guiding clinical decision-making and informing antimicrobial stewardship strategies. Particular attention has been directed toward the ESKAPE pathogens, which include *Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa*, and *Enterobacter* species. These microorganisms are recognized for their ability to evade the activity of multiple antimicrobial agents, representing a major challenge for infection control and clinical management because of their high levels of resistance and association with healthcare-associated infections (5–7).

Despite growing awareness of the consequences of antibiotic misuse, antimicrobial consumption remains excessive in many regions of the world, where antibiotics may still be obtained without medical prescription or through inappropriate distribution channels (8). Inappropriate prescribing practices continue to contribute substantially to the selection and dissemination of resistant microorganisms. To address this challenge, the World Health Organization (WHO) has promoted multiple strategies aimed at improving antimicrobial use, including antimicrobial stewardship programs (ASPs), which seek to optimize prescribing practices through educational and restrictive interventions. These programs have demonstrated their ability to reduce inappropriate antimicrobial use, lower healthcare costs, and contribute to reductions in antimicrobial resistance (9,10).

Antimicrobial stewardship programs are coordinated multidisciplinary interventions designed to promote the appropriate use of antimicrobial agents, improve patient outcomes, reduce the emergence of resistance, and limit the spread of multidrug-resistant organisms. Common strategies include prescriber education, antimicrobial restriction policies, optimization of dosing regimens, antibiotic cycling, combination therapies, and conversion from parenteral to oral therapy when clinically appropriate (11,12). Continuous evaluation of these programs is essential to assess their effectiveness and guide future interventions. Evidence from healthcare institutions in Latin America has demonstrated the potential benefits of stewardship initiatives in reducing antimicrobial consumption and improving prescribing practices (13).

To further support the rational use of antibiotics, the WHO developed the Access, Watch, and Reserve (AWaRe) classification, a tool designed to promote appropriate antimicrobial prescribing and help contain the progression of antimicrobial resistance. The AWaRe framework categorizes antibiotics into three groups according to their spectrum of activity, resistance potential, and recommended use: Access, Watch, and Reserve. This classification provides guidance regarding first-line treatments, antibiotics requiring careful monitoring, and agents that should be reserved for specific situations such as last-resort therapies (14).

In the present study, the AWaRe framework was modified according to previously reported local antimicrobial resistance patterns within the hospital (2). This study aimed to evaluate the implementation of a modified AWaRe guideline and its association with antimicrobial resistance patterns in a tertiary-care hospital.

Materials and Methods

A retrospective comparative study was conducted at a tertiary-care hospital in Chihuahua, Mexico. During 2023, a modified AWaRe guideline was implemented as part of an antimicrobial stewardship initiative. The guideline was adapted according to previously reported antimicrobial resistance patterns within the institution and the antibiotics available in the hospital formulary (2).

The modified AWaRe tool classified antibiotics using a color-coded system based on their reported susceptibility profiles. Antibiotics with the lowest levels of resistance were categorized as green (susceptible), those with intermediate resistance levels were categorized as yellow (intermediate susceptibility), and those with the highest resistance levels were categorized as red (non-susceptible). The modified AWaRe classification and the corresponding susceptibility and resistance profiles observed during 2022 and 2023 are presented in Table 4. Modified AWaRe Guideline and Antimicrobial Susceptibility Profiles Reported During 2022 and 2023.

Table 4
Modified AWaRe Guideline and Antimicrobial Susceptibility Profiles Reported During 2022 and 2023

Group	Antibiotic	2022 Profile		2023 Profile	
		Susceptibility (%)	Resistance (%)	Susceptibility (%)	Resistance (%)
Access	Clindamycin	79	21	79	21
	Trimethoprim/Sulfamethoxazole	83	17	83	17
	Trimethoprim/Sulfamethoxazole	85	15	85	15
	Amikacin	86	14	86	14
	Nitrofurantoin	95	5	95	5
	Gentamicin	80	20	80	20
	Metronidazole	87	13	87	13
Watch	Vancomycin	93	7	93	7
	Levofloxacin	87	13	87	13
	Daptomycin	94	6	94	6
	Ceftriaxone	93	7	93	7
	Ceftazidime	76	24	76	24
	Ciprofloxacin	79	21	79	21
	Meropenem	87	13	87	13
	Imipenem	86	14	86	14
	Azithromycin	80	20	80	20
Reserve	Linezolid	94	6	94	6
	Fosfomycin	85	15	85	15
	Tigecycline	86	14	86	14
	Colistin	90	10	90	10

To evaluate the implementation of the modified AWaRe guideline, antimicrobial susceptibility test results from two periods were compared. The pre-implementation period included antibiograms reported from January to December 2022, whereas the post-implementation period included antibiograms reported from January to October 2023.

The study included hospitalized patients of either sex with documented infections affecting any organ system and with complete culture and antimicrobial susceptibility testing results. Patients treated exclusively in outpatient settings, those with incomplete medical records, hospital readmissions, and cultures or antimicrobial susceptibility test results older than one month were excluded.

Bacterial identification and antimicrobial susceptibility testing were performed using the automated BD Phoenix system according to the institution's laboratory procedures and the standards established by the Clinical and Laboratory Standards Institute (CLSI). Susceptibility interpretations were based on minimum inhibitory concentration values or inhibition zone diameters used to classify isolates as susceptible, intermediate, or resistant according to bacterial growth in the presence of the antimicrobial agent under evaluation (15).

A total of 1,126 bacterial isolates were included in the analysis. Descriptive statistics and univariate analysis were performed to characterize the frequency of isolated microorganisms and their antimicrobial susceptibility profiles. Resistance and susceptibility rates were determined by cross-referencing antimicrobial susceptibility data with the corresponding antibiogram results. Comparisons between the pre-implementation (2022) and post-implementation (2023) periods were performed using the chi-square test. Statistical analyses were conducted using IBM SPSS Statistics software (IBM Corp., Armonk, NY, USA).

Results

A total of 1,126 microorganisms were reported during the study period. Of these, 568 isolates (50.44%) were identified during 2022, prior to implementation of the modified AWaRe guideline, whereas 558 isolates (49.56%) were identified during 2023 following its implementation.

Regarding microorganism prevalence, similar distributions were observed across both study periods. Among Gram-negative bacteria, the most frequently isolated organisms were *Escherichia coli* (124 isolates in 2022 and 137 in 2023), *Klebsiella pneumoniae* (72 and 50 isolates, respectively), and *Pseudomonas aeruginosa* (47 and 44 isolates, respectively). Among Gram-positive bacteria, *Staphylococcus epidermidis* remained the most prevalent species in both years (54 isolates each year), followed by *Staphylococcus aureus* (46 isolates in 2022 and 41 in 2023) and *Enterococcus faecalis* (37 and 32 isolates, respectively). A marked reduction was observed in *Acinetobacter baumannii* isolates, decreasing from 31 isolates (5.5%) in 2022 to 7 isolates (1.25%) in 2023. In contrast, *Candida albicans* increased from 3 isolates (0.5%) in 2022 to 39 isolates (6.99%) in 2023. The complete distribution of microorganisms is presented in Table 1. Distribution of Microorganisms Isolated Before (2022) and After (2023) Implementation of the Modified AWaRe Guideline.

Table 1
Distribution of Microorganisms Isolated Before (2022) and After (2023) Implementation of the Modified AWaRe Guideline

Microorganism	**2022**		**2023**	
	#	**%**	**#**	**%**
Gram-Negative				
Acinetobacter baumannii	31	5.5%	7	1.25%
Achromobacter xylosoxidans ss. Denitrificans	0	0.0%	2	0.36%
Aeromonas hydrophila	0	0.0%	3	0.54%
Acinetobacter haemolyticus	0	0.0%	1	0.18%
Aeromonas salmonicida	1	0.2%	1	0.18%
Acinetobacter ursingii	0	0.0%	2	0.36%
Achromobacter xylosoxidans ss. Xylosoxidans	0	0.0%	1	0.18%
Brucella melitensis	1	0.2%	0	0.00%
Burkholderia cepacia	1	0.2%	0	0.00%
Brevundimonas diminuta	0	0.0%	2	0.36%
Citrobacter braakii	0	0.0%	1	0.18%
Citrobacter sedlakii	2	0.4%	0	0.00%
Citrobacter koseri	3	0.5%	0	0.00%
Citrobacter freundii	2	0.4%	5	0.90%
Chryseomonas luteola	2	0.4%	0	0.00%
Enterobacter cloacae	14	2.5%	8	1.43%
Escherichia coli	**124**	**21.8%**	**137**	**24.55%**
Escherichia fergusonii	1	0.2%	0	0.00%
Klebsiella aerogenes	6	1.1%	3	0.54%
Klebsiella oxytoca	3	0.5%	3	0.54%
Klebsiella pneumoniae ss. Pneumoniae	**72**	**12.7%**	**50**	**8.96%**
Morganella morganii ss. Morganii	7	1.2%	3	0.54%
Pantoea sp.	1	0.2%	1	0.18%
Pantoea agglomerans	2	0.4%	0	0.00%
Proteus mirabilis	11	1.9%	11	1.97%
Proteus vulgaris	1	0.2%	0	0.00%

Microorganism	2022		2023	
	#	%	#	%
Gram-Negative				
Providencia stuartii	0	0.0%	1	0.18%
Providencia rettgeri	2	0.4%	0	0.00%
Pseudomonas aeruginosa	**47**	**8.3%**	**44**	**7.89%**
Pseudomonas fluorescens	1	0.2%	0	0.00%
Raoultella planticola	2	0.4%	0	0.00%
Salmonella sp.	2	0.4%	0	0.00%
Serratia fonticola	0	0.0%	2	0.36%
Serratia liquefaciens	0	0.0%	1	0.18%
Serratia marcescens	10	1.8%	5	0.90%
Sphingomonas paucimobilis	2	0.4%	1	0.18%
Yersinia enterocolitica	1	0.2%	0	0.00%
Gram-Positive				
Globicatella sanguinis	2	0.4%	0	0.00%
Enterococcus faecalis	**37**	**6.5%**	**32**	**5.73%**
Enterococcus faecium	3	0.5%	12	2.15%
Enterococcus gallinarum	0	0.0%	1	0.18%
Kocuria sp.	1	0.2%	0	0.00%
Kocuria kristinae	3	0.5%	1	0.18%
Kocuria rosea	1	0.2%	0	0.00%
Kocuria varians	1	0.2%	0	0.00%
Listeria monocytogenes	1	0.2%	0	0.00%
Micrococcus luteus	1	0.2%	1	0.18%
Pediococcus pentosaceus	0	0.0%	1	0.18%
Staphylococcus aureus ss. Aureus	**46**	**8.1%**	**41**	**7.35%**
Staphylococcus auricularis	1	0.2%	0	0.00%
Staphylococcus capitis ss. Capitis	2	0.4%	0	0.00%
Staphylococcus epidermidis	**54**	**9.5%**	**54**	**9.68%**

Microorganism	2022		2023	
	#	%	#	%
Gram-Negative				
Staphylococcus haemolyticus	9	1.6%	4	0.72%
Staphylococcus hominis ss. Hominis	9	1.6%	6	1.08%
Staphylococcus lugdunensis	1	0.2%	3	0.54%
Staphylococcus pseudintermedius	0	0.0%	1	0.18%
Staphylococcus saprophyticus ss. Saprophyticus	1	0.2%	0	0.00%
Staphylococcus sciuri ss. Lentus	5	0.9%	2	0.36%
Staphylococcus sciuri ss. Sciuri	1	0.2%	0	0.00%
Staphylococcus warneri	1	0.2%	0	0.00%
Stenotrophomonas maltophilia	9	1.6%	8	1.43%
Streptococcus sp	0	0.0%	1	0.18%
Streptococcus anginosus	1	0.2%	0	0.00%
Streptococcus agalactiae	16	2.8%	14	2.51%
Streptococcus constellatus	1	0.2%	0	0.00%
Streptococcus dysgalactiae ss. Equisimilis	0	0.0%	2	0.36%
Streptococcus intermedius	0	0.0%	1	0.18%
Streptococcus mitis	1	0.2%	3	0.54%
Streptococcus parasanguinis	0	0.0%	1	0.18%
Streptococcus pneumoniae	0	0.0%	2	0.36%
Streptococcus pyogenes	0	0.0%	4	0.72%
Streptococcus sanguinis	0	0.0%	1	0.18%
Streptococcus salivarius	1	0.2%	0	0.00%
Streptococcus suis	0	0.0%	1	0.18%
Streptococcus thoraltensis	1	0.2%	1	0.18%
Yeasts				
Candida albicans	3	0.5%	39	6.99%
Candida glabrata	2	0.4%	12	2.15%
Candida parapsilosis	0	0.0%	2	0.36%

Microorganism	2022		2023	
	#	%	#	%
Gram-Negative				
Candida tropicalis	1	0.2%	3	0.54%
Debaryomyces hansenii	0	0.0%	1	0.18%
Trichomonascus ciferrii	0	0.0%	5	0.90%
Pichia kudriavzevii	0	0.0%	2	0.36%
Yarrowia lipolytica	0	0.0%	1	0.18%
Total	568		558	

Analysis of antimicrobial susceptibility profiles showed that erythromycin (60.7%), clindamycin (58.5%), and oxacillin (57.7%) exhibited the highest resistance rates during 2022. Conversely, gentamicin high-level and high-level erythromycin demonstrated susceptibility rates of 100%, followed by ertapenem (97.3%) and amikacin (92.3%). Detailed resistance, intermediate susceptibility, and susceptibility rates for all evaluated antimicrobial agents are presented in Table 2. Antimicrobial Susceptibility and Resistance Profiles Reported During 2022 and 2023.

Table 2
Antimicrobial Susceptibility and Resistance Profiles Reported During 2022 and 2023*

Antibiotic	**2022**				**2023**			
	#	**%R**	**%I**	**%S**	**#**	**%R**	**%I**	**%S**
Amikacin	311	5.5	2.3	92	281	5.3	2.1	92.5
Ampicillin	277	56	6.1	38	249	47.4	4.0	48.6
Ampicillin/Sulbactam	255	40	0	60	214	32.2	0.0	67.8
Cephalothin	342	0	0	0	289	0.0	0.0	0.0
Cefepime	341	15	2.9	82	289	7.3	4.8	87.9
Cefotaxime	342	47	1.5	52	271	40.6	0.4	59.0
Ceftazidime	342	23	4.4	73	287	16.0	3.5	80.5
Ceftriaxone	342	48	0.6	52	287	39.0	1.0	59.9
Cefuroxime	342	52	4.1	44	273	44.0	5.5	50.5
Ciprofloxacin	504	37	4.6	58	440	34.5	6.6	58.9
Ertapenem	261	2.7	0	97	231	2.6	0.4	97.0
Fosfomycin	342	7	2	67	288	3.8	1.0	74.3
Gentamicin	466	25	2.8	72	395	21.3	3.0	75.7
Meropenem	342	13	2.6	85	284	4.9	3.5	91.5
Nitrofurantoin	437	14	14	73	394	8.4	13.2	78.4
Norfloxacin	311	26	2.9	70	277	26.7	3.2	70.0
Clindamycin	118	59	0.8	41	110	59.1	0.9	40.0
Daptomycin	161	1.2	3.7	85	142	0.0	4.9	95.1
Doxycycline	165	6.7	15	78	155	8.4	12.9	78.7
Erythromycin	163	61	8	31	155	49.0	21.9	29.0
High-Level Gentamicin	39	0	0	100	45	0.0	0.0	100.0
Levofloxacin	177	31	0.6	68	169	29.6	3.0	67.5
Linezolid	177	14	0.6	86	169	1.8	1.2	97.0
Moxifloxacin	137	23	15	51	124	29.8	7.3	51.6
Oxacillin	123	58	0	42	110	60.0	0.0	40.0
Rifampin	123	11	0	89	110	4.5	0.0	95.5
High-Level Streptomycin	39	0	0	100	45	0.0	0.0	100.0

Antibiotic	2022				2023			
	#	%R	%I	%S	#	%R	%I	%S
Tetracycline	177	35	1.7	64	169	32.0	1.2	66.9
Tigecycline	179	0	0	0	167	0.0	0.0	0.0
Vancomicina	173	9.8	2.3	88	166	0.6	0.6	98.8
Trimethoprim/Sulfamethoxazole	1	0	0	100	358	37.7	0.0	62.3
*2022 (pre-ASP implementation) and 2023 (post-ASP implementation). R, resistant; I, intermediate; S, susceptible.								

Comparisons between the pre-implementation and post-implementation periods were performed using the chi-square test. Within the Access group, nitrofurantoin demonstrated a statistically significant difference between periods ($\chi^2 = 5.529$, $p = 0.0187$). Within the Watch group, significant differences were observed for ceftazidime ($\chi^2 = 4.531$, $p = 0.0332$), ceftriaxone ($\chi^2 = 4.730$, $p = 0.0296$), and meropenem ($\chi^2 = 10.953$, $p = 0.0009$). Within the Reserve group, linezolid demonstrated a significant difference between periods ($\chi^2 = 16.687$, $p < 0.001$). Additional significant differences were identified for ampicillin ($\chi^2 = 4.188$, $p = 0.0407$), cefepime ($\chi^2 = 8.558$, $p = 0.0034$), cefuroxime ($\chi^2 = 3.979$, $p = 0.0162$), and erythromycin ($\chi^2 = 5.383$, $p = 0.0203$). Results for all evaluated antimicrobial agents are shown in Table 3. Comparison of Antimicrobial Resistance Profiles Between the Pre-Implementation (2022) and post-implementation (2023) Periods.

Table 3
Comparison of Antimicrobial Resistance Profiles Between the Pre-Implementation (2022) and post-implementation (2023) Periods

Antibiotic	**2022**	**2023**	**Chi2**	***p***
Access Group				
Amikacin	17	15	0.0005	0.9451
Clindamycin	69	65	0.009	0.9247
Gentamicin	118	84	1.959	0.1616
Nitrofurantoin	**59**	**33**	**5.529**	**0.0187**
Rifampin	13	5	2.956	0.085
Watch Group				
Ceftazidime	**78**	**46**	**4.531**	**0.0332**
Ceftriaxone	**163**	**112**	**4.73**	**0.0296**
Ciprofloxacin	187	152	0.668	0.4138
Daptomycin	2	0	1.776	0.1827
Ertapenem	7	6	0.003	0.9534
Meropenem	**43**	**14**	**10.953**	**0.0009**
Moxifloxacin	32	37	1.406	0.2358
Reserve Group				
Fosfomycin	24	11	3.048	0.0808
Linezolid	**24**	**3**	**16.687**	**0**
Others				
Ampicillin	**156**	**118**	**4.188**	**0.0407**
Ampicillin/Sulbactam	102	69	3.022	0.0821
Cefepime	**50**	**21**	**8.558**	**0.0034**
Cefotaxime	159	110	2.138	0.1437
Cefuroxime	**178**	**120**	**3.979**	**0.0162**
Doxycycline	11	13	0.341	0.5593
Erythromycin	**101**	**76**	**5.383**	**0.0203**
Levofloxacin	55	50	0.091	0.7635
Norfloxacin	81	74	0.034	0.854

Antibiotic	2022	2023	Chi2	*p*
Access Group				
Oxacillin	71	66	0.124	0.7245

When antimicrobial agents were analyzed according to the modified AWaRe classification, antibiotics included in the Access group exhibited susceptibility rates ranging from 79% to 95%, whereas resistance rates ranged from 5% to 21%. Within the Watch group, vancomycin, daptomycin, and ceftriaxone demonstrated the highest susceptibility rates and the lowest resistance rates. Similarly, antibiotics included in the Reserve group maintained high susceptibility profiles, particularly linezolid, tigecycline, and colistin, which exhibited susceptibility rates ranging from 86% to 94%. Detailed results are presented in Table 4. Modified AWaRe Guideline and Antimicrobial Susceptibility Profiles Reported During 2022 and 2023.

Analysis of ESKAPE pathogens did not reveal statistically significant differences in isolation frequency between 2022 and 2023 according to the corresponding chi-square tests (Table 5. Chi-Square Analysis of ESKAPE Pathogens Reported in 2022 and 2023). Evaluation of antimicrobial susceptibility profiles among these pathogens showed distinct resistance patterns. *Escherichia coli* exhibited high resistance to ampicillin (70%), whereas susceptibility remained high for amikacin (90%) and nitrofurantoin (95%). *Staphylococcus aureus* demonstrated considerable resistance to oxacillin (60%), while maintaining high susceptibility to linezolid (95%) and daptomycin (99%). *Klebsiella pneumoniae* showed elevated resistance to ampicillin (80%) but retained high susceptibility to carbapenems. *Acinetobacter baumannii* exhibited resistance rates of 25–30% against carbapenems, while maintaining susceptibility to tigecycline and colistin. *Pseudomonas aeruginosa* demonstrated notable resistance to ceftazidime (40%), whereas *Enterococcus faecium* maintained susceptibility rates above 80% for all evaluated antimicrobials. Detailed susceptibility profiles are presented in Table 6. Panel of antibiotics reported in ESPAKE group bacteria during 2022 and 2023.

Table 5
Chi-Square Analysis of ESKAPE Pathogens Reported in 2022 and 2023

Bacteria	2022	2023	Chi2	*p*
E. Coli	124	137	0.009	1
S. Aureus	46	41	0.038	1
K. Pneumoniae	72	50	0.004	1
A. Baumannii	31	7	1.12	0.8911
E. Faecium	3	12	0	1
P. Aeuriginosa	47	44	0.007	1

Table 6
Panel of antibiotics reported in ESPAKE group bacteria during 2022 and 2023

Bacteria	Antibiotic	2022	2023
Escherichia coli	Ampicillin	30% S, 70% R	30% S, 70% R
	Ceftazidime	80% S, 20% R	80% S, 20% R
	Ciprofloxacin	70% S, 30% R	70% S, 30% R
	Amikacin	90% S, 10% R	90% S, 10% R
	Nitrofurantoin	95% S, 5% R	95% S, 5% R
	Fosfomycin	85% S, 15% R	85% S, 15% R
Staphylococcus aureus	Vancomycin	90% S, 10% R	90% S, 10% R
	Oxacillin	40% S, 60% R	40% S, 60% R
	Clindamycin	70% S, 30% R	70% S, 30% R
	Levofloxacin	80% S, 20% R	80% S, 20% R
	Trimethoprim/Sulfamethoxazole	80% S, 20% R	80% S, 20% R
	Linezolid	95% S, 5% R	95% S, 5% R
	Daptomycin	99% S, 1% R	99% S, 1% R
Klebsiella pneumoniae	Ampicillin	20% S, 80% R	20% S, 80% R
	Ceftazidime	70% S, 30% R	70% S, 30% R
	Ciprofloxacin	60% S, 40% R	60% S, 40% R
	Amikacin	80% S, 20% R	80% S, 20% R
	Meropenem	90% S, 10% R	90% S, 10% R
	Imipenem	95% S, 5% R	95% S, 5% R
Acinetobacter baumannii	Imipenem	70% S, 30% R	70% S, 30% R
	Meropenem	75% S, 25% R	75% S, 25% R
	Amikacin	80% S, 20% R	80% S, 20% R
	Tigecycline	85% S, 15% R	85% S, 15% R
	Colistin	90% S, 10% R	90% S, 10% R
Pseudomonas aeruginosa	Piperacillin-Tazobactam	70% S, 30% R	70% S, 30% R
	Ceftazidime	60% S, 40% R	60% S, 40% R
	Ciprofloxacin	75% S, 25% R	75% S, 25% R
	Amikacin	85% S, 15% R	85% S, 15% R

Bacteria	Antibiotic	2022	2023
	Gentamicin	80% S, 20% R	80% S, 20% R
	Tobramicin	80% S, 20% R	80% S, 20% R
Enterococcus faecium	Ampicillin	80% S, 20% R	80% S, 20% R
	Vancomycin	85% S, 15% R	85% S, 15% R
	Linezolid	90% S, 10% R	90% S, 10% R
	Daptomycin	85% S, 15% R	85% S, 15% R
	Quinupristin-Dalfopristin	90% S, 10% R	90% S, 10% R

Discussion

Antimicrobial resistance continues to represent a major challenge for healthcare systems worldwide. Since the relationship between inappropriate antibiotic use and the emergence of bacterial resistance was recognized, multiple antimicrobial stewardship strategies have been developed to promote the rational use of antibiotics and preserve their effectiveness (9,16).

Among these initiatives, the World Health Organization introduced the Access, Watch, and Reserve (AWaRe) classification as a practical tool to support antimicrobial stewardship programs and monitor antibiotic use patterns (14,17). In the present study, the AWaRe framework was adapted according to local resistance patterns and implemented as part of an institutional antimicrobial stewardship strategy.

The results demonstrated a slight reduction in the total number of isolates reported during 2023 compared with 2022. Despite this difference, the most prevalent microorganisms remained largely unchanged between both periods. *Escherichia coli, Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* continued to be the predominant Gram-negative pathogens, whereas *Staphylococcus epidermidis, Staphylococcus aureus*, and *Enterococcus faecalis* remained the most frequently isolated Gram-positive microorganisms. These findings are consistent with previous reports describing these organisms among the most common causes of healthcare-associated infections and antimicrobial resistance worldwide (5,6).

Analysis of antimicrobial susceptibility profiles revealed differences between the two study periods. Erythromycin, clindamycin, and oxacillin exhibited the highest resistance rates, whereas amikacin, ertapenem, and high-level gentamicin maintained high susceptibility rates. Several antibiotics demonstrated statistically significant differences between periods, including nitrofurantoin, ceftazidime, ceftriaxone, meropenem, linezolid, ampicillin, cefepime, cefuroxime, and erythromycin. These findings suggest changes in antimicrobial susceptibility patterns over time and highlight the importance of continuous surveillance of resistance trends within healthcare institutions (4,18).

When antibiotics were evaluated according to the modified AWaRe classification, agents included in the Access group maintained high susceptibility rates and relatively low resistance levels. Similarly, antibiotics classified within the Watch and Reserve groups generally preserved favorable susceptibility profiles, particularly vancomycin, daptomycin, ceftriaxone, linezolid, tigecycline, and colistin. These findings support

the value of periodic monitoring of susceptibility profiles to guide antimicrobial stewardship activities and optimize antibiotic selection (10,19).

Evaluation of ESKAPE pathogens revealed stable susceptibility profiles between study periods, with no statistically significant differences in isolation frequency. However, important resistance patterns persisted among specific organisms. *Escherichia coli* and *Klebsiella pneumoniae* exhibited high resistance rates to ampicillin, *Staphylococcus aureus* demonstrated substantial resistance to oxacillin, and Acinetobacter baumannii maintained resistance to carbapenems. These findings are consistent with previous reports describing ESKAPE pathogens as major contributors to antimicrobial resistance in healthcare settings (5,6).

The findings of this study emphasize the importance of maintaining antimicrobial stewardship programs and continuous microbiological surveillance within hospitals. Periodic evaluation of resistance patterns may facilitate evidence-based decision-making and support local strategies aimed at optimizing antimicrobial use. Given the dynamic nature of antimicrobial resistance, ongoing monitoring remains essential to identify changes in susceptibility profiles and to guide future stewardship interventions (20–23).

This study has some limitations. The analysis was conducted in a single tertiary-care hospital and was based on retrospective microbiological records from two time periods. Therefore, the findings should be interpreted within the context of the study setting and may not be generalizable to other institutions. Nevertheless, the results provide valuable information regarding local resistance patterns and the implementation of a modified AWaRe-based stewardship strategy.

Conclusions

The implementation of a modified AWaRe guideline was associated with changes in antimicrobial susceptibility patterns observed between the pre-implementation and post-implementation periods. Although the most prevalent microorganisms remained largely consistent across both years, statistically significant differences were identified for several antimicrobial agents, highlighting the dynamic nature of antimicrobial resistance within the hospital setting.

The findings suggest that local adaptation of the AWaRe classification according to institutional resistance patterns may provide a useful framework for monitoring antimicrobial susceptibility profiles and supporting antimicrobial stewardship activities. In addition, the persistence of resistance among specific pathogens and antimicrobial agents underscores the need for continuous microbiological surveillance and periodic review of treatment guidelines.

Given the growing global burden of antimicrobial resistance, the integration of stewardship strategies and resistance monitoring tools may support evidence-based decision-making and contribute to the optimization of antimicrobial use in tertiary-care hospitals. Continued evaluation of resistance trends remains essential to guide future interventions and preserve the effectiveness of currently available antimicrobial agents.

Declarations

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Authors' Contributions

- Luis A Camacho-Silvas: Conceptualization, methodology, data collection, formal analysis, interpretation of results, and manuscript writing.
- Jorge H Portillo-Gallo: Supervision, methodology, interpretation of results, and critical review of the manuscript.
- María C Ishida-Gutiérrez: Manuscript writing, language editing, and critical review.
- Yazmin A Hernández-Acosta: Manuscript writing, language editing, and critical review.
- Jorge M Sánchez-González: Manuscript writing, language editing, and critical review.
- Antonio E Rivera-Cisneros: Manuscript writing, language editing, and critical review.
- Rafael Franco-Santillán: Manuscript writing, language editing, and critical review.

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Availability of Data and Materials

The datasets generated and/or analyzed during the current study are available from the corresponding author on reasonable request.

Ethics Approval and Consent to Participate

This study was based on retrospective analysis of microbiological records routinely generated during patient care. All data were anonymized prior to analysis, and no identifying patient information was collected. At hospital admission, patients provide informed consent authorizing the use of their clinical information in accordance with institutional policies regarding confidentiality and data management. The study was conducted in accordance with the ethical principles of the Declaration of Helsinki. The protocol was approved by the research committee of the Faculty of Medicine and Biomedical Sciences of the UACH, registration number CI-018-23.

Consent for Publication

Not applicable.

Clinical trial number

Not applicable.

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