DEPARTMENT OF HEALTH
RESEARCH INSTITUTE FOR TROPICAL MEDICINE
ANTIMICROBIAL RESISTANCE SURVEILLANCE PROGRAM

ANTIMICROBIAL RESISTANCE SURVEILLANCE PROGRAM ANNUAL REPORT 2023

Antimicrobial Resistance Surveillance Program

2023 Annual Report

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Preface

As the steadfast national AMR surveillance, the Antimicrobial Resistance Surveillance Program (ARSP), aims to provide relevant AMR information for action. The surveillance provides current AMR data and documents developing AMR trends among pathogens of public health importance.

The surveillance's long-time sentinel sites, which had been partners of ARSP for more than 3 decades, ensure the performance of standard laboratory and data management methods in their respective hospitals and have actively contributed data to the surveillance. The Antimicrobial Resistance Surveillance Reference Laboratory (ARSRL), in turn serves as the national coordinating laboratory for ARSP, and implements quality assurance programs for both laboratory and data management processes. ARSRL, on behalf of ARSP, has likewise incorporated genomics into the surveillance and continuously implement trainings to strengthen capacities across the surveillance participants.

In the 2023 annual report, few changes in data presentation and reporting will be noted. The reader will note that the range of percent resistance in the graphs is visually illustrated by color to allow the readers to immediately spot the antibiotics with relatively low, intermediate or high resistance rates. Resistance analysis for additional subsets of isolates such as respiratory isolates and presumptive hospital acquired isolates for *Klebsiella pneumonia, Pseudomonas aeruginosa* and *Acinetobacter baumannii* were also included to provide insight on resistance profile of these isolates of interest. Further, when a notable increase in resistance rates may be due to changes in the breakpoints, a precaution in the interpretation of trend was indicated. Also included in this report is the monitoring of oxacillin resistance of *Staphylococcus aureus* isolates causing blood stream infections (BSI) as well as extended spectrum cephalosporins resistance of *Escherichia coli* isolates causing BSI as part of the monitoring of the AMR targets in the Sustainable Development Goals 3: Good Health and Well-being.

While there are no notable considerable increases in the resistance among most of the pathogens included in this surveillance, there are persistence of occurrence of isolates of emerging resistance phenotypes. There were confirmed reports of meropenem resistant *S. pneumonia* isolates, vancomycin- and linezolid resistant Staphylococcus aureus, and linezolid resistant Enterococcus faecalis (for validation). Among the gram-negative rods, colistin resistance was continuously observed. Although the surveillance is not as of yet able to provide estimate of resistance rates to the new generation combination antibiotics such as ceftazidime-avibactam and ceftolozane-tazobactam among gram-negative rods, the 2023 Annual Report mentions sporadic reports of occurrence of resistance among the gram-negative rods to ceftazidime-avibactam. Further, while wide confidence intervals of percentage resistance estimates are noted for isolates with fewer reported data such as for *Streptococcus pneumonia, Haemophilus influenze, Neisseria gonorrhoeae*, and the food- and water-borne pathogens, narrow confidence intervals of percentage resistance estimates are noted for the *Enterococcus sp*, *Staphylococcus aureus, E. coli, Klebsiella pneumonia, Pseudomonas aeruginosa* and *Acinetobacter baumannii*.

The continuing efforts to integrate genomics into ARSP is reflected in the 2023 ARSP Annual Report as genomic characterization of isolates with emerging resistance phenotypes. The genomic reports are included to provide insight in the potential for spread of the resistance phenotype within the hospital and inform possible infection and prevention control measures across the sentinel sites and possibly in all hospitals in the country. Such characterization may likewise provide information on possible treatment options against the respective pathogens.

Executive Summary

Resistance data for **117,398** bacterial isolates coming from 24 hospital based bacteriology laboratories and 1 gonococcal surveillance site were analyzed for 2023.

Streptococcus pneumoniae

Cumulative resistance rate of *S. pneumoniae* isolates against penicillin using non-meningitis breakpoint at 1.24% (n=223) remained low making this a viable antibiotic option for non-meningitis infections. A continued decrease in resistance to erythromycin was noted for the second consecutive year reversing the previous trend of increasing resistance to this antibiotic. Resistance to the alternative antibiotics are as follows: ceftriaxone (NM) 0.84%, ceftriaxone (M) 1.67%, clindamycin 6.22% and levofloxacin 0.89%. Compared with 2022, the overall resistance rates for *S. pneumoniae* decreased in 2023 for most antibiotics except for co-trimoxazole and meropenem.

Haemophilus influenzae

Resistance rate of *H. influenzae* for 2023 to ampicillin was at 14.48% which was significantly higher than the observed rate of 9.80% in 2022. These isolates remained mostly susceptible to ceftriaxone with non-susceptibility rate for 2023 being at 0.59%. Resistance to ampicillin/sulbactam and amoxicillin/clavulanic acid were 10.96% and 4.40%, respectively. Levofloxacin resistance was at 1.06% while no resistance to azithromycin was reported for 2022.

Salmonella enterica serotype Typhi

Salmonella Typhi isolates remained susceptible to ciprofloxacin, imipenem, and meropenem with no resistance detected against these antibiotics for 2023. Resistance to co-trimoxazole was at 14.63% while azithromycin resistance based mostly on disc diffusion testing was at 13.43%.

Nontyphoidal *Salmonella*

As in the past years, resistance of non-typhoidal *Salmonella* to ampicillin (29.25%), co-trimoxazole (17.97%) and azithromycin (31.71%) are higher compared to that of *Salmonella* Typhi. Resistance to ciprofloxacin remained within 10-12% range in the past seven years with 2023 resistance at 11.02%.

Shigella species

Resistance to ceftriaxone and ciprofloxacin for 2023 among *Shigella* were at 18.03% and 16.95% respectively. These two antibiotics both showed higher resistance rates as compared in their 2022 rates, however, these increases were not statistically significant. Co-trimoxazole and azithromycin resistance were at 55.74% and 6.45% respectively.

Vibrio cholerae

Resistance of *Vibrio cholerae* isolates to ampicillin at 16.67% this was significantly higher (p=0.0002) than the observed resistance rate to this antibiotic at 3.76%in 2022. Resistance to co-trimoxazole was 6.38%. No reported resistance to tetracycline and chloramphenicol for 2023.

Neisseria gonorrhoeae

There is no reported resistance to ceftriaxone, cefixime and azithromycin for 2023. Resistance to tetracycline and ciprofloxacin continues to be very high for 2022 at 71.43% (n=77) and 87.84% (n=74) respectively.

Staphylococcus aureus

There is a continued decrease of oxacillin resistance among *Staphylococcus aureus* to its present rate of 40.53% (n=6,682) in 2023. Erythromycin resistance was at 11.94% (n=7,451) and clindamycin 9.92% (n=7,350) with both rates appearing to be stable for the past years. Vancomycin resistance was noted to be at 2.01% (n=6,776) for 2023 and the increase in the resistance to vancomycin in the past decade was noted to be statistically significant (p=0.0069). All isolates tested against daptomycin were susceptible to this antibiotic.

Enterococcus species

Resistance of *Enterococcus faecalis* to penicillin and ampicillin were at 14.85% and 7.02% respectively. Vancomycin resistance increased in 2023 at 3.11%. There were 2 confirmed vancomycin-resistant isolates from urine specimens of 34-year old 64-year old patients from VSM. The isolates were both resistant to ciprofloxacin and tetracycline, but susceptible to ampicillin, daptomycin, linezolid, penicillin and gentamicin high-level. *Enterococcus faecium* continue to show higher antibiotic resistance with rates for vancomycin and nitrofurantoin being 25.54% and 44.01% respectively for 2023. The percent increase for linezolid (3.10%) in 2023 from the previous year was not statistically significant.

Escherichia coli

Carbapenem resistance among *E. coli* remained above 8% for meropenem and imipenem and above 7% for ertapenem for year 2023 with increase in rates over the past decade noted to be statistically significant. There were three confirmed colistin resistant *E. coli* isolates in 2023. Overall ESBL positivity rate among *E. coli* tested for ESBL production was 24.71%. MDR and possible XDR rates for *E.coli* were at 59.4% and 14.2% respectively for 2023.

Klebsiella pneumoniae

Carbapenem resistance among *K. pneumoniae* isolates continued to increase in 2023 with resistance rates for meropenem at 16.70% (n= 15,580), imipenem at 16.59% (n=15, 629) and ertapenem at 15.67% (n=14,427). When the subset of *K. pneumoniae* isolates from blood specimens were analysed, even higher carbapenem resistance rates were noted with meropenem resistance rate at 20.85% (n=1,544). The overall ESBL positivity rate among *K. pneumoniae* tested for ESBL production was 31.80%. MDR and possible XDR rates for *K. pneumoniae* were at 57.7% and 26.1% respectively for 2023.

Pseudomonas aeruginosa

For 2023, resistance to *Pseudomonas aeruginosa* isolates to ceftazidime and piperacillin/tazobactam were 17.23% and 23.53%. Carbapenem resistance was reported at 18.97% for imipenem and 15.12% for meropenem. Colistin resistance was at 4.32% (n= 2,917). MDR and possible XDR rates for *P. aeruginosa* were at 28.3% and 18.2% respectively for 2023.

Acinetobacter baumannii

For 2023, resistance to most antibiotics remained above 50%. There were significant decrease in rates for ceftazidime, meropenem, imipenem, co-trimoxazole, ceftriaxone and amikacin. There was an overall decrease in resistance rate seen for colistin (p=0.0000) and overall increase for piperacillin-tazobactam (p=0.0000), co-trimoxazole (p=0.0000) imipenem (p=0.0039), meropenem (p=0.2396) and amikacin (p=0.0001).

Introduction

Antimicrobial Resistance (AMR) is the change that occurs over time among bacteria, viruses, fungi and parasites where these organisms no longer respond to medicines making infections harder to treat and increasing the risk of disease spread, severe illness and death[1]. *AMR is a serious public health threat* because of its far reaching and serious implications in health care as well as economies. AMR hampers the control of infectious diseases because patients remain infectious for a longer time increasing the risk of spreading resistant microorganisms to others. AMR increases the cost of health care as more expensive therapies must be used when infections become resistant to first-line medicines. Infections due to resistant microorganisms increases economic burden to families and societies as it often results in longer duration of illness and treatment.

With the loss of antimicrobials to resistance, the achievements of modern medicine such as organ transplant, cancer chemotherapy and major surgery would be compromised as these would not be possible without effective antimicrobials for prevention and treatment of infections. Losing antimicrobials to resistance can result in many infectious diseases becoming untreatable and uncontrollable. This can bring us back to the pre-antibiotic era.

The Philippine Committee on Antimicrobial Resistance Surveillance Program was created in 1988 through the Department of Health's Department Order 339-J. The program aims to provide critical inputs to the Department of Health's effort to promote rational drug use by determining the status and developing trends of antimicrobial resistance of selected bacteria to specific antimicrobials.

AMR surveillance remains an essential component in the control of AMR in the country. Surveillance data enable correct decisions to be made about treatment options and guide policy recommendations. The Philippine National Action Plan on Antimicrobial Resistance 2019-2023 [2] reiterates the importance of surveillance as it identifies the strengthening of surveillance and laboratory capacity as among its key strategy.

The culture and susceptibility reports submitted into the program was noted to have increased by more than 33% compared with the reports submitted in 2022. This difference must be kept in mind in the interpretation of the surveillance data in the past two years.

SURVEILLANCE, TESTING METHODS, DATA ANALYSIS & LIMITATIONS

The Surveillance

The DOH-ARSP is a sentinel laboratory-based antimicrobial resistance surveillance on aerobic bacteria from clinical specimens.

Currently participating in the program are 24 sentinel sites, and 2 gonococcal surveillance sites, representing 16 out of the 17 regions of the country (**Figure 1** & **Table 1**).

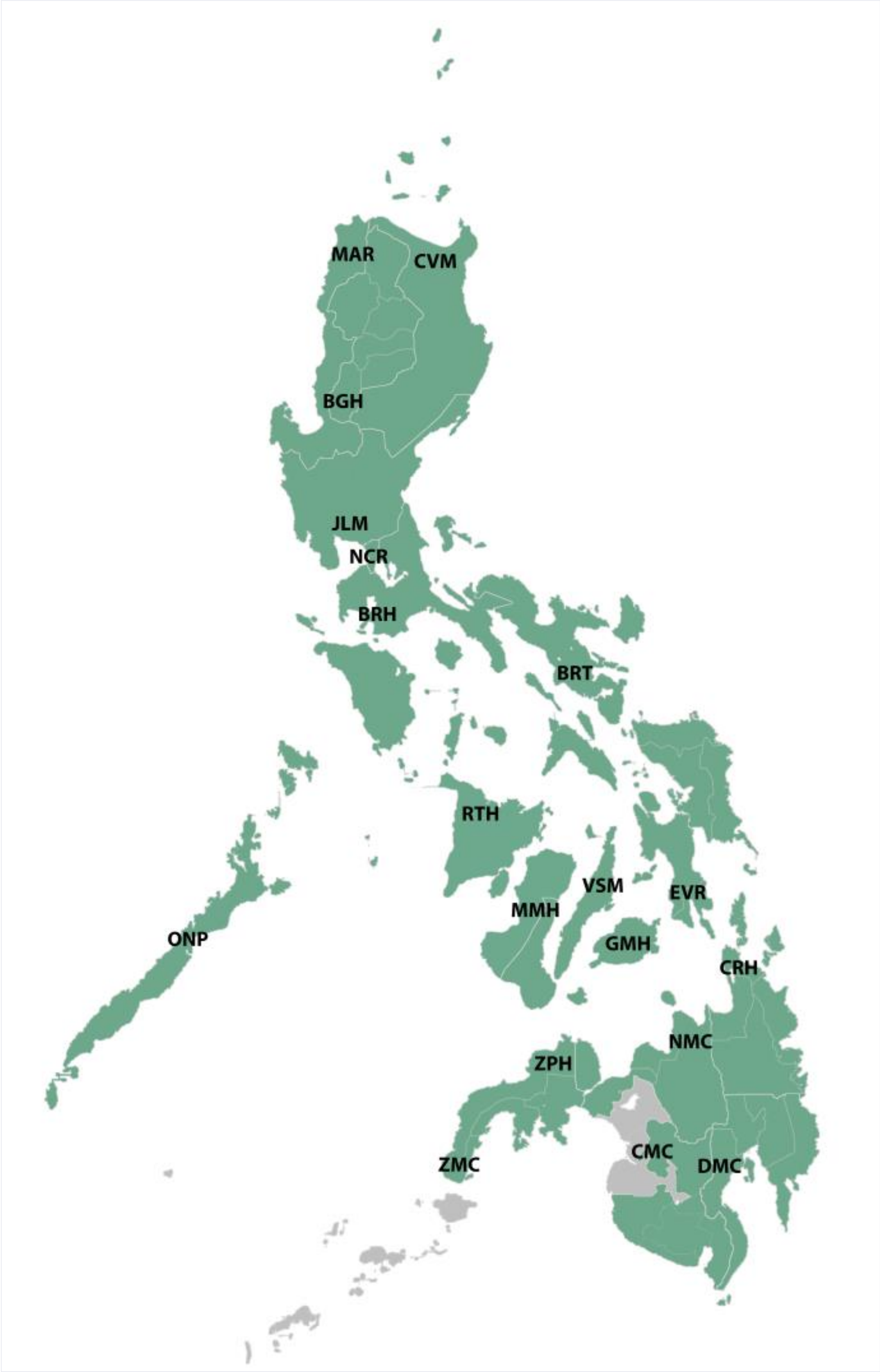

Figure 1. Regional representation in the ARSP 2023

Table 1. ARSP 2022 sentinel sites by region

Region	Sentinel Site
National Capital Region (NCR)	Lung Center of the Philippines National Kidney and Transplant Institute Rizal Medical Center San Lazaro Hospital Philippine General Hospital Research Institute for Tropical Medicine University of Santo Tomas Hospital Far Eastern University Nicanor Reyes Medical Foundation Medical Center
Cordillera Administrative Region (CAR)	Baguio General Hospital and Medical Center
Region 1—Ilocos Region	Mariano Marcos Memorial Hospital and Medical Center
Region 2—Cagayan Valley	Cagayan Valley Medical Center
Region 3—Central Luzon	Jose B. Lingad Memorial Regional Hospital
Region 4-A—CALABARZON	Batangas Medical Center
Region 4-B—MIMAROPA	Ospital ng Palawan
Region 5—Bicol Region	Bicol Regional Training and Teaching Hospital
Region 6—Western Visayas	Corazon Locsin Montelibano Memorial Regional Hospital Dr. Rafael S. Tumbokon Memorial Hospital
Region 7—Central Visayas	Celestino Gallares Memorial Hospital Vicente Sotto Memorial Medical Center
Region 8—Eastern Visayas	Eastern Visayas Regional Medical Center
Region 9—Zamboanga Peninsula	Zamboanga City Medical Center Zamboanga del Norte Medical Center
Region 10—Northern Mindanao	Northern Mindanao Medical Center
Region 11—Davao Region	Southern Philippines Medical Center
Region 12—SOCCSKSARGEN	Cotabato Regional Hospital and Medical Center
Region 13—CARAGA Region	Caraga Regional Hospital
Legend: CALABARZON: Cavite, Laguna, Batangas, Rizal, Quezon; MIMAROPA: Mindoro, Marinduque, Romblon, Palawan; SOCCSKSARGEN: South Cotabato, Cotabato, Sultan Kudarat, Sarangani, General Santos City.	

The surveillance collects data on culture and antimicrobial susceptibility from its *24 sentinel sites and 2* gonococcal surveillance sites*.* Case finding is based on priority specimens sent routinely to sentinel sites laboratories for clinical purposes.

TESTING METHODS

All sentinel sites implement standard methods for culture and susceptibility testing based on the WHO Manual for the Laboratory Identification and Antimicrobial Susceptibility Testing of Bacterial Pathogens of Public Health Importance in the Developing World [3] and the updated Clinical Laboratory Standards Institute (CLSI) references for antibiotic susceptibility testing and quality control [4].

Panel of antibiotics for testing are based on the latest CLSI recommendations. In the analysis of antimicrobial susceptibility testing, an isolate is considered resistant to an antimicrobial agent when tested and interpreted as resistant (R) in accordance with the clinical breakpoint criteria based on the most recent Clinical Laboratory Standards Institute (CLSI) references for antibiotic susceptibility testing.

The culture and antimicrobial susceptibility test results are encoded using a database software called *WHONET*. WHONET is Windows-based database software developed by the WHO Collaborating Centre for Surveillance of Antimicrobial Resistance based at the Brigham and Women's Hospital in Boston for the management and analysis of microbiology laboratory data with a special focus on the analysis of antimicrobial susceptibility test results[5]

Using a standard format, routine culture and antimicrobial susceptibility test results are sent by the sentinel sites to the coordinating laboratory of the program – the *Antimicrobial Resistance Surveillance Reference Laboratory (ARSRL) at the Research Institute for Tropical Medicine*. Beginning January 2018, sentinel sites transmit data daily to the reference laboratory. The automated data transfer facilitates prompt identification of resistant isolates of public health importance as well the identification of clustering of cases and potential outbreaks among sentinel sites. The ARSRL's Data Management Unit manages the cleaning, analysis, storage and security of the program's surveillance data.

Sentinel sites likewise send isolates with unusual antimicrobial susceptibility patterns to ARSRL for phenotypic and genotypic confirmatory testing.

At the reference laboratory, all isolates with unusual susceptibility patterns received for confirmatory testing are re-identified using both automated (Vitek) and conventional methods. Both minimum inhibitor concentration (MIC) - via automated method (Vitek) and gradient E-test, and disk diffusion are employed in antimicrobial susceptibility testing. As indicated, additional testing are done for specific antibiotics which are not included in AST card in use in the reference laboratory and for susceptibility testing for specific bacteria such as *N. gonorrhea* which requires manual AST methods. Serotyping for *S. pneumoniae, H. influenzae*, Salmonellae, *Shigellae* and *Vibrio cholera* were done for 2023.

Further, select isolates with resistance phenotype which have not been previously reported or have been only rarely reported to date under-went whole genome sequencing (WGS) at the ARSRL. The genomic characterization of these isolates is meant to allow for the understanding of resistance mechanisms of these isolates as well as their potential for spread in order to inform control and prevention measures. The Isolates were grown on tryptic soy broth overnight at 35°C. DNA was extracted from single colonies using NexttecTM 1 –STEP DNA Isolation systems. The DNA extracts were sequenced through Illumina Miseq platform (Illumina, San Diego, CA, USA) with 100-bp paired- end reads.

The program sentinel sites participate in an external quality assessment scheme (EQAS) conducted by the reference laboratory to ensure quality of laboratory results. Conditions permitting, periodic monitoring visits to sentinel sites were likewise done.

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DATA ANALYSIS

Analysis is restricted to the first isolate received (per genus under surveillance) per patient in the calendar year. Data are expressed as a cumulative resistance percentage, i.e. the percentage of resistant isolates out of all isolates with antimicrobial susceptibility testing (AST) information on that specific organism–antimicrobial agent combination. A 95% confidence interval is determined for the resistance percentage. Cumulative percentages of resistance are compared as proportions using the either Chi square of Fischer's test, using a p value of <0.05 as statistically significant. Only species with testing data for 30 or more isolates are included in the analysis.

Bioinformatics processing and analysis of whole genome sequences were primarily conducted using Bactopia v. 3.0.1[5]. Within this pipeline, Shovill v. 1.1.0 was employed for sequence assembly. Multi-locus sequence typing (MLST) was performed using MLST v2.23.0, which utilized the database version 2.23.0-20230907, to classify the sequence type of the assembled genomes. AMRFinderPlus v3.11.18, with its database updated to 2023-08-08.2, was used to detect antimicrobial resistance (AMR), virulence, and stress genes. Gene annotation was conducted using Prokka v1.14.6, and plasmid replicon genes were identified through PlasmidFinder v2.1.6, all integrated within the Bactopia toolkit. Species-specific tools, also part of the Bactopia analysis, included SISTR v1.1.1 and Seqsero v1.2.1 for Salmonella serotype prediction, Ectyper v1.0.0 and SerotypeFinder for E. coli, and Kleborate v2.3.0 for various analyses on Klebsiella spp. Pasty v1.0.3 was used for Pseudomonas spp. serotyping. The pangenome analysis was performed using Roary v3.13.0 to generate a phylogenetic tree and SNP distance matrices, which helped infer the evolutionary relationships among the strains, further supported by phylogenetic tree construction using IQ-TREE v2.2.2.7.

An annual report with a summary of the surveillance data focusing on aerobic bacterial pathogens of public health importance causing common infectious diseases with significant morbidity and mortality locally are disseminated to the program's stakeholders.

LIMITATIONS

Interpretation of data in this annual report should be undertaken with caution taking into consideration that there may be several factors that could influence and introduce bias to the data resulting in over- or underestimation of resistance percentages. Potential sources of bias include population coverage, sampling, and laboratory capacity.

1) Most of the resistance data in the program come from regional hospitals which typically cater to patients from towns and cities within the vicinity of the hospital. Resistance variations in local areas not covered by regional hospitals are not represented in the program data.
2) Data for the National Capital Region come from 8 sentinel sites while data for other regions come from 1 or 2 sentinel sites.
3) Given that the program data are from routine clinical samples, differences in factors indicating need for microbiological cultures may introduce variations in the resistance data.
4) Performance of culture and susceptibility tests in the sentinel sites is dependent on the diagnostic habits of the clinicians as well as the financial capability of patients for such test. Differential sampling can occur if cultures are typically only performed after empirical treatment shows no adequate therapeutic response. Predictably, this will lead to a serious overestimation of the percentage resistance by not including susceptible isolates in the denominator.
5) Lastly, the ability of the laboratory to identify the microorganism and its associated antimicrobial susceptibility pattern may differ.

The 2023 ARSP Data

Resistance data for **117,398** isolates were reported and analyzed for 2023. A 33.33% increase was observed when compared with the reported 88,049 isolates in 2022. **Table 2** shows that all 24 sentinel sites had an increase in data submission for 2023.

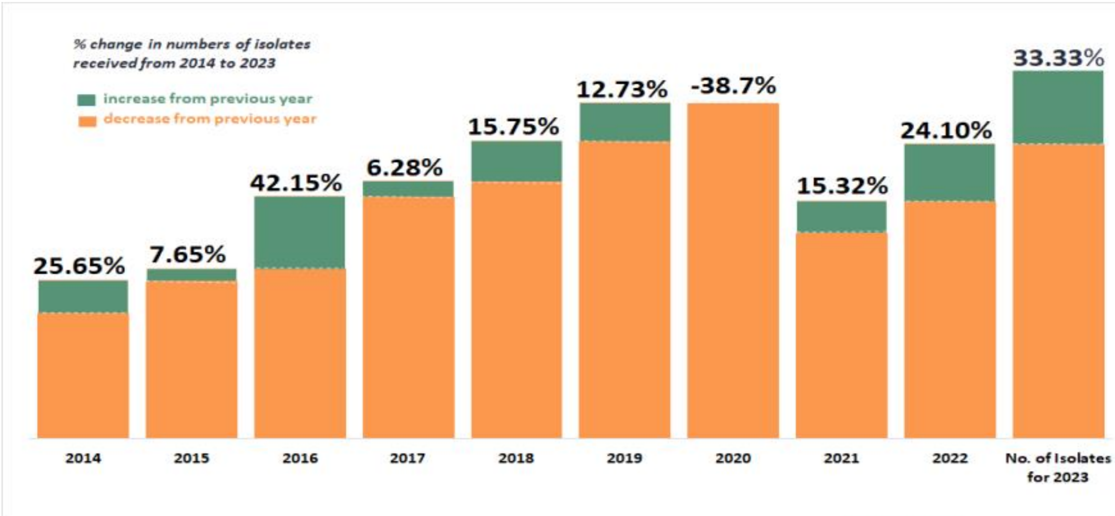


Figure 2. Number and percentage difference of isolates received from 2014-2023

Table 2. Sentinel sites isolate contribution, DOH-ARSP, 2014-2023

SENTINEL	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	Change %
BGH	2583	2625	3214	4628	4842	5775	5234	2968	3191	5459	7997	31.74
BRH	-	1022	1294	2075	2472	3133	3633	1569	1472	2570	3118	17.58
BRT	611	1047	1251	1584	1640	1842	2521	1176	1903	3055	4118	25.81
CMC	796	833	1300	1599	1704	2642	3181	2076	2021	3257	4430	26.48
CRH	-	-	-	10	624	879	1205	1115	1314	2075	3876	46.47
CVM	1100	1223	1512	3473	4141	4276	5668	3782	2687	4207	5714	26.37
DMC	3456	4062	5109	8058	8680	10762	12177	7412	8189	9135	11471	20.36
EVR	697	823	1514	1731	3303	3879	3874	4056	4584	5388	5585	3.53
FEU	1050	956	712	810	1201	1173	548		322	413	784	47.32
GMH	1307	1351	1807	1669	3153	3258	3957	2624	2818	4254	6676	36.28
JLM	502	638	1266	2768	3261	3880	4824	3248	3753	5229	5881	11.09
LCP	2253	2921	2905	3115	1367	3098	4433	2713	3205		3984	100.00
MAR	1773	1706	1849	2759	3565	4293	4462	3581	3302	4492	6196	27.50
MMH	1413	2289	2940	2886	3133	3026	2539	1425	1140	1575	2007	21.52
NKI	2179	2918	1455	5894	627	2959	4358		5571	5911	6688	11.62
NMC	2131	2416	2237	3105	2245	2961	3409	3735	2780	4868	6817	28.59
ONP	-	-	-	2	5	68	90	13	31	202	204	0.98
PGH	7093	12471	11710	12860	14572	12808	13895	6818	9557	12343	15716	21.46
RMC	1207	320	1054	3252	3160	3241	2375	2027	1968	2298	2873	20.01
RTH	-	-	-	25	69	159	352	289	0	4	5	20.00
RTM	303	303	336	410	513	598	507	255	423	528	554	4.69
SLH	1132	575	824	1410	2460	2044	2371	1019	1157	1060	1348	21.36
STU	2050	2002	1923	2275	2088	2184	2722	1419	1250	854	1121	23.82
VSM	3171	3951	3834	4803	6838	8714	10286	6886	6971	7596	8327	8.78
ZMC	822	819	841	1142	1222	1346	1644	1192	1341	1276	1908	33.12
ZPH	-	9	8	4	7	3	69	129	1			
TOTAL	37629	47280	50895	72347	76892	89001	100334	61527	70951	88049	117398	33.33%

** RTH and ZPH are the 2 gonococcal surveillance sites*

The 2023 ARSP data were collected from all 24 sites and 1 *N. gonorrhoeae* surveillance site of the program which represents data from 16 of 17 regions in the Philippines. More than half (59.47%) of the isolates were from Luzon, 24.28% from Mindanao and 19.25% from Visayas (**Figure 3**). The eight sentinel sites from NCR contributed 28.17% of the total 2023 data. Majority (51.27%) of the isolates were from male patients and from the 20-64 age group (58.44%) (**Figure 4**). The most common specimen types were respiratory (26.20%), blood (24.79%) and urine (20.84%) (**Figure 4**). Many of the data are from patients from the Medicine ward (22.26%). **Table 3** shows the most common isolates by specimen type.

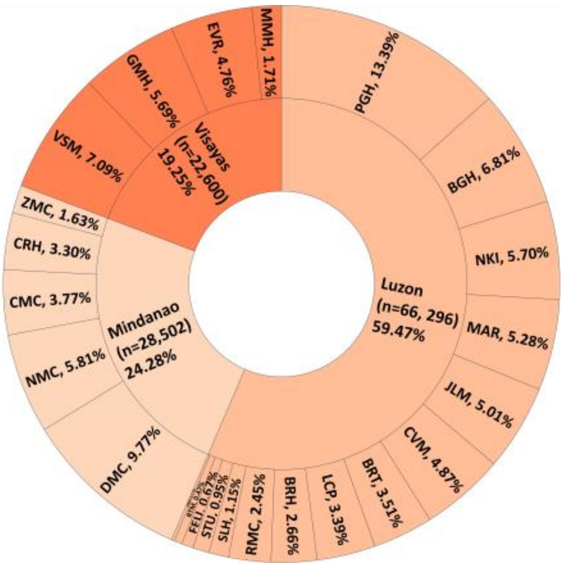
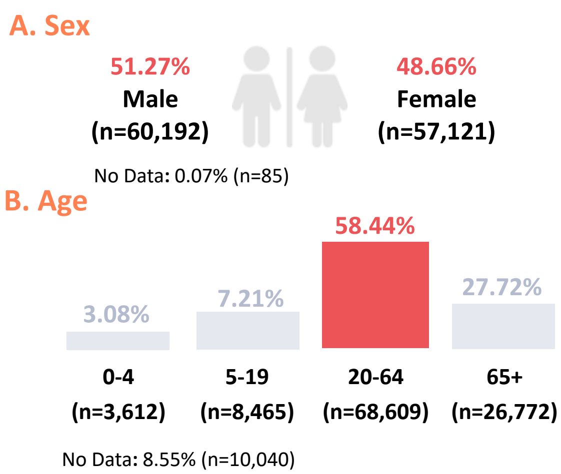


Figure 3. Sentinel sites isolate contribution, DOH-ARSP, 2023, (N=117,398)



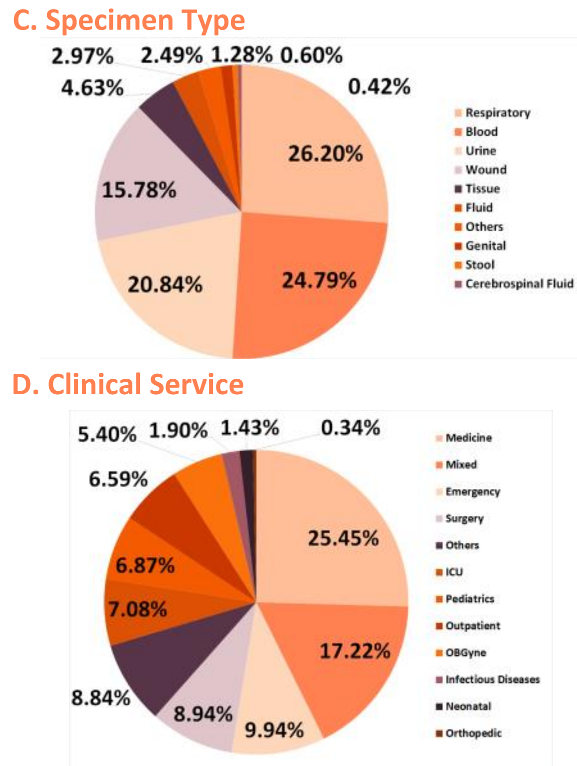


Figure 4. Patient characteristics of the 2023 ARSP isolates, DOH-ARSP, 2023 (N=117,398)

Table 3. Most common isolates by specimen type, DOH-ARSP, 2023 (N=117,398)

Respiratory Specimens	
1	*Klebsiella pneumoniae ss. pneumoniae*
2	*Pseudomonas aeruginosa*
3	*Acinetobacter baumannii*
Cutaneous or Wound	
1	*Staphylococcus aureus ss. aureus*
2	*Escherichia coli*
3	*Klebsiella pneumoniae ss. pneumoniae*
Cerebrospinal Fluid	
1	*Acinetobacter baumannii*
2	*Klebsiella pneumoniae ss. pneumoniae*
3	*Pseudomonas aeruginosa*
Blood	
1	*Staphylococcus aureus ss. aureus*
2	*Klebsiella pneumoniae ss. pneumoniae*
3	*Escherichia coli*
Stool	
1	*Salmonella sp.*
2	*Vibrio cholerae*
3	*Shigella sp.*
Urine	
1	*Escherichia coli*
2	*Klebsiella pneumoniae ss. pneumoniae*
3	*Enterococcus faecalis*

Streptococcus pneumoniae

There were **427** *Streptococcus pneumoniae* isolates reported for 2023. Sentinel sites located in Luzon contributed most (61.12%) of the isolates with 32.55% coming from NCR, 19.67% from Visayas and 19.20% from Mindanao (Figure 5).

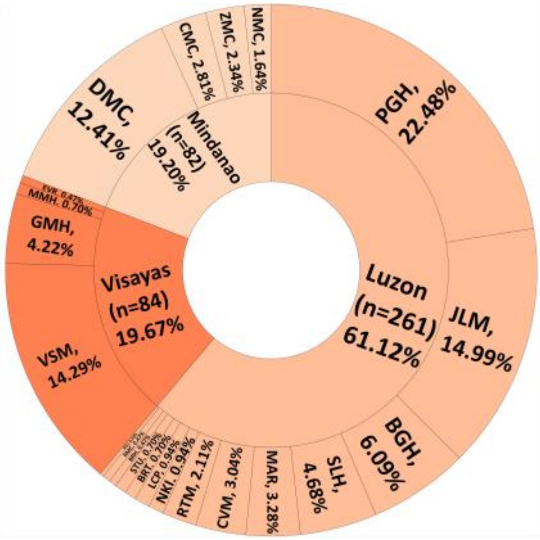


Figure 5. Isolate distribution *of S. pneumoniae*, DOH-ARSP, 2023 (n=427)

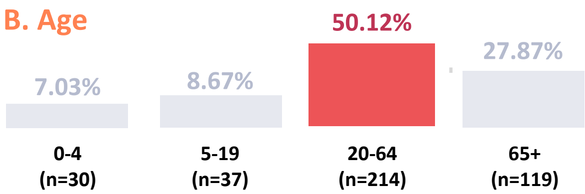
A. Sex

60.89% Male (n=260)

38.64% Female (n=165)

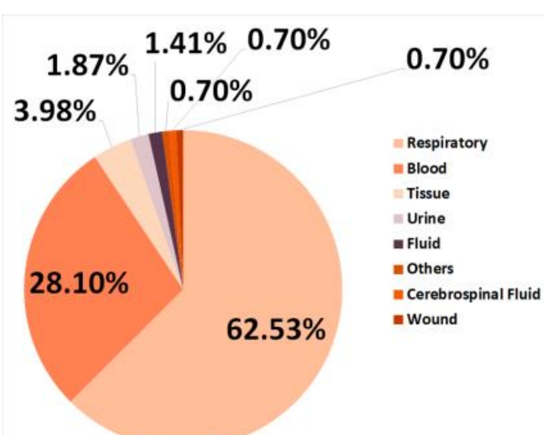
No Data: 0.47% (n=2)

B. Age



Unknown: 28.81% (n=123)

C. Specimen Type



D. Clinical Service

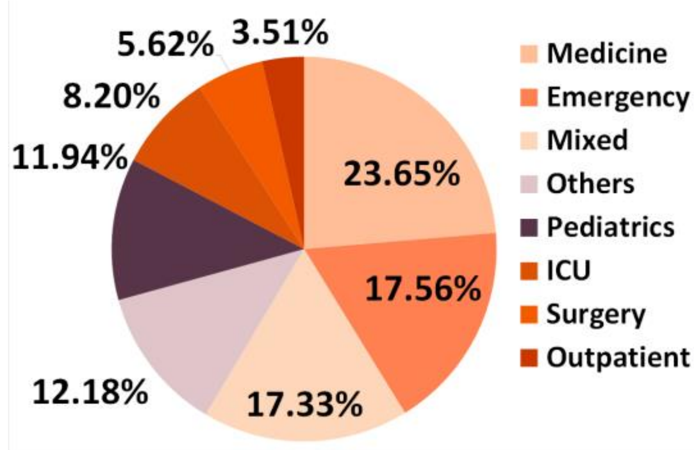


Figure 6. Patient characteristics of *S. pneumoniae* isolates, DOH-ARSP, 2023 (n=427)

Most (60.89%) isolates came from male patients and most (50.12%) were from aged 20-64 years old. Most isolates were detected from respiratory (62.53%) and blood (28.10%) specimens.

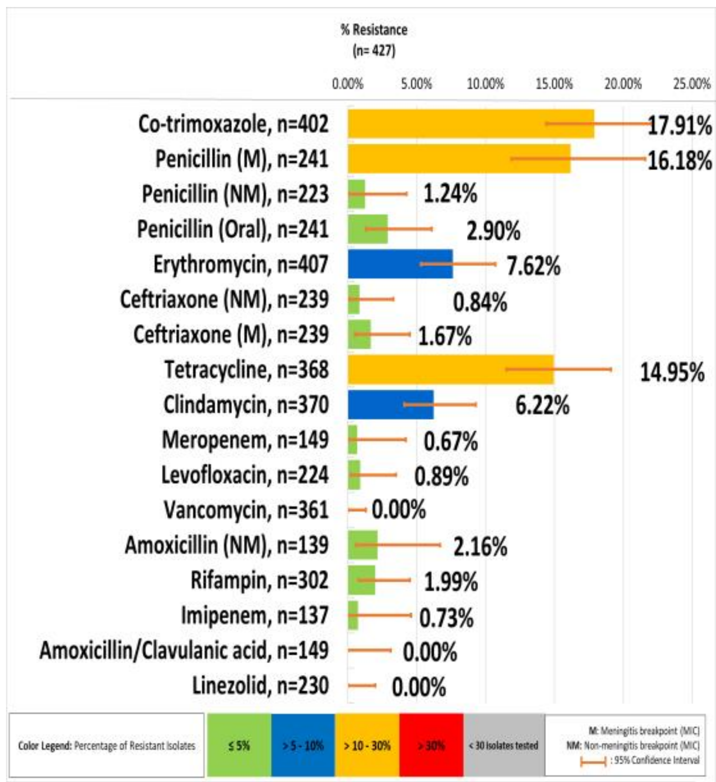
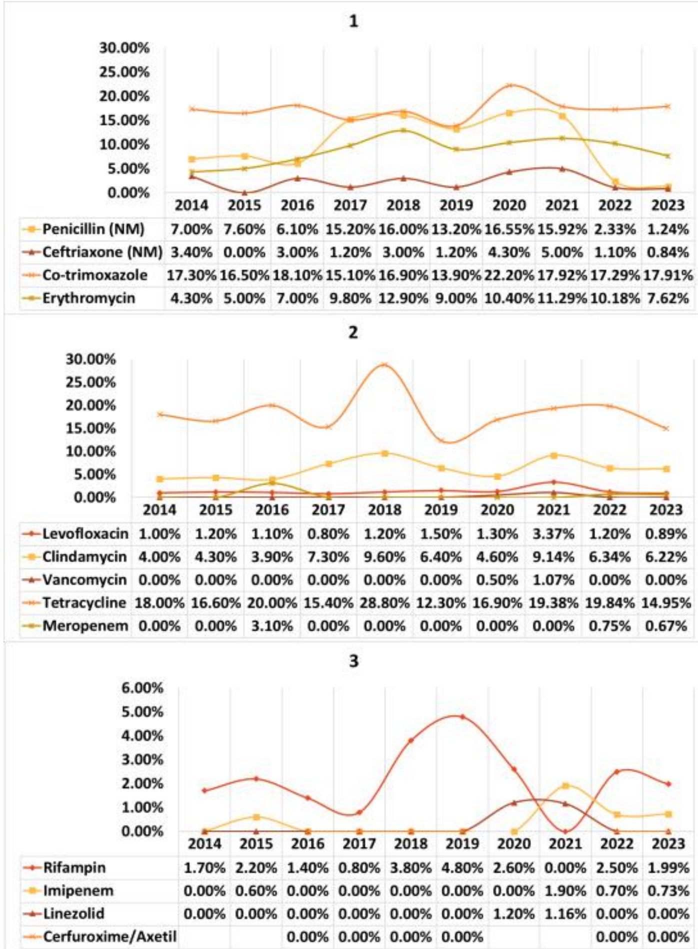


Figure 7. Resistance rates of *S. pneumoniae* isolates for all specimens, DOH-ARSP, 2023

For 2023, penicillin resistance in *S. pneumoniae* isolates is at 16.18% (n=241) using meningitis breakpoint, 1.24% (n=223) for non-meningitis breakpoint and 2.90% (n=241) using oral breakpoints (**Figure 7**). Resistance to co-trimoxazole was at 17.91 and to erythromycin at 7.62%. Resistance to the alternative antibiotics are as follows: ceftriaxone (NM) 0.84%, ceftriaxone

(M) 1.67%, clindamycin 6.22% and levofloxacin 0.89%. Compared with 2022, the overall resistance rates for *S. pneumoniae* decreased in 2023 for most antibiotics except for co-trimoxazole and meropenem (Figure 8). The observed changes in resistance rates for all antibiotics were not statistically significant.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Penicillin (NM)	7.00%	7.60%	6.10%	15.20%	16.00%	13.20%	16.55%	15.92%	2.33%	1.24%
Ceftriaxone (NM)	3.40%	0.00%	3.00%	1.20%	3.00%	1.20%	4.30%	5.00%	1.10%	0.84%
Co-trimoxazole	17.30%	16.50%	18.10%	15.10%	16.90%	13.90%	22.20%	17.92%	17.29%	17.91%
Erythromycin	4.30%	5.00%	7.00%	9.80%	12.90%	9.00%	10.40%	11.29%	10.18%	7.62%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Levofloxacin	1.00%	1.20%	1.10%	0.80%	1.20%	1.50%	1.30%	3.37%	1.20%	0.89%
Clindamycin	4.00%	4.30%	3.90%	7.30%	9.60%	6.40%	4.60%	9.14%	6.34%	6.22%
Vancomycin	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.50%	1.07%	0.00%	0.00%
Tetracycline	18.00%	16.60%	20.00%	15.40%	28.80%	12.30%	16.90%	19.38%	19.84%	14.95%
Meropenem	0.00%	0.00%	3.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.75%	0.67%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Rifampin	1.70%	2.20%	1.40%	0.80%	3.80%	4.80%	2.60%	0.00%	2.50%	1.99%
Imipenem	0.00%	0.60%	0.00%	0.00%	0.00%	0.00%	0.00%	1.90%	0.70%	0.73%
Linezolid	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	1.20%	1.16%	0.00%	0.00%
Cerfuroxime/Axetil			0.00%	0.00%	0.00%	0.00%			0.00%	0.00%

Figure 8. Yearly resistance rates of *S. pneumoniae* isolates DOH-ARSP, 2014-2023

Multiple year analysis results showed an overall decrease in the resistance rates over the past decade (Figure 8) for meropenem (p= 0.0000), tetracycline (p= 0.0000), penicillin (p= 0.2689) and ceftriaxone (p=0.8866).

Resistance to meropenem, considered as among the treatment options for penicillin-resistant pneumococcal (penRP) infections, is not commonly observed among *S. pneumoniae* isolates in the Philippines. For 2023, there was one isolate confirmed to test intermediate to meropenem. This isolate was from the respiratory sample of a 4-month old male from Region VII which was identified as serotype 9N. It was also noted that the isolate tested intermediate to imipenem and co-trimoxazole and resistant to amoxicillin, erythromycin and tetracycline making the isolate multidrug resistant. The isolate, however, showed susceptibility to penicillin (NM), ceftriaxone, amoxicillin-clavulanic acid, clindamycin, linezolid and vancomycin. In 2022, there was a reported *S. pneumonia* isolate (serotype 9N) likewise noted to be meropenem resistant.

Inclusion of rifampicin in empiric treatment when there is a risk of decreased susceptibility to penicillin has been recommended[7]. For 2023, there were 2 confirmed rifampin-resistant isolates from the respiratory specimens of a 27-year-old male and 30-year-old-male from Region III and NCR respectively. The isolates were both susceptible to amoxicillin, ceftriaxone, imipenem, linezolid, meropenem, penicillin, co-trimoxazole, tetracycline and vancomycin. Another isolate from the respiratory specimen of a 73-year-old male tested intermediate to rifampin, this isolate showed susceptibility to all other antibiotics tested.

Given the very limited treatment options for penRP infections, a continued surveillance to watch out for potential emergence and spread of these resistance phenotypes will guide prevention and control measures.

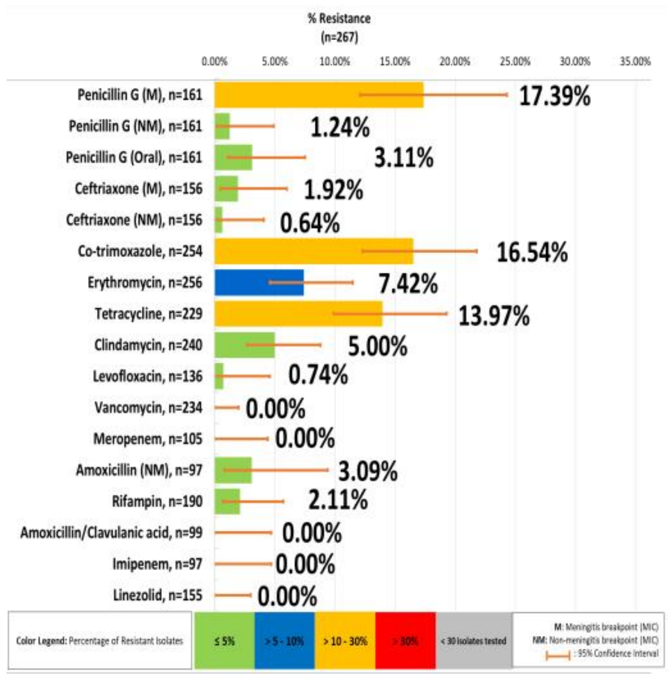


Figure 9. Resistance rates of *S. pneumoniae* respiratory isolates DOH-ARSP, 2023

Figure 9 shows the percent resistance of *S. pneumoniae* isolates from respiratory samples. Penicillin (M) resistance was 17.39%, penicillin (NM) was 1.24% and oral penicillin was 3.11%. Co-trimoxazole resistance was at 16.54% and ceftriaxone resistance for M and NM were 1.92% and 0.64% respectively. Tetracycline resistance was at 13.97%. No respiratory isolate was found resistant to linezolid, vancomycin, imipenem and amoxicillin-clavulanic acid. Compared with overall resistance of *S. pneumoniae* from all samples, resistance to most of the antibiotics are higher for the respiratory isolates except for lower resistance to co-trimoxazole, tetracycline, clindamycin and levofloxacin.

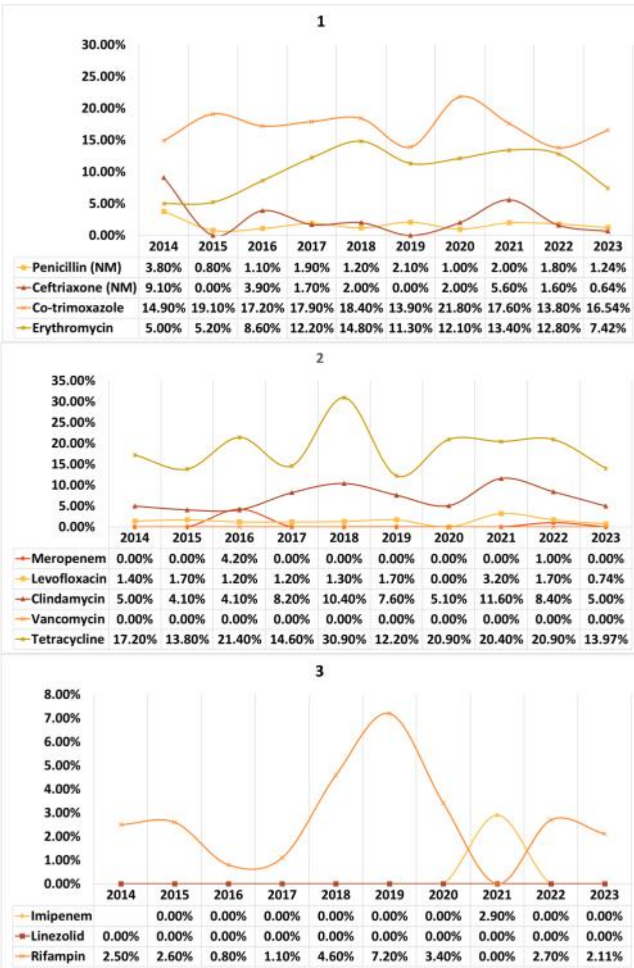


Figure 10. Yearly resistance rates of *S. pneumoniae* respiratory isolates DOH-ARSP, 2014-2023

Figure 10 shows the resistance rates of *S. pneumoniae* respiratory isolates in the last ten years. Multi-year analysis showed an overall decrease in resistance to penicillin (p=0.0000) and tetracycline (p=0.0000) and increased resistance to co-trimoxazole (p=0.0000) and erythromycin (p=0.0000).

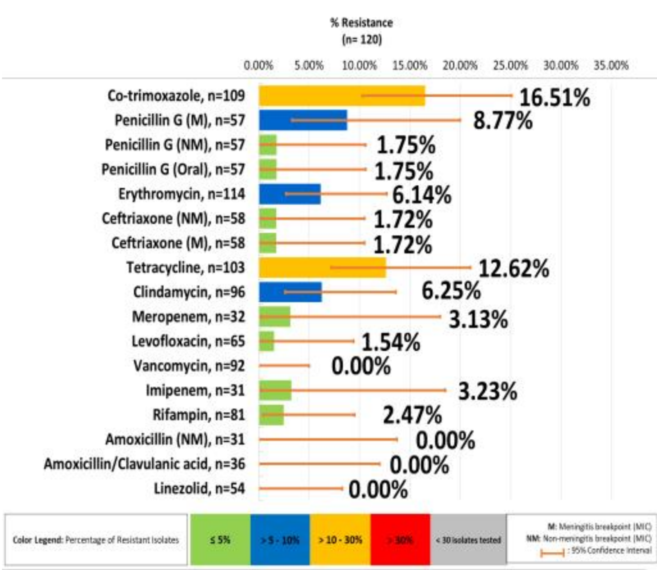


Figure 11. Resistance rates of *S. pneumoniae* blood isolates DOH-ARSP, 2023

Among *S. pneumoniae* blood isolates (Figure 11), penicillin (M) resistance was 8.77% and penicillin (NM) was 1.75%. Resistance to co-trimoxazole was highest at 16.51% followed by tetracycline at 12.62%. Resistance to ceftriaxone meningitis and non-meningitis breakpoints were both 1.72. Resistance rate for erythromycin was 6.14%. Compared with the overall resistance of *S. pneumoniae* from all samples, resistance to most of the antibiotics were noted to be lower for the blood isolates except for higher resistance to clindamycin, both M and NM breakpoints for ceftriaxone, meropenem, levofloxacin, rifampin, imipenem and penicillin NM. The observed wide confidence interval of the resistance rates of antibiotics can be attributed to the few numbers of *S. pneumoniae* blood isolates tested.

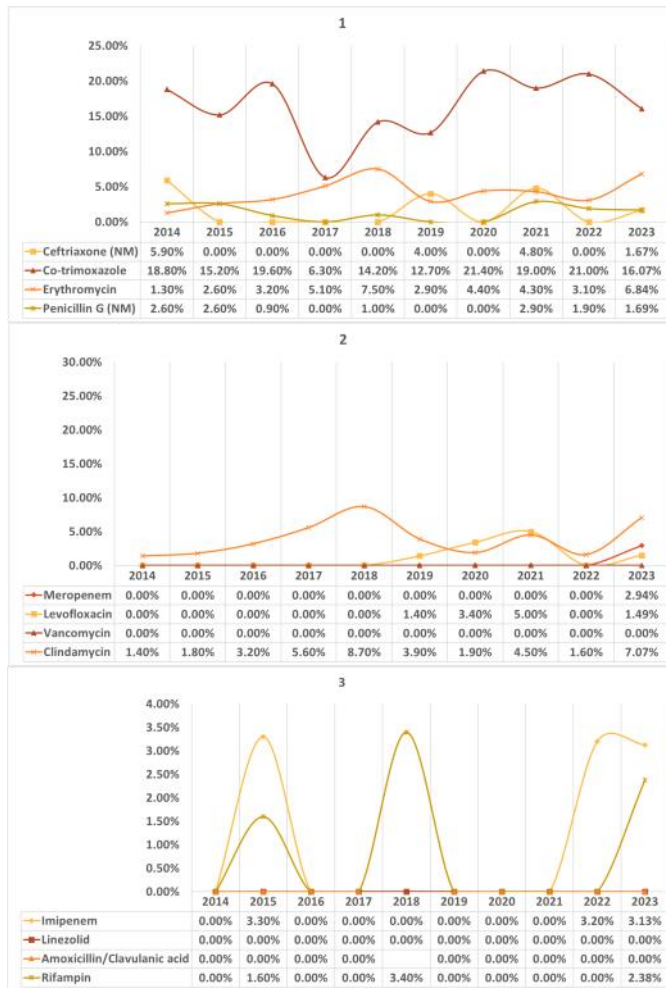


Figure 12. Yearly resistance rates of *S. pneumoniae* blood and CSF isolates DOH-ARSP, 2019-2023

The yearly resistance rates of *S. pneumoniae* blood and CSF isolates are shown in **Figure 12**. The multi-year analysis showed an overall decrease in resistance to penicillin NM (p=0.0000), co-trimoxazole (p=0.0000), and an overall increase in resistance to erythromycin (p=0.0000), clindamycin (p=0.0000) and linezolid (p=0.0000).

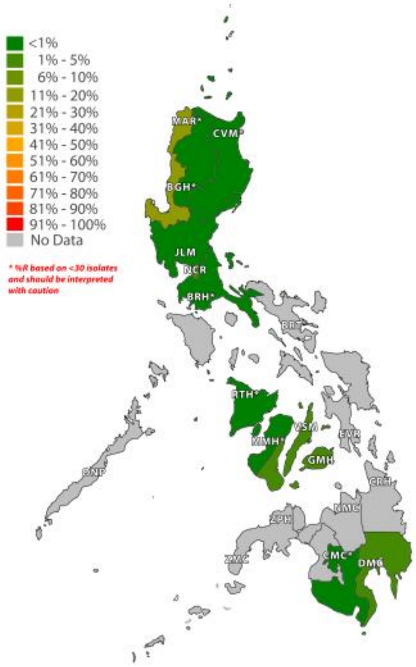


Figure 13. Geographic distribution of penicillin-resistant *S. pneumoniae* in the Philippines, DOH-ARSP, 2023

A look at the penicillin (NM) resistance (all specimens) of *S. pneumoniae* isolates across the different sentinel sites shows that most are within less than 5% except for DMC (within 6-10% range) and for MAR and BGH (within 11-20%).

A total of **119** *S. pneumoniae* isolates were referred to ARSRL in 2023 with 71 *S. pneumoniae* serogroup/ serotypes identified. Most (n=46, 38.65%) of the isolates were from ≥ 60 years old, 18-49 years old (n=34, 28.57%) and 50-59 years old (n=19, 15.96%) (**Table 4**).

Of the few *S. pneumoniae* isolates from patients 5 years old and below (n= 12), there were 10 serogroups /serotypes noted: 18C (PCV7), 3 (PCV13), 11A (PPS23), 11 (serogroup; not serotyped), 19 (serogroup; not serotyped), and the non-vaccine serogroup/serotypes 24, 29, 9N and 15C.

Among 6-11 and 12-17 age groups, PCV serotypes 23F and 3, PPSV serotype 11A and non-PCV/ PPSV serotypes 10 and 12 were seen. More common among the 18-49 years old were PPSV3 serotype 10A (n=4, 11.76%) and non-PCV serotype 34 (n=4, 11.76%). Among the 50-59 years old, PPSV23 serotype 11A, and non-PCV serotypes 13 and 15 were mostly observed. Finally, among the geriatric population (≥ 60 years old), PCV13 serotype 3 (n=7, 15.21%) was the most frequent serotype seen. Serotype 3 (PCV 13) was also the overall most common serotype across all age groups, followed by non-vaccine serotypes 29, 34 and 16F with 3 isolates each. There was one *S. pneumoniae* isolate with serotype 22F (PCV15) from the ≥ 60 years old age group.

Penicillin (NM) resistant *S. pneumoniae* isolates are of serotypes 9N (n=1; PPSV) and 24 (n=1; non-vaccine type). Serotypes of cotrimoxazole resistant isolates were variable and include 6/6B (n=2; PCV7), 19A (n=1; PVC13), 19F (n=1; PCV7), 14 (n=1; PCV7) and PPSV-23 serotypes 11A (n=2) and 10A (n=2). Serotypes of erythromycin resistant isolates were likewise variable and include 19A (n=1; PCV13), 19F (n=1; PCV7), PPSV serotypes 9N (n=1) and 11A (n=1) and non-vaccine types 15A (n=1), 18(n=1) and 24(n=2). There appears to be no specific serotypes that drive resistance to specific antibiotics among the *S. pneumoniae* isolates.

Percent PCV and PPSV coverage (overall and per age group) of *S. pneumoniae* isolates sent to ARSRL for confirmation were determined by dividing the number of isolates with serotypes included in PCV or PPSV over the total number of isolates (overall and per age group). The overall (N=119) PCV7 and PCV10 coverage were 10.08% and 13.44% respectively while the overall vaccine coverage for PCV 13 is 23.52% and 24.36% for both PCV15 and PCV20.

The overall coverage for all PCV vaccines decreased for 2023 (24.36%) compared with 2022 (27.73%). PPSV-23 vaccine coverage this year is 40.23% which is higher than the coverage in 2022 (38.66%).

For age specific vaccine coverage among less than 5 years old (n=12), vaccine coverage for PCV7 and PCV 10 were both at 8.33%, while 16.66% for PCV13, PCV15 and PCV20. PPSV-23 vaccine coverage was 25%.

Among the geriatric population, vaccine coverage for PCV7, PCV10 and PCV13 were 8.69%, 13.04%, and 30.43%, respectively. On the other hand, vaccine coverage for both PCV15 and PCV20 was 32.61% while 41.3% PPSV-23 among ≥ 60 years old.

The overall non-vaccine coverage for 2023 was 58.82% (70/119), while it is 75% (9/12) for the population less than 5 years old and 58.69% (27/46) for ≥ 60 years old population. The overall non-vaccine coverage for 2022 was 48.47% which is lower than the vaccine coverage for 2023 at 58.69%, the observed increase was statistically significant (p=0.0036).

Table 4. *S. pneumoniae* serotypes and PCV serotypes per age group, DOH-ARSP, 2023

SEROTYPE		AGE																																						TOTAL
		<1					1-5					6-11					12-17					18-49					50-59					>=60								
		1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	6	7	8	
PCV-7	4																																							4
	6B																																							2
	9																																							0
	9V																																							0
	14																																							1
	18C																																							2
	19F																																							2
	23F																																							1
PCV-10	1																																							1
	5																																							0
	7F																																							3
PCV-13	3																																							10
	6A																																							1
	19A																																							1
PCV-15	22F																																							1
	33F																																							0
PCV-20	15BC																																							0
PPSV-23	2																																							0
	8																																							0
	9N																																							0
	10A																																							5
	11A																																							8
	12F																																							0
	15B																																							1
	17F																																							3
	20																																							2
Non-PCV/PPSV	6																																							4
	10																																							3
	11																																							2
	12																																							2
	13																																							6
	15																																							2
	16																																							1
	18																																							2
	19																																							2
	21																																							2
	23																																							1
	24																																							2
	28																																							1
	29																																							7
	31																																							0
	34																																							7
	35																																							0
	36																																							1
	47																																							0
	6C																																							1
	7C																																							2
	9L																																							0
	9N																																							1
	10B																																							0
	10X																																							2
	11B																																							1
	11E																																							0
	15A																																							4
	15C																																							1
	16F																																							5
	17A																																							1
	18A																																							1
	18B																																							0
	23A																																							2
	23B																																							2
	28F																																							0
	32F																																							1
	35A																																							0
	35B																																							0
	35F																																							1
Untypable																																								1
TOTAL		7					5					3					5					34					19					46								119

*__PCV__ – Pneumococcal Conjugate Vaccine, **PPSV** – Pneumococcal Polysaccharide Vaccine

Haemophilus influenzae

A total of 390 *H. influenzae* isolates were reported for 2023 which increased by 13.04% from 345 isolates in 2022. The highest contributors are PGH at 28.72%, BGH at 28.46% and DMC at 15.64% (**Figure 14**) Based on island group distribution, the highest was in Luzon with 74.87% followed by Mindanao at 15.64%, and Visayas at 9.49%.

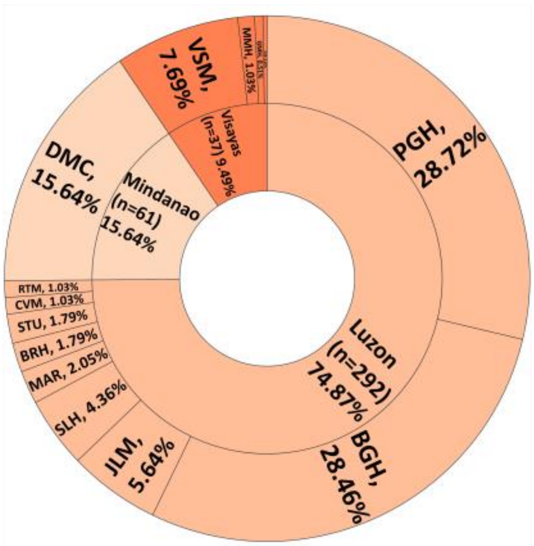
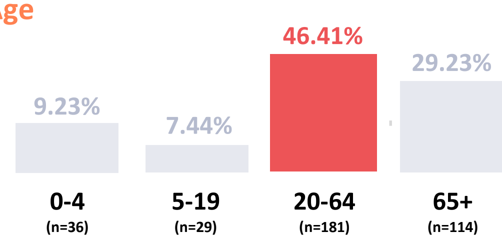


Figure 14. Isolate distribution of *H. influenzae,* DOH-ARSP, 2023 (n=390)

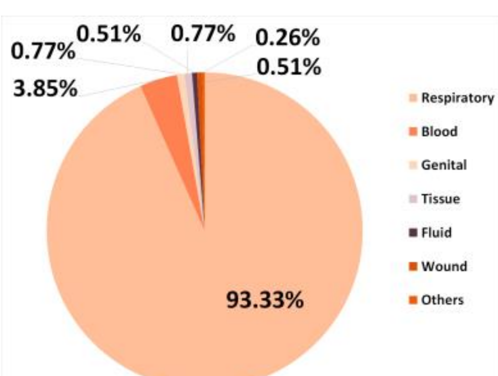
A. Sex

B. Age



Unknown: 7.69% (n=30)

C. Specimen Type



D. Clinical Service

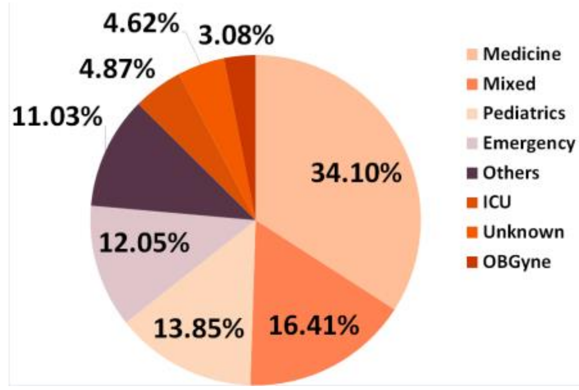


Figure 15. Patient characteristics of *H. influenzae* isolates, DOH-ARSP, 2023 (n=390)

Most *H. influenzae* were isolated from male patients at 60.26%, adult patients aged 20-64 years old at 46.41%, and many (34.10%) were from patients in the medicine department. (**Figure 15**) Respiratory specimens remain to be the most common source of *H. influenzae* at 93.33%.

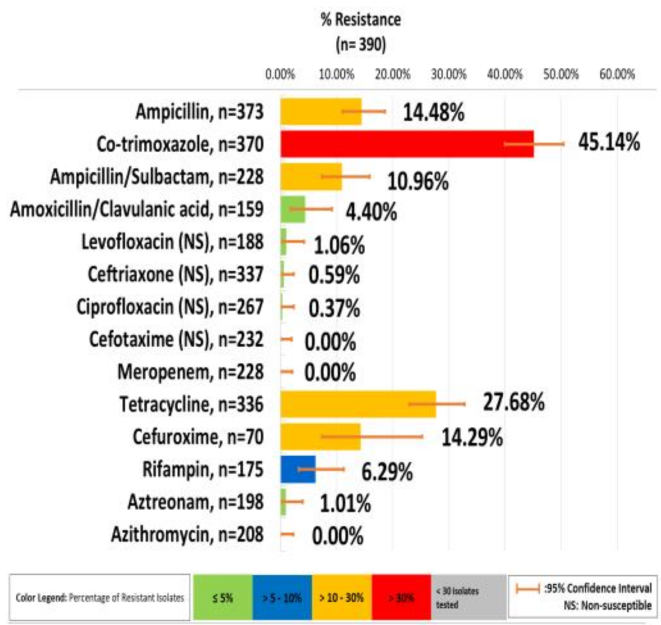


Figure 16. Resistance rates of *H. influenzae* isolates for all specimens, DOH-ARSP, 2023

A cumulative analysis of resistance rates of *H. influenzae* isolates from all specimens (**Figure 16**) show resistance to ampicillin, ampicillin/sulbactam, and amoxicillin/clavulanic acid to be 14.48%, 10.96% and 4.40%, respectively. Resistance to ceftriaxone was at 0.59% and 14.29% to cefuroxime. No *H.influenzae* isolate was noted to be resistant to cefotaxime for 2023. Non-susceptibility to ciprofloxacin and levofloxacin was at 0.37% and 1.06% respectively.

There were 2 isolates confirmed to be resistant to amoxicillin/clavulanic acid. One isolate was from an 81-year old female from the medical ward of BGH, and was presumptively community acquired. Another isolate was from a 56- year old male from VSM. Both isolates were susceptible to azithromycin, ciprofloxacin, ceftriaxone, cefotaxime, and meropenem, and resistant against cotrimoxazole. The isolate from BGH was also found to be resistant against ampicillin and tetracycline.

For 2023, six (6) isolates were confirmed to be non-susceptible to ciprofloxacin. Four (4) of these were from BGH, while one (1) each were from SLH and VSM. Only one (1) was nosocomial, while four (4) were presumptively community-acquired. All the isolates were from adults, with ages ranging from 36-71. Majority (n=4) of the isolates were male. All were susceptible to ampicillin sulbactam, these isolates were susceptible to amoxicillin/clavulanic acid, ampicillin, azithromycin, ceftriaxone, cefotaxime, meropenem and tetracycline. Five (5) out of the 6 were resistant to co-trimoxazole.

Molecular characterization of ciprofloxacin resistant *Haemophilus influenzae*

Haemophilus influenzae is a Gram-Negative coccobacillus pathogen which presents a wide-range of pathology from benign otitis media to invasive diseases such as septicemia.[1] Antibiotic resistance in this organism was observed from the first line antibiotics such as amoxicillin, ampicillin-sulbactam, and amoxillin-clavulanate, to newer compounds such as fluoroquinolones.[2] Of the six confirmed ciprofloxacin non-susceptible isolates of *H. influenzae* for 2023, three were available for whole genome sequencing (WGS). We describe in this report the molecular characteristics of three *H. influenzae* isolates which exhibited non-susceptibility to ciprofloxacin.

Table 5 show the characteristics of the isolates. All isolates were recovered from respiratory specimens collected from adult patients.

Table 5. Demographic and genomic characteristics of ciprofloxacin non- susceptible *H. influenzae* isolates, DOH-ARSP, n=3

Isolate No.	Region	Specimen Source	MLST	Resistance Profile	AMR Gene
1	VII	tracheal aspirate	ST 1524	Ciprofloxacin	*hmrM*
2	NCR	sputum	ST 1524	Ciprofloxacin	*hmrM*
3	CAR	sputum	ST 1524	Ciprofloxacin –Co-trimoxazole	*hmrM*

The 3 isolates were all ST 1524. Similar sequence type was also seen in a clinical isolate from a tertiary hospital in Spain which showed beta-lactamase production. [3]

The most extensively described mechanism of fluoroquinolone resistance among *H. influenzae* is the occurrence of amino acid modifications in the quinolone resistance-determining region (QRDR) of the topoisomerase II and I genes. [4] However, there were also reports on the effects of efflux pumps overexpression and permeability defects on the susceptibility of this organism to quinolone. [5] The utilization of *H. influenzae* intrinsic redox-driven sodium extrusion pump plays an important role for the detoxification in this microorganism. [6]

The 3 isolates harbored *hmrM,* a sodium-coupled multidrug efflux pump gene among the three isolates which facilitates fluoroquinolone resistance when overstimulated. The elevated expression of *hmrM* gene could lead to enhanced resistance not only to fluoroquinolones but also to many other antimicrobial agents in *H. influenzae*,[6] this may explain the observed resistance of isolate 3 against co-trimoxazole.

Continued monitoring and surveillance of this emerging resistance phenotype is necessary to guide treatment as well as prevention and control of the spread of these resistant pathogens.

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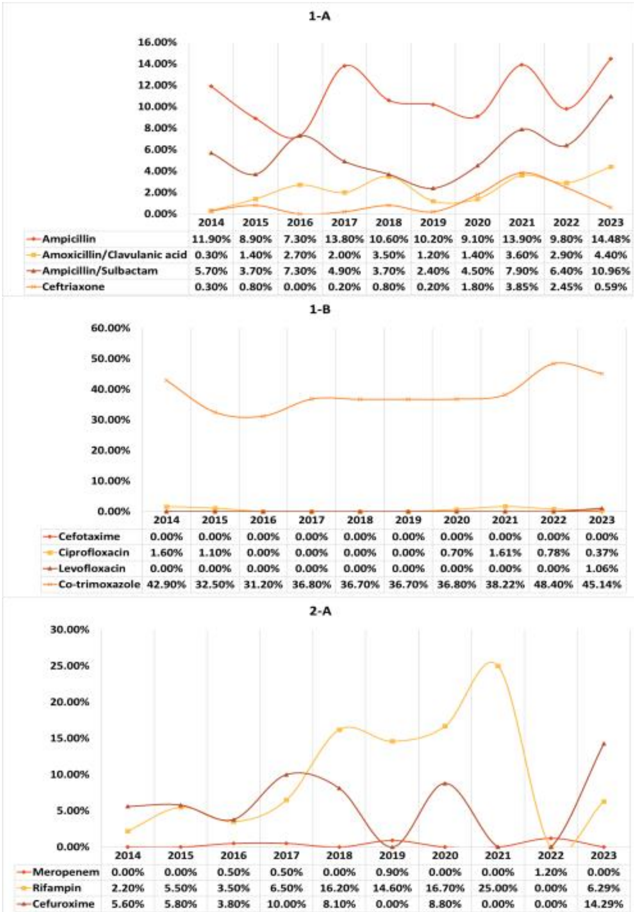


Figure 17. Yearly resistance rates of *H. influenzae*, DOH-ARSP, 2014-2023

Figure 17 shows the trend in resistance rates of *H. influenzae* in the last 10 years. Resistance rates in 2023 increased from that of 2022 rates for ampicillin, co-amoxiclav, and ampicillin/sulbactam, and said increases were all statistically significant. Multi-year analysis showed an overall increase in ampicillin (p=0.0069), ampicillin/sulbactam (p=0.0139), cotrimoxazole (p=0.0000), ceftriaxone (p = 0.0099), and tetracycline (p=0.0000).

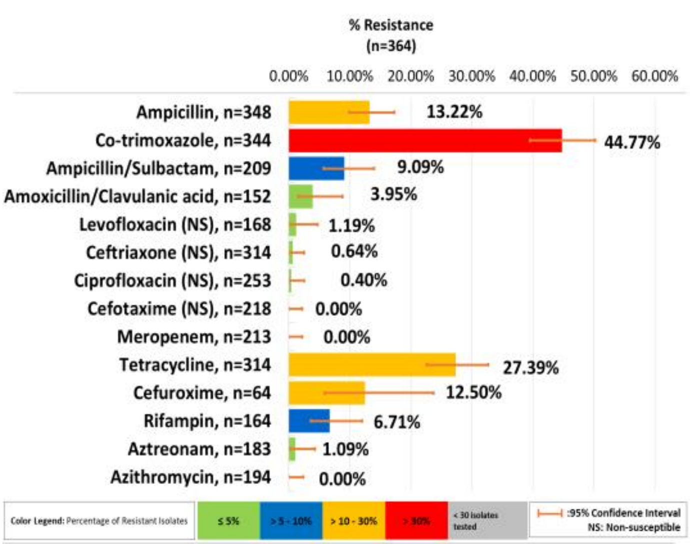


Figure 18. Percent resistance of *H. influenzae* from respiratory specimens , DOH-ARSP, 2023

Resistance rates among respiratory isolates of *H. influenzae* are shown in **Figure 18**. Resistance to ampicillin, ampicillin/sulbactam, and amoxicillin/clavulanic acid were 13.22%, 9.09% and 3.95%, respectively while resistance to ceftriaxone was at 0.64% and 12.50% to cefuroxime. Non-susceptibility to ciprofloxacin and levofloxacin was at 0.40% and 1.19% respectively. Highest resistance rate was observed for co-trimoxazole at 44.77%, followed by tetracycline at 27.39% For 2023, all isolates from respiratory specimens were found to be susceptible to cefotaxime, meropenem, and azithromycin Compared with cumulative resistance rates for isolates from all specimens, higher resistance rates of *H. influenzae* respiratory isolates were noted for ceftriaxone, ciprofloxacin and levofloxacin.

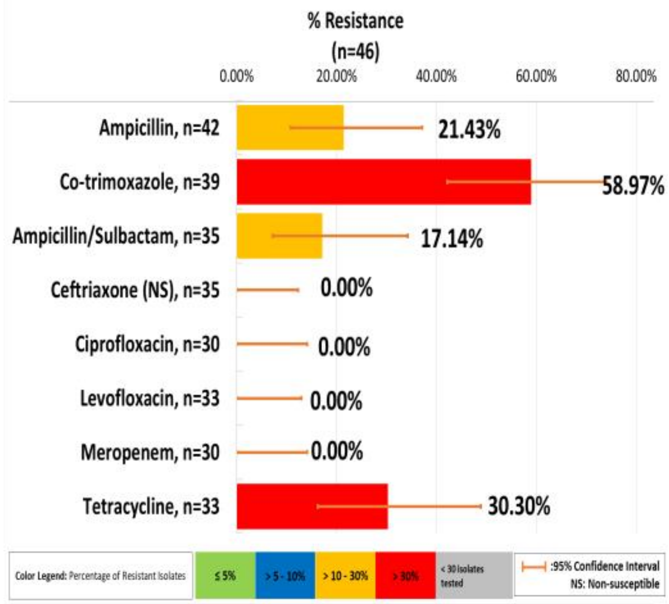


Figure 19. Percent resistance of *H. influenzae* from blood and CSF isolates, DOH-ARSP, 2021-2023

Cumulative percentage resistance for *H. influenzae* from blood and CSF samples from 2021-2023 are shown in Figure 19. Data from the past three years were presented in order to obtain reasonable statistical estimates of resistance rates. Resistance to ampicillin and ampicillin/sulbactam were 21.43%, and 17.14% respectively. Resistance rate against co-trimoxazole was still highest at 58.97%, followed by tetracycline at 30.30%. For 2023, all isolates from blood and CSF were found to be susceptible to ceftriaxone, ciprofloxacin, levofloxacin and meropenem. Compared with cumulative resistance rates for isolates from all specimens, higher resistance rates of *H. influenzae* blood isolates were noted for ampicillin, ampicillin-sulbactam, cotrimoxazole and tetracycline while lower rates were noted for ceftriaxone, ciprofloxacin and levofloxacin.

Salmonella enterica serovar Typhi

A total of **83** *S.* Typhi isolates were reported for 2023, a similar number of isolates analyzed in 2022. The highest contributors were ZMC (33.73%), CMC (18.07%) and CVM and BRT, which are both at 10.84%. According to island group distribution, 60.24% was from Mindanao, 31.33% from Luzon and 8.43% from Visayas.

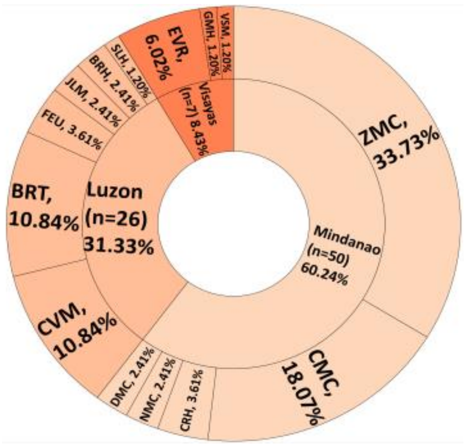


Figure 20. Isolate distribution of *S. Typhi*, DOH-ARSP, 2023 (n= 83)

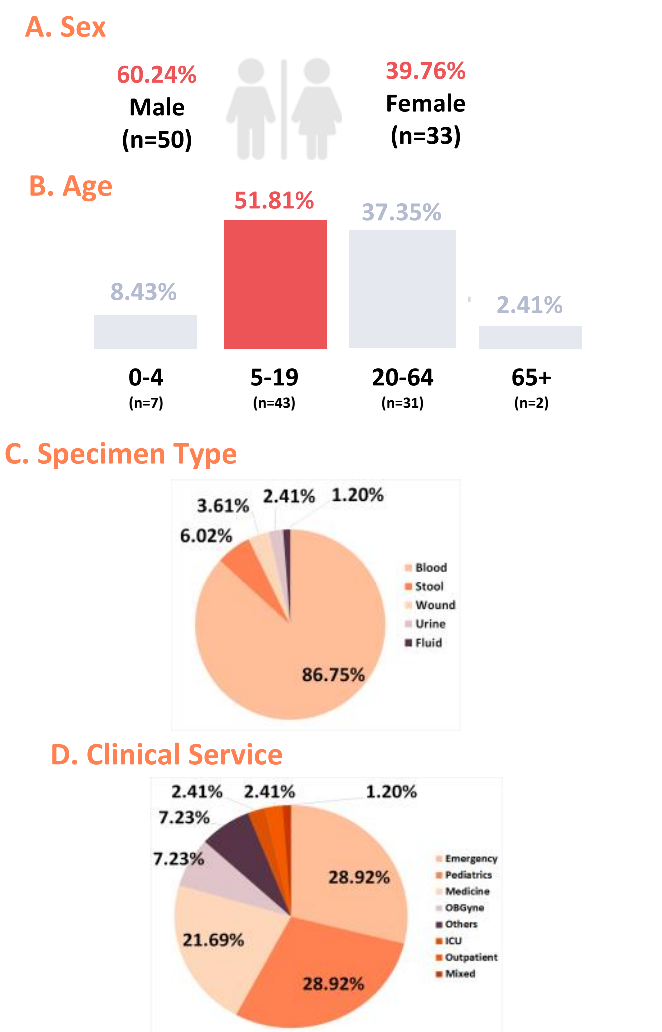


Figure 21. Patient characteristics of *S. Typhi* isolates, DOH-ARSP, 2023

More than half (60.24%) of the *S. Typhi* isolates were recovered from male patients. Most (51.81%) were from patients aged 5-19 years old, many (28.92%) were from patients from the Emergency clinical service (**Figure 21**). Most (86.75%) of the isolates were from blood specimens.

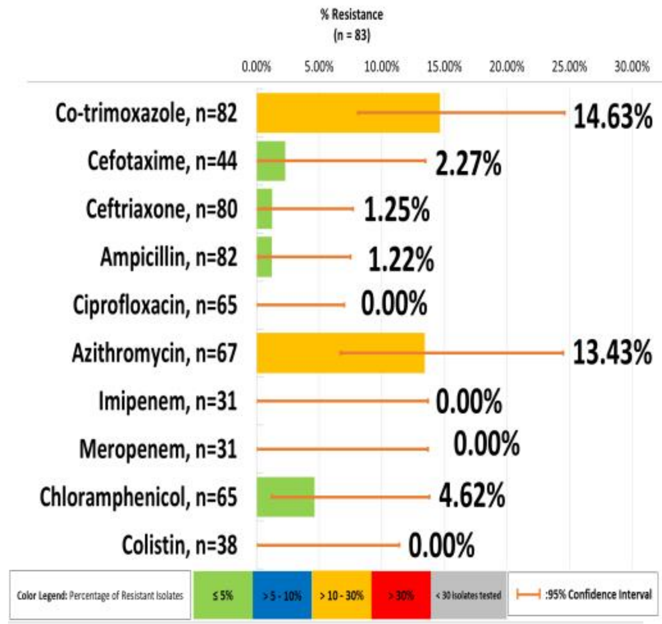
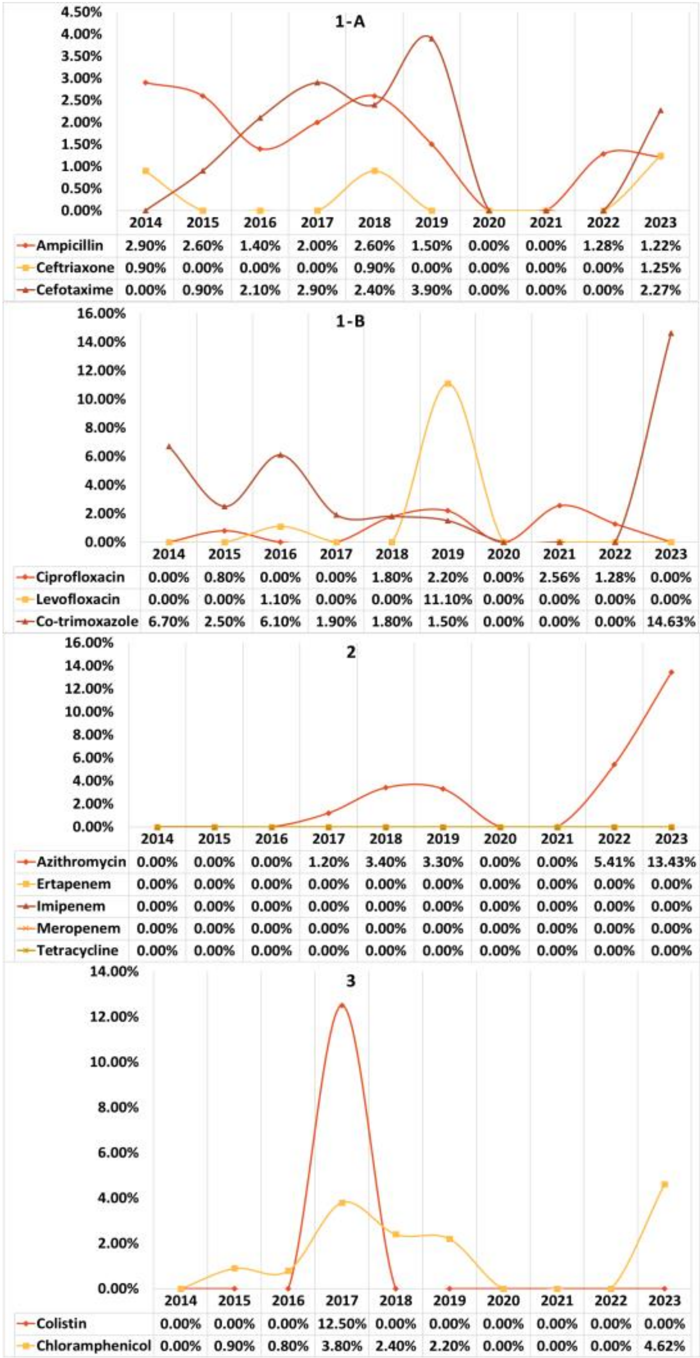


Figure 22. Resistance rates of *S. Typhi* isolates for all specimens, DOH-ARSP, 2023

Resistance rates of *S.* Typhi isolates for 2023 are shown in **Figure 22**. Resistance to ampicillin was at 1.22% and to chloramphenicol at 4.62%. The isolates were all susceptible to ciprofloxacin but resistance to azithromycin was at 13.43%. Azithromycin resistance indicated here are mostly based on disc diffusion method with few isolates having MIC confirmation. Resistance to cefotaxime was at 2.27% and to ceftriaxone at 1.25%. Resistance to co-trimoxazole was highest at 14.63%. The isolates remained susceptible to imipenem, meropenem and colistin.

There were two (2) confirmed azithromycin resistant *S.* Typhi isolates from Region IV-A. The first isolate was from the blood specimen of a 51-year-old male and was noted to be resistant to ampicillin, chloramphenicol, ceftriaxone and cefotaxime making the isolate multidrug-resistant. The isolate tested intermediate to ciprofloxacin and colistin but was susceptible to co-trimoxazole. The second isolate was from the blood specimen of a 31-year-old male, tested intermediate to ciprofloxacin and colistin, and noted to be susceptible to ampicillin, chloramphenicol and ceftriaxone. There were likewise several unconfirmed reports of azithromycin resistance in 2022 but the occurrence of azithromycin resistance among *Salmonella* Typhi appears to remain sporadic in the country.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ampicillin	2.90%	2.60%	1.40%	2.00%	2.60%	1.50%	0.00%	0.00%	1.28%	1.22%
Ceftriaxone	0.90%	0.00%	0.00%	0.00%	0.90%	0.00%	0.00%	0.00%	0.00%	1.25%
Cefotaxime	0.00%	0.90%	2.10%	2.90%	2.40%	3.90%	0.00%	0.00%	0.00%	2.27%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ciprofloxacin	0.00%	0.80%	0.00%	0.00%	1.80%	2.20%	0.00%	2.56%	1.28%	0.00%
Levofloxacin	0.00%	0.00%	1.10%	0.00%	0.00%	11.10%	0.00%	0.00%	0.00%	0.00%
Co-trimoxazole	6.70%	2.50%	6.10%	1.90%	1.80%	1.50%	0.00%	0.00%	0.00%	14.63%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Azithromycin	0.00%	0.00%	0.00%	1.20%	3.40%	3.30%	0.00%	0.00%	5.41%	13.43%
Ertapenem	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Imipenem	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Meropenem	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Tetracycline	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Colistin	0.00%	0.00%	0.00%	12.50%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Chloramphenicol	0.00%	0.90%	0.80%	3.80%	2.40%	2.20%	0.00%	0.00%	0.00%	4.62%

Figure 23. Yearly resistance rates of *S. Typhi*, DOH-ARSP, 2014-2023

Yearly resistance rates of *S*. Typhi for all antibiotics used to treat infections against them remained low in the past ten years with no reports of resistance against ciprofloxacin, imipenem, and meropenem for the year 2023 (Figure 23). However, the occurrence of resistance to ceftriaxone (p=1.000), cefotaxime (p=0.9182), co-trimoxazole (p= 0.0014) and chloramphenicol (p=0.0233) in 2023 where there had been no such occurrence in the past three years is herewith noted with the observed increase for the two latter antibiotics being statistically significant. Moreover, the increase in resistance rate for azithromycin from 5.4% in 2022 to 11.84% in 2023 was statistically significant (p= 0.0267).

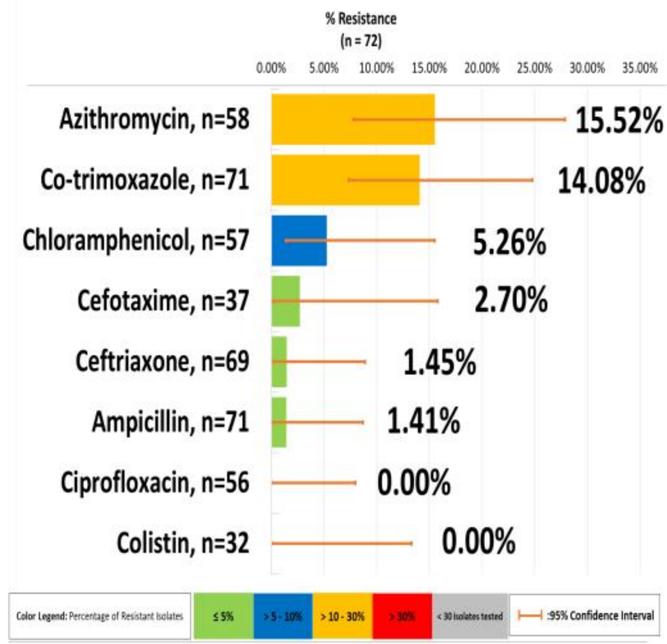


Figure 24. Resistance rates of *S. Typhi* blood isolates, DOH-ARSP, 2023

S. Typhi blood isolates were noted to be susceptible to ciprofloxacin. Resistance to ampicillin was at 1.41%, to chloramphenicol was at 5.26%, to co-trimoxazole at 14.08%, and to azithromycin at 15.52%. Resistance to ceftriaxone was at 1.45% and to cefotaxime at 2.70%.

Non-Typhodial *Salmonella*

A total of **321** non-typhoidal *Salmonella* (NTS) isolates were reported for 2023. This was a 12.24% increase than the 286 isolates in 2022. The highest contributing sites were VSM (14.95%), PGH (14.64%) and JLM (9.97%). Isolates were mostly reported from Luzon at 58.88% followed by Mindanao (20.87%) and Visayas (20.25%).

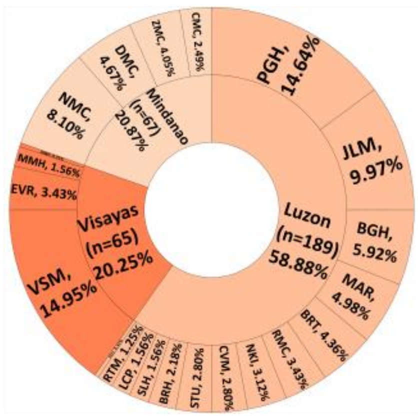


Figure 25. Isolate distribution of Non-typhoidal *Salmonella*, DOH-ARSP, 2023 (n=321)

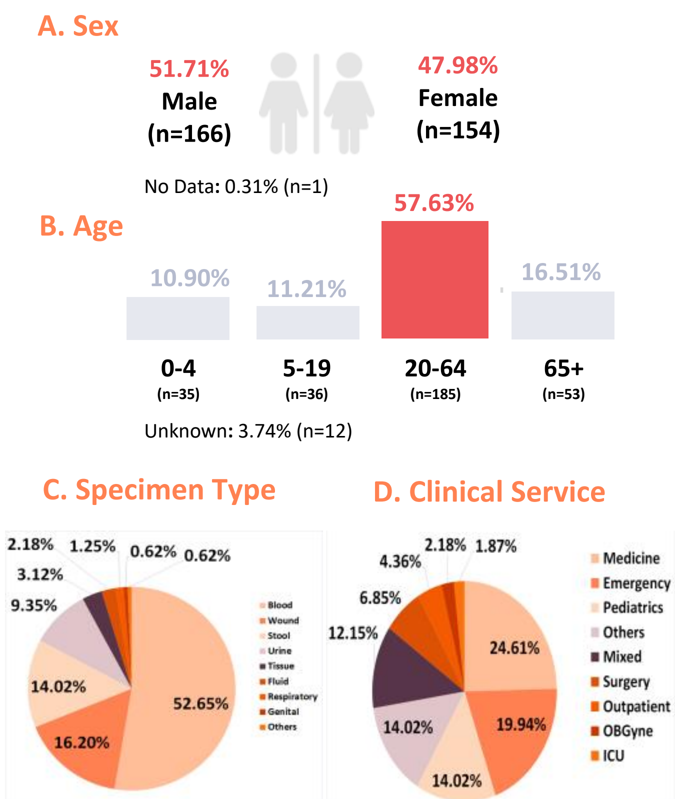


Figure 26. Patient characteristics of Non-typhoidal *Salmonella* isolates, DOH-ARSP, 2023 (n=321)

More than half (51.71%) of NTS isolates were from male patients and 57.63% were from the 20-64 age group (**Figure 26**). Most (52.65%) isolates reported were from blood samples and many (24.61%) were from Medicine clinical service.

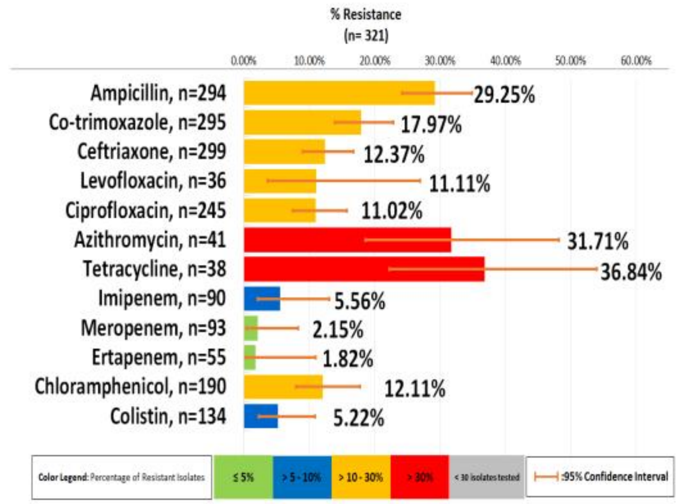


Figure 27. Resistance rates of Non-typhoidal *Salmonella* for all specimens, DOH-ARSP, 2023

Resistance rates for NTS isolates for 2023 are shown in **Figure 27**. Resistance to ciprofloxacin and ceftriaxone were at 11.02% and 12.37%, respectively. Resistance rates to co-trimoxazole was 17.97% which was higher than the observed resistance rate 13.1 last year, however the increase was not statistically significant (p=0.2133). The resistance rates for ceftriaxone (12.37%) and ciprofloxacin (11.02%) were both lower than the previous year but the decreases for both antibiotics were not statistically significant.

There was a confirmed ciprofloxacin resistant isolate from urine of a 58 year old female. The isolate was also resistant to ampicillin but susceptible to ceftriaxone, cefotaxime, and co-trimoxazole.

For 2023, there were 5 confirmed ceftriaxone and cefotaxime resistant isolates from stool samples (4 isolates) and a single blood specimen. The isolate from blood was *Salmonella* Cotonou and was from a 50-year-old female from Region III, showed resistance to ampicillin, and chloramphenicol making the isolate multidrug resistant. The isolate was susceptible to co-trimoxazole and tested intermediate to colistin.

There was one isolate of *Salmonella* Anatum confirmed to be resistant to cefotaxime. The isolate was from a fluid specimen of a 50-year old male. The isolate was resistant to ampicillin, chloramphenicol and co-trimoxazole but susceptible to ceftriaxone.

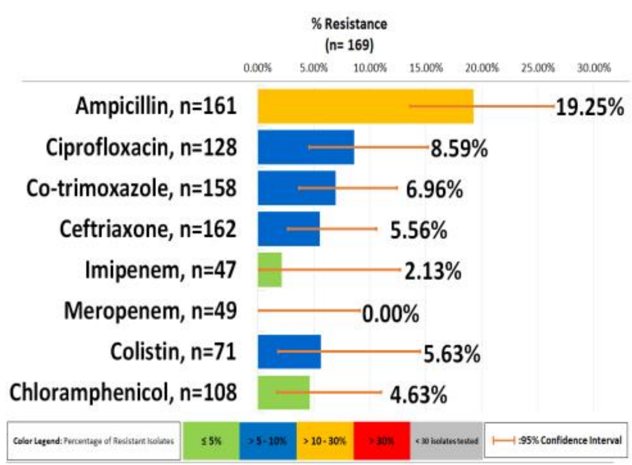
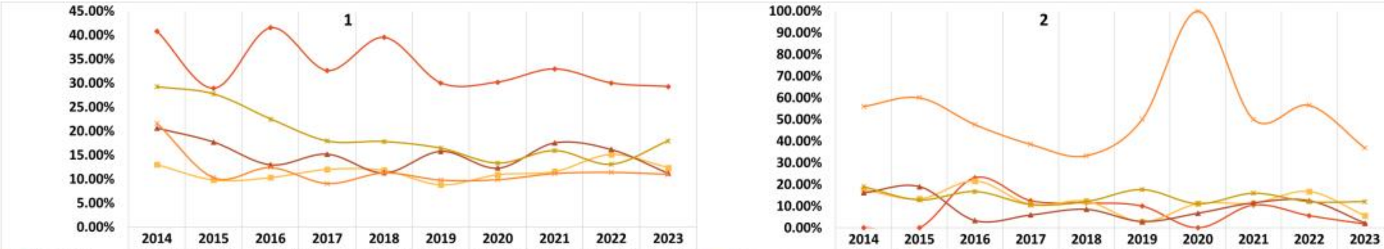


Figure 28. Resistance rates of non-typhoidal blood isolates, DOH-ARSP, 2023

Among NTS isolates from blood, resistance rates were at 19.25% for ampicillin, 8.59% for ciprofloxacin, 4.63% for chloramphenicol and 5.56% for ceftriaxone. Resistance rate to imipenem was 2.13%, while no resistance was observed for meropenem. Compared with overall resistance of NTS isolates from all samples, resistance to all antibiotics was lower for NTS isolates from blood.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ampicillin	40.80%	28.90%	41.50%	32.60%	39.50%	30.00%	30.20%	32.93%	30.00%	29.25%
Ceftriaxone	13.00%	9.80%	10.30%	12.00%	11.80%	8.80%	10.90%	11.56%	15.09%	12.37%
Cefotaxime	20.60%	17.70%	13.00%	15.20%	11.30%	15.80%	12.30%	17.54%	16.15%	11.22%
Ciprofloxacin	21.60%	10.30%	12.40%	9.10%	11.30%	9.80%	9.90%	11.18%	11.42%	11.02%
Co-trimoxazole	29.20%	27.70%	22.50%	17.90%	17.80%	16.40%	13.30%	15.91%	13.06%	17.97%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ertapenem	0.00%	0.00%	23.10%	12.50%	11.50%	10.00%	0.00%	10.50%	5.60%	1.82%
Imipenem	17.60%	13.30%	21.60%	10.70%	12.20%	2.80%	11.10%	11.40%	16.70%	5.56%
Meropenem	16.10%	19.00%	3.30%	5.90%	8.50%	2.90%	6.70%	11.50%	12.50%	2.15%
Tetracycline	56.00%	60.00%	47.60%	38.50%	33.30%	50.00%	100.00%	50.00%	56.50%	36.84%
Chloramphenicol	19.00%	12.90%	16.80%	10.80%	12.10%	17.70%	11.10%	16.00%	12.02%	12.11%

Figure 29. Yearly resistance rates of NTS isolates from 2014-2023

Yearly resistance rates for non-typhoidal isolates are shown in **Figure 29**. In the last three years, there is an observed decrease in the resistance rates for ampicillin (p=0.0041) and cefotaxime (p=0.6497). The resistance rates were noted to be decreasing for co-trimoxazole (p=0.0000), ceftriaxone (p=0.4446) and chloramphenicol (p=0.1328).

Table 6. *Salmonella* serotypes per age group, DOH-ARSP, 2023

SEROTYPE	AGE 0-4	AGE 5-19	AGE 20-64	AGE >=65
	5 10 15 20 25 30	5 10 15 20 25 30	5 10 15 20 25 30	5 10 15 20 25 30
Salmonella Enteritidis (n=43)				
Salmonella Typhi (n=41)				
Salmonella Typhimurium (n=21)				
Salmonella species (n=13)				
Salmonella Amager (n=8)				
Salmonella Infantis (n=6)				
Salmonella Weltevreden (n=6)				
Salmonella Newport (n=4)				
Salmonella Paratyphi B (n=4)				
Salmonella Stanley (n=3)				
Salmonella Group E1 (n=2)				
Salmonella Group I (n=2)				
Salmonella Hvittingfoss (n=2)				
Salmonella Rissen (n=2)				
Salmonella Senftenberg (n=2)				
Salmonella Anatum (n=1)				
Salmonella Corvallis (n=1)				
Salmonella Cotonou (n=1)				
Salmonella Derby (n=1)				
Salmonella Group C (n=1)				
Salmonella Group F (O:11) (n=1)				
Salmonella Group Y (n=1)				
Salmonella London (n=1)				
Salmonella Ohio (n=1)				
Salmonella Virchow (n=1)				

There were **169** *Salmonellae* referred to the reference laboratory for serotyping. There were 25 *Salmonella* serotypes identified for 2023. Most of the isolates were *Salmonella enterica* serovar Enteritidis (25.44%) and *Salmonella enterica* serovar Typhi (24.26%) (**Table 6**). Among the 128 confirmed non-typhoidal *Salmonella*, most common serotypes were *Salmonella enterica* serovar Enteritidis (n=43) followed by *Salmonella enterica* serovar Typhimurium (n=21). These two serotypes had been the most common serotypes reported for the past three years. Antimicrobial resistance among NTS may reflect variations in serotypes, its distribution or both.

Shigella species

There were **39** *Shigella* species reported in 2023. Most isolates were from VSM at 41.03%, CVM at 10.26%, and PGH at 7.69%. Based on island group distribution, the majority were from Visayas at 46.15%, Luzon at 36.90%, and Mindanao at 17.95% (**Figure 30**). Most of the isolates (63.41%) were from patients aged 20-64 with 61.54% from stool samples. (**Figure 31**)

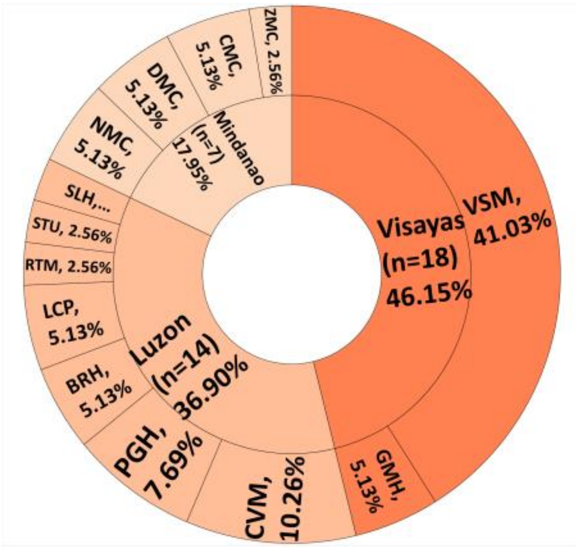
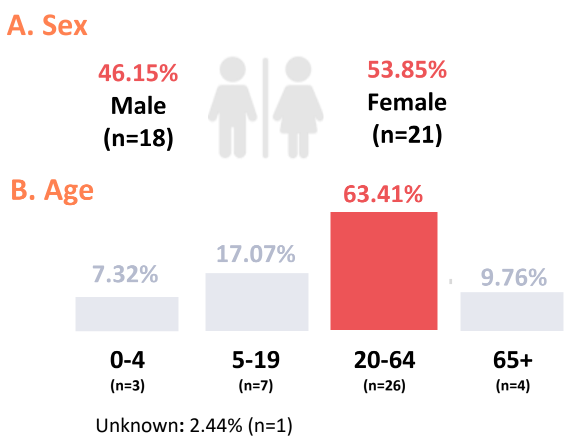
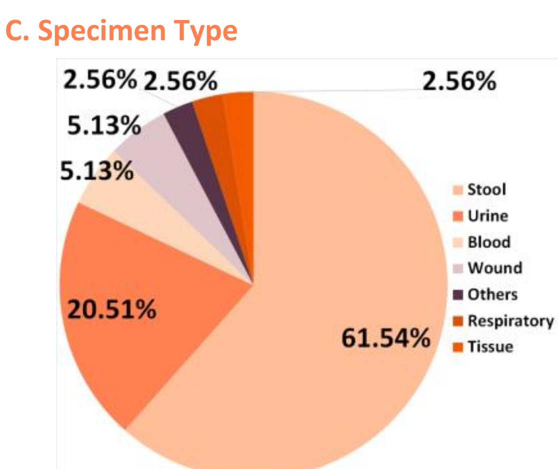


Figure 30. Isolate distribution of *Shigella* species, DOH-ARSP 2023 (n= 39)





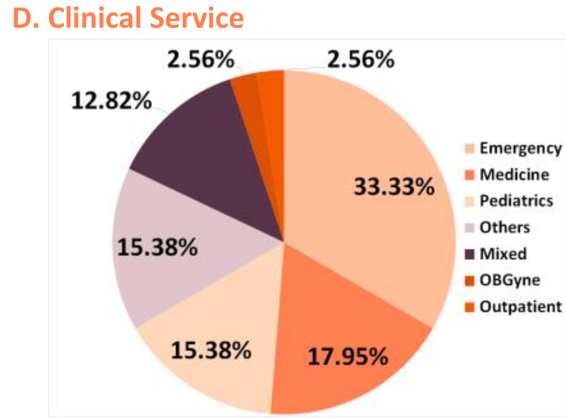


Figure 31. Patient characteristics of *Shigella species* isolates, DOH-ARSP, 2023 (n=39)

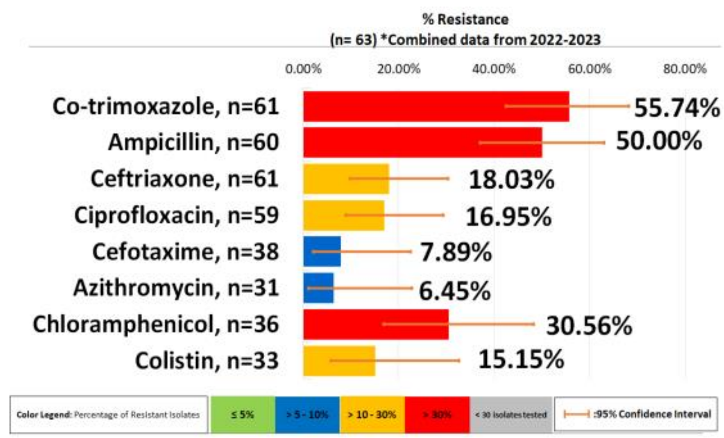
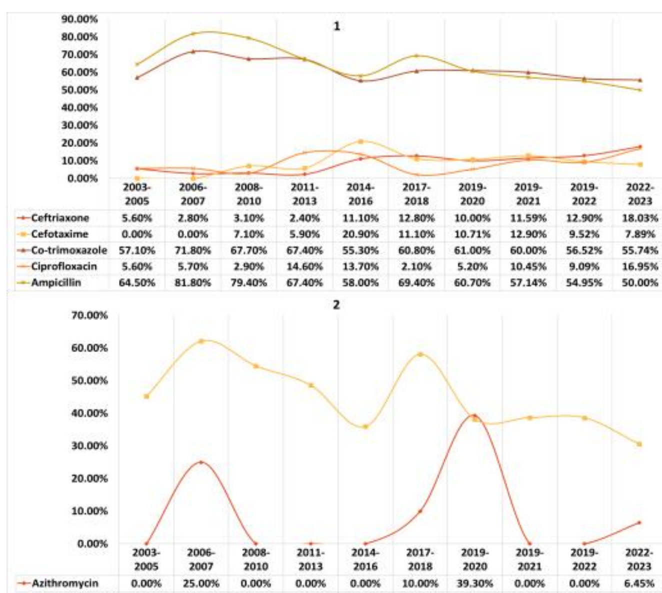


Figure 32. Resistance rates of *Shigella* species from all specimens, DOH-ARSP, 2022-2023 (n=63)

Figure 32 shows the cumulative resistance rates of *Shigella* species for all specimens from 2022-2023. Resistance to ceftriaxone was 18.03%, to cefotaxime at 7.89%, 16.95% to ciprofloxacin and 6.45% for azithromycin. Co-trimoxazole, ampicillin and chloramphenicol resistance remained high at 55.74%, 50.0%, and 30.56%, respectively.



	2003-2005	2006-2007	2008-2010	2011-2013	2014-2016	2017-2018	2019-2020	2019-2021	2019-2022	2022-2023
Ceftriaxone	5.60%	2.80%	3.10%	2.40%	11.10%	12.80%	10.00%	11.59%	12.90%	18.03%
Cefotaxime	0.00%	0.00%	7.10%	5.90%	20.90%	11.10%	10.71%	12.90%	9.52%	7.89%
Co-trimoxazole	57.10%	71.80%	67.70%	67.40%	55.30%	60.80%	61.00%	60.00%	56.52%	55.74%
Ciprofloxacin	5.60%	5.70%	2.90%	14.60%	13.70%	2.10%	5.20%	10.45%	9.09%	16.95%
Ampicillin	64.50%	81.80%	79.40%	67.40%	58.00%	69.40%	60.70%	57.14%	54.95%	50.00%

	2003-2005	2006-2007	2008-2010	2011-2013	2014-2016	2017-2018	2019-2020	2019-2021	2019-2022	2022-2023
Azithromycin	0.00%	25.00%	0.00%	0.00%	0.00%	10.00%	39.30%	0.00%	0.00%	6.45%
Chloramphenicol	45.20%	62.10%	54.50%	48.60%	35.90%	58.10%	38.10%	38.64%	38.60%	30.56%

Figure 33. Yearly resistance rates of *Shigella* species from 2003-2023.

A comparison of the cumulative rates obtained from 2003 – 2023 (**Figure 33**) shows the changes in resistance rates of *Shigella* sp. over the 11-year period. Statistical analyses showed that there were no significant changes in resistance rates from 2022-2023. The decreasing resistance rates from 2003 were statistically significant for ampicillin (p=0.0302) and chloramphenicol (p=0.0095), while increasing trends for azithromycin (p=0.0021) and ceftriaxone (p=0.0020) were likewise significant.

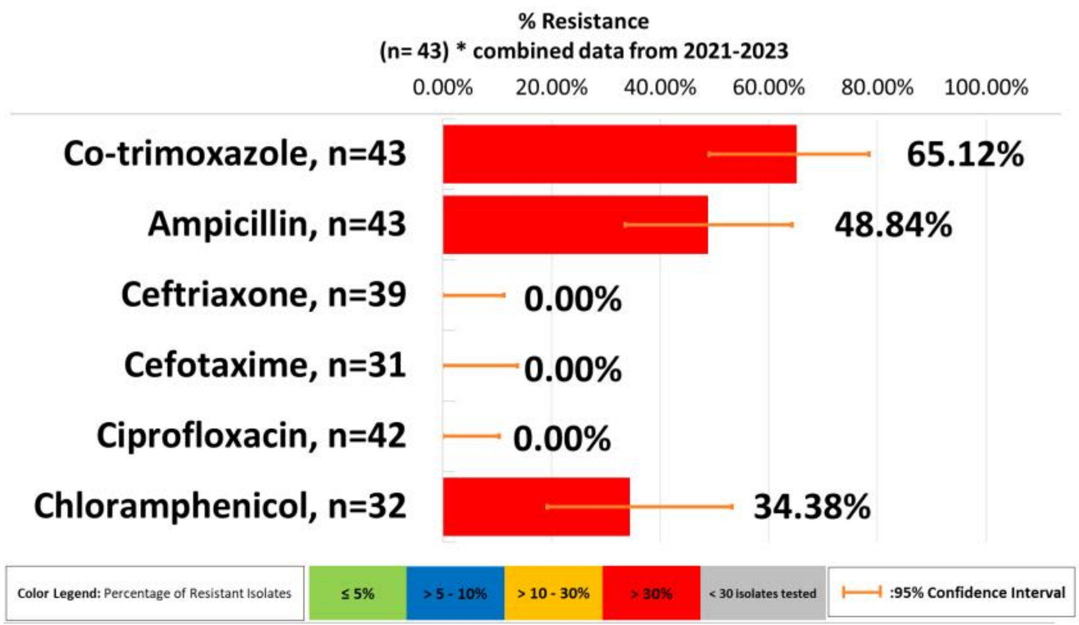


Figure 34. Resistance rates of *Shigella species* from stool isolates, DOH-ARSP, 2022-2023 (n=43)

Resistance rates for *Shigella* sp from stool samples from 2022-2023 were shown in **Figure 34**. Isolates from stool remained susceptible to ceftriaxone, cefotaxime, and ciprofloxacin. Co-trimoxazole, ampicillin,and chloramphenicol resistance were high at 65.12%, 48.84%, and 34.38%, respectively. Compared with the cumulative resistance rates of isolates from all samples, *Shigella* sp isolates from stool have lower resistance to ceftriaxone, cefotaxime, ciprofloxacin and ampicillin and have higher resistance to co-trimoxazole and chloramphenicol.

There was one *Shigella* sp isolate from the Visayas that was confirmed to be extensively drug-resistant. The isolate was from a urine specimen of a 22-year old male and was noted to be resistant to ampicillin, azithromycin, cefotaxime, ciprofloxacin, colistin, and co-trimoxazole. The occurrence of this phenotype appears to be an isolated case and no report of a similar isolate was further noted for the year.

Vibrio cholerae

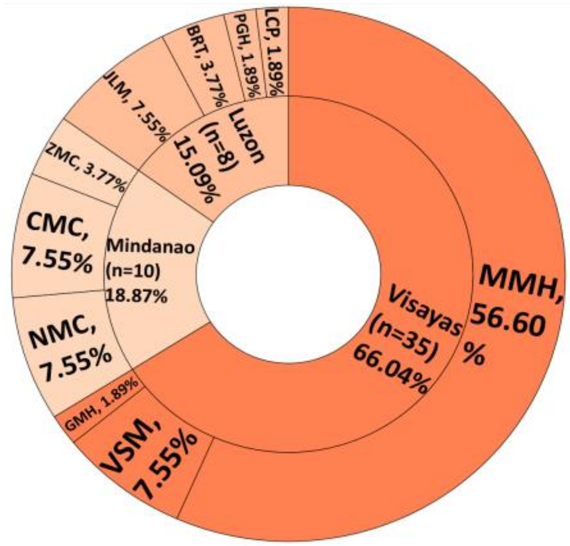


Figure 35. Isolate distribution of *V. cholerae* isolates, 2023, DOH-ARSP (n=53)

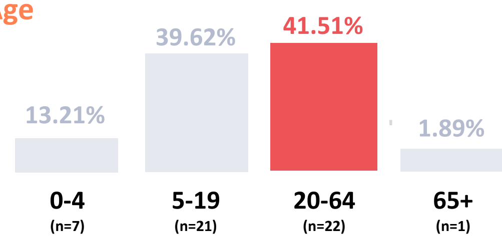
There were a total of **53** *Vibrio cholerae* isolates reported for 2023 (Figure 35). This is 70% lower than the reported isolates in 2022. Majority of the isolates were from MMH at 56.60% followed by CMC, JLM and NMC at 7.55%. Distribution by island group shows the Visayas having the majority of isolates at 66.04%, Mindanao at 18.87%, and Luzon at 15.09%.

A. Sex

50.94%
Male
(n=27)

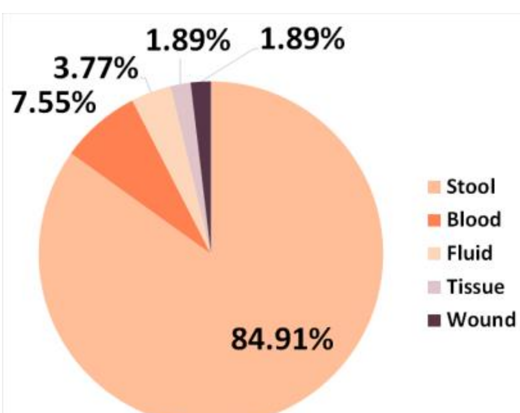
49.06%
Female
(n=26)

B. Age



Unknown: 3.77% (n=2)

C. Specimen Type



D. Clinical Service

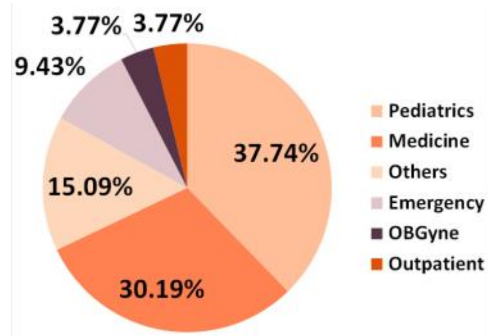


Figure 36. Patient characteristics of *V. cholerae* isolates, DOH-ARSP, 2023 (n=69)

Many of *V. cholerae* isolates reported were from the 20-64 age group (41.51%) and many of the patients were from the pediatric and medicine wards. (**Figure 36**) Majority (84.91%) were isolated from stool samples.

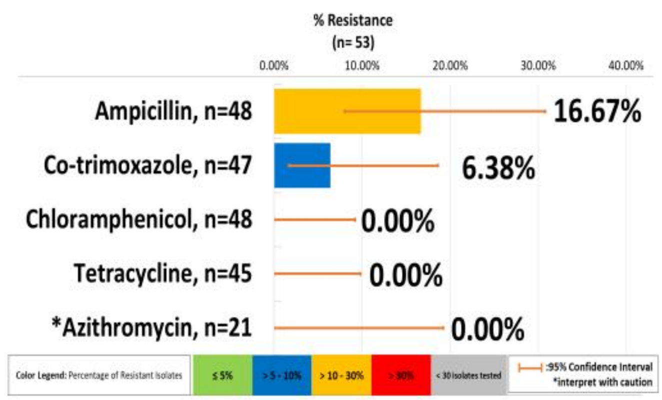
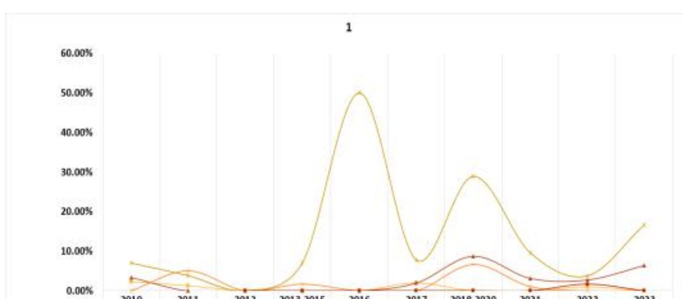


Figure 37. Resistance rates of *V. cholerae* isolates from all specimens, DOH-ARSP, 2023 (n=69)

For 2023, *V. cholerae* isolates remained susceptible to tetracycline, azithromycin and chloramphenicol. Resistance to ampicillin was at 16.67% and this was higher (p=0.0002) than the observed resistance rate to this antibiotic at 3.76% in 2022. Resistance to co-trimoxazole was at 6.38%.



	2010	2011	2012	2013-2015	2016	2017	2018-2020	2021	2022	2023
Chloramphenicol	2.30%	1.30%	0.00%	0.00%	0.00%	2.00%	0.00%	0.00%	1.00%	0.00%
Co-trimoxazole	3.40%	0.00%	0.00%	0.00%	0.00%	2.00%	8.70%	3.16%	2.76%	6.38%
Tetracycline	0.00%	5.10%	0.00%	1.70%	0.00%	0.00%	6.70%	1.05%	0.00%	0.00%
Ampicillin	7.00%	3.80%	0.00%	7.00%	50.00%	7.80%	28.90%	9.57%	3.76%	16.67%
Azithromycin			0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	1.68%	0.00%

Figure 38. Yearly resistance rates of *V. cholerae* isolates, DOH-ARSP 2010-2023

Yearly resistance rates for *V. cholerae* are shown in **Figure 38**. Except for ampicillin, resistance rates for most of the antibiotics remained largely less than 5%. Multiple year analyses for all antibiotics showed no significant difference.

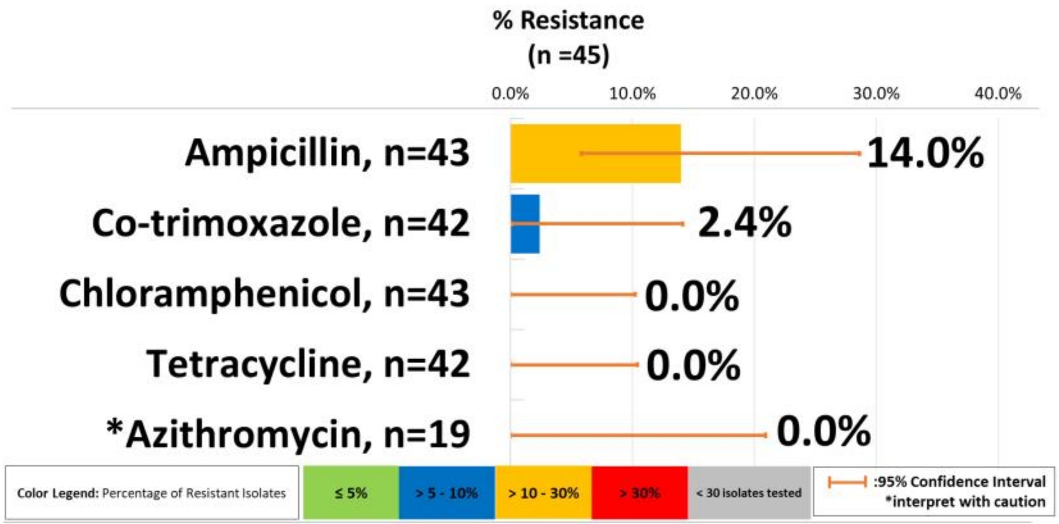


Figure 39. Resistance rates of *V. cholerae* isolates from stool specimens, DOH-ARSP, 2023 (n=61)

Resistance rates of *V. cholerae* from stool specimens are shown in **Figure 39**. *V. cholerae* isolates from stool specimens remained susceptible to tetracycline, azithromycin and chloramphenicol. Resistance to ampicillin was at 13.95% and to co-trimoxazole at 2.38%.

Neisseria gonorrhoeae

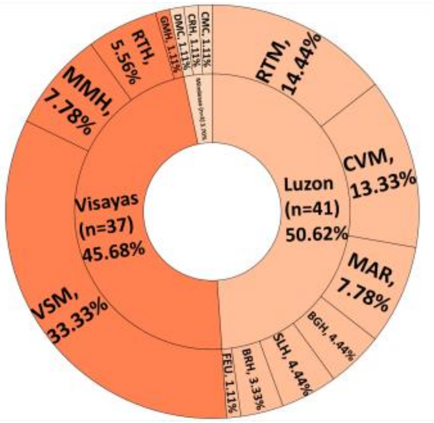


Figure 40. Isolate distribution of *N. gonorrhoeae* isolates, DOH – ARSP, 2023 (n=81)

There were **81** isolates of *Neisseria gonorrhoeae* reported for 2023 (**Figure 40**). This is 84% higher than the number reported in 2022 (n=44). The largest contributor was VSM at 33.33%, RTM at 14.44% and CVM at 13.33%. Based on island group distribution, many isolates were from patients in Luzon at 50.62%.

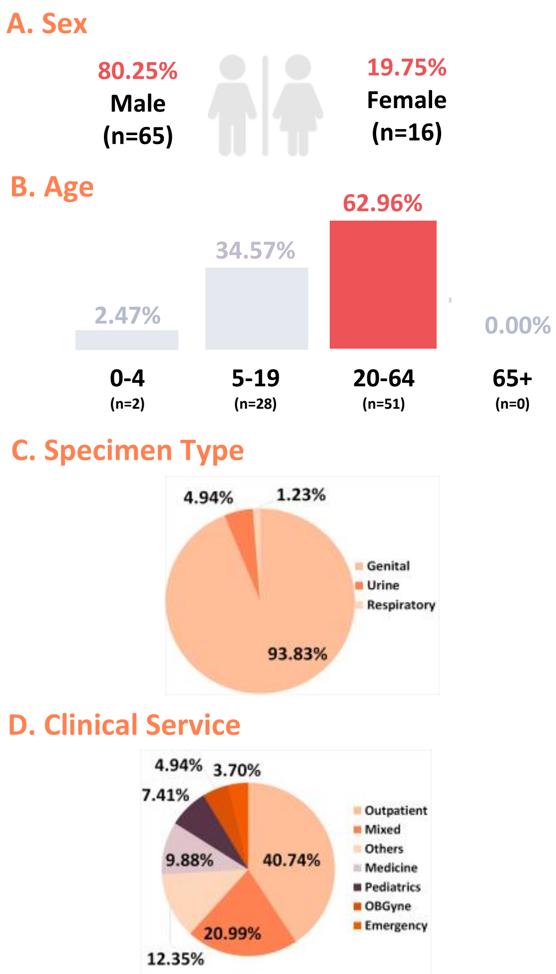


Figure 41. Patient characteristics of *N. gonorrohoeae* isolates, DOH-ARSP, 2023 (n=90)

Most isolates were from male (80.25%) and adult (62.96%) patients (**Figure 41**) and were mostly from genital specimens (93.83%).

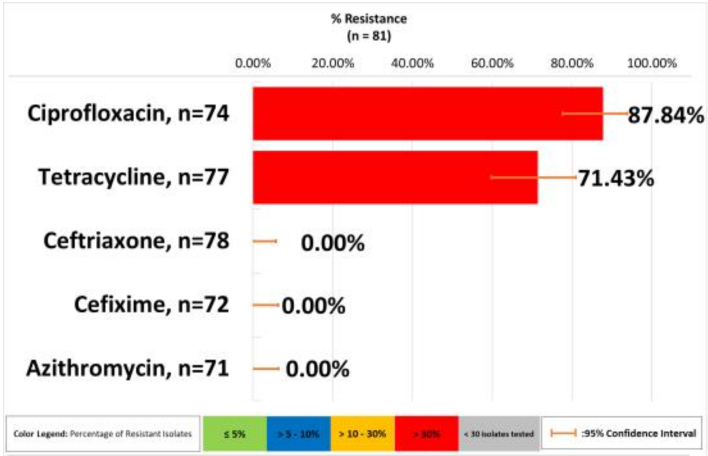


Figure 42. Percent resistance of *N. gonorrhoeae* isolates, DOH-ARSP, 2023 (n=81)

Figure 42 shows the resistance rates of *N. gonorrhoeae* isolates in 2023. All isolates tested remained susceptible to ceftriaxone, cefixime, and azithromycin. The highest resistances were for ciprofloxacin at 87.84% and tetracycline at 71.43%.

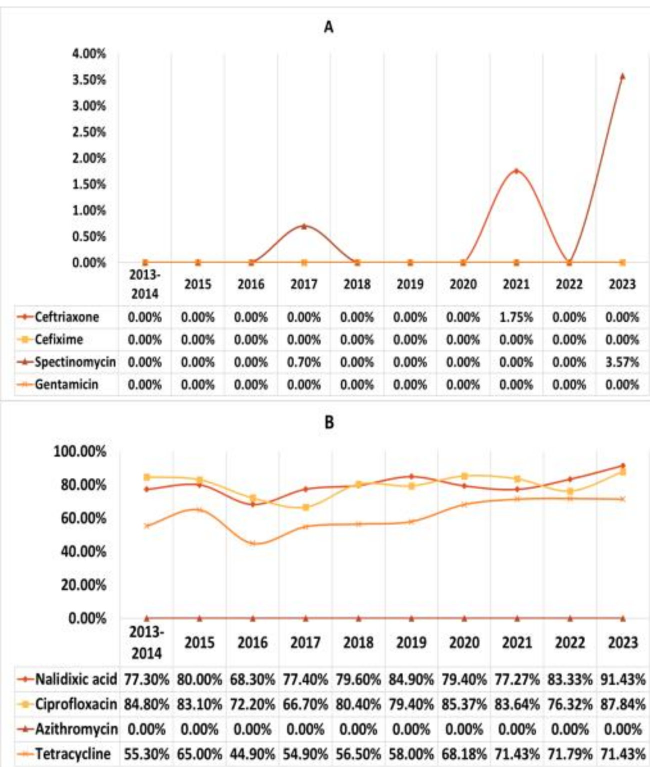


Figure 43. Yearly resistance rates of *N. gonorrhoeae* isolates from 2013-2023, DOH-ARSP

Multi-year analysis of *N. gonorrhoeae* resistance rates from 2013-2023 are shown in **Figure 43**. In the past 11 years, the isolates remained susceptible to azithromycin (p=0.09901), cefixime (p=0.9979) and ceftriaxone (p=0.9983).

Staphylococcus aureus

There were **7,834** *Staphylococcus aureus* isolates reported for 2023. This is a 38.37% increase from the number reported in 2022 (n=5,663). The largest contributors were PGH (13.49%), DMC (9.11%) and BGH (7.37%) (**Figure 44**). Luzon had the highest number of isolates at 61.46%, Mindanao at 23.41% and Visayas at 15.13%.

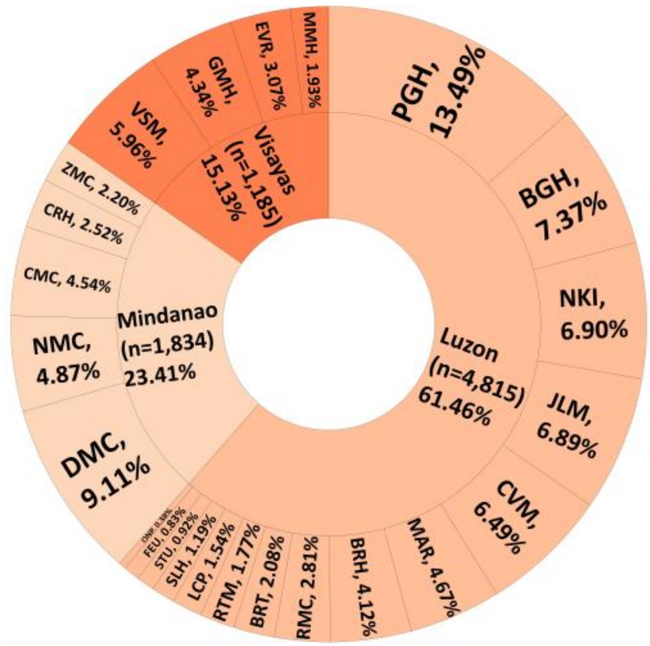
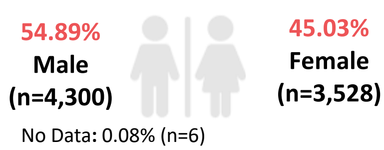
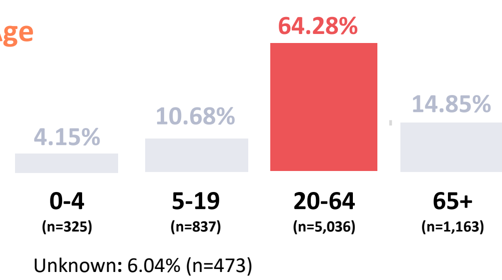


Figure 44. Isolate distribution of *S. aureus*, DOH-ARSP, 2023, (n= 7,834)

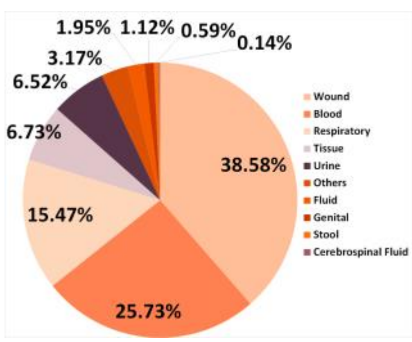
A. Sex



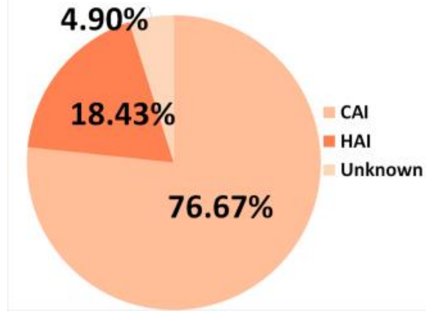
B. Age



C. Specimen Type



D. Infection Type



E. Clinical Service

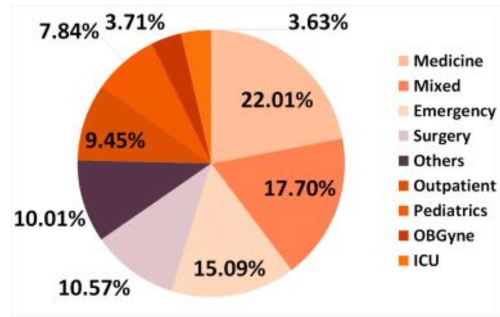


Figure 45. Patients characteristics of *S. aureus* isolates, DOH-ARSP, 2023, (n=7,834)

More than half (64.28%) of the isolates were from 20-64 years old and more frequently (54.89%) obtained from male patients (**Figure 45**). The highest percentage of the specimens are wound samples (38.58%) followed by blood (25.73%) and respiratory (15.47%) samples. Majority (76.67%) of the isolates were from community-acquired infections.

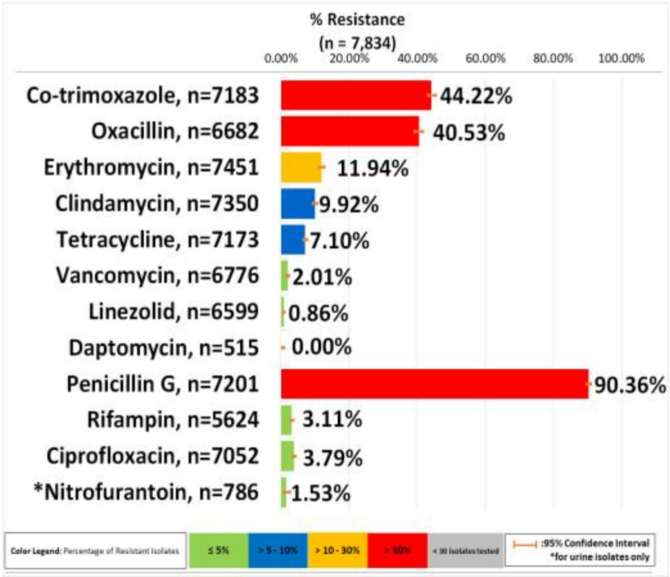
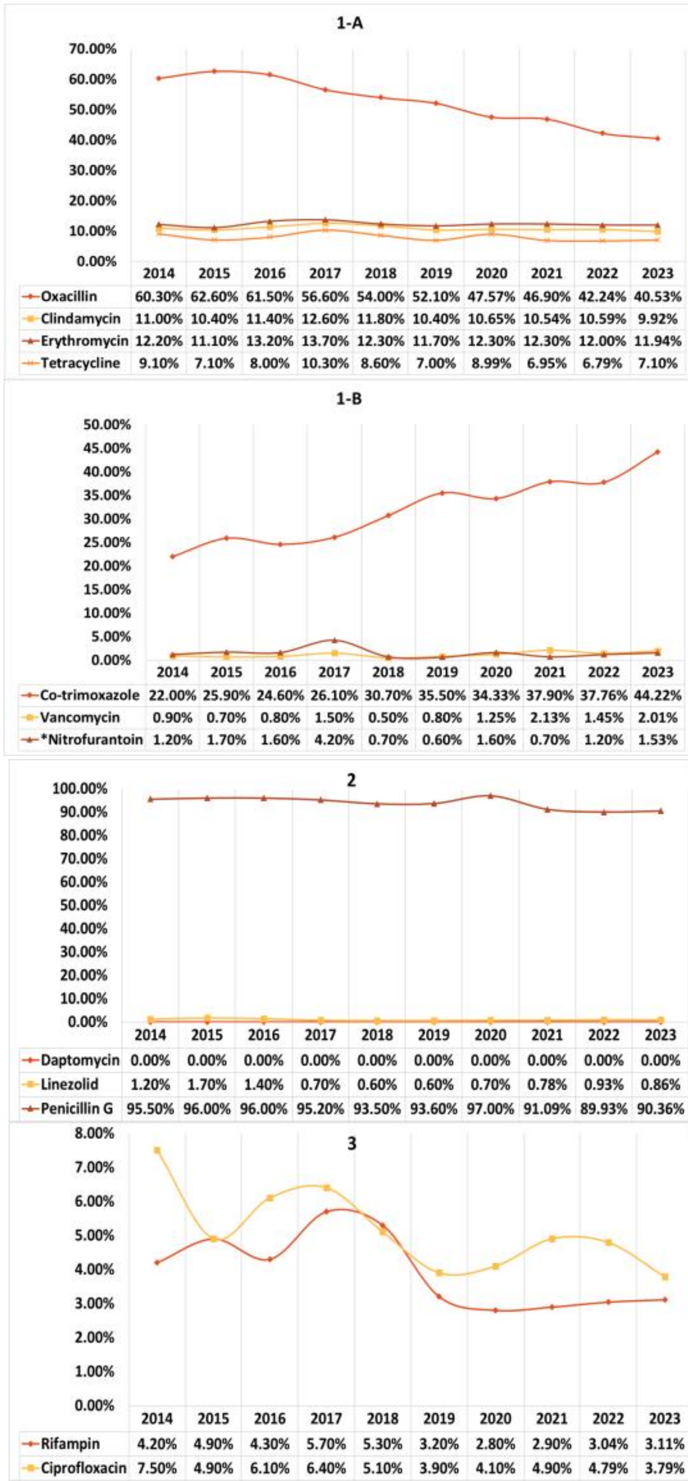


Figure 46. Resistance rates of *S. aureus* for all specimens, DOH-ARSP, 2023

The overall resistance rate of *S. aureus* for all specimens reported for 2023 is shown in Figure 46. Resistance to oxacillin was 40.53%, to clindamycin at 9.92% and co-trimoxazole at 44.22%. Resistance to erythromycin was at 11.94% and to tetracycline at 7.10%. Resistance to vancomycin and linezolid were below 3% while no resistance to daptomycin was reported. The observed increase in the resistance rates in 2023 from that of 2022 for vancomycin and co-trimoxazole were both statistically significant as well as the noted decrease in resistance rates for clindamycin and ciprofloxacin (Figure 46).



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Oxacillin	60.30%	62.60%	61.50%	56.60%	54.00%	52.10%	47.57%	46.90%	42.24%	40.53%
Clindamycin	11.00%	10.40%	11.40%	12.60%	11.80%	10.40%	10.65%	10.54%	10.59%	9.92%
Erythromycin	12.20%	11.10%	13.20%	13.70%	12.30%	11.70%	12.30%	12.30%	12.00%	11.94%
Tetracycline	9.10%	7.10%	8.00%	10.30%	8.60%	7.00%	8.99%	6.95%	6.79%	7.10%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Co-trimoxazole	22.00%	25.90%	24.60%	26.10%	30.70%	35.50%	34.33%	37.90%	37.76%	44.22%
Vancomycin	0.90%	0.70%	0.80%	1.50%	0.50%	0.80%	1.25%	2.13%	1.45%	2.01%
*Nitrofurantoin	1.20%	1.70%	1.60%	4.20%	0.70%	0.60%	1.60%	0.70%	1.20%	1.53%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Daptomycin	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Linezolid	1.20%	1.70%	1.40%	0.70%	0.60%	0.60%	0.70%	0.78%	0.93%	0.86%
Penicillin G	95.50%	96.00%	96.00%	95.20%	93.50%	93.60%	97.00%	91.09%	89.93%	90.36%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Rifampin	4.20%	4.90%	4.30%	5.70%	5.30%	3.20%	2.80%	2.90%	3.04%	3.11%
Ciprofloxacin	7.50%	4.90%	6.10%	6.40%	5.10%	3.90%	4.10%	4.90%	4.79%	3.79%

Figure 47. Yearly resistance rates of *S. aureus* isolates from 2014-2023

Yearly resistance rates for *S. aureus* are shown in Figure 47. Oxacillin resistance continues to decrease since 2014 and multiple year analysis showed that the noted changes in resistance rates were statistically significant (p=0.0000). Over the past decade, resistance to clindamycin (p = 0.0000) and erythromycin (p=0.0006) were noted to be decreasing while resistance to co-trimoxazole was noted to be increasing (p=0.0000). Vancomycin resistance rates in the past decade remained less than 5%.

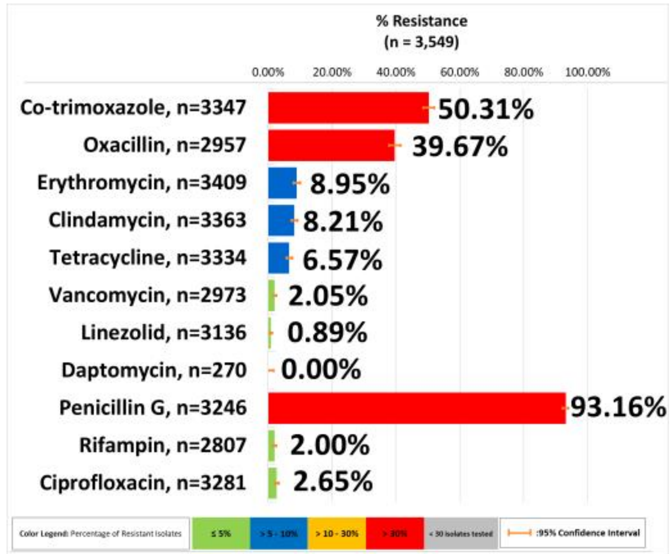
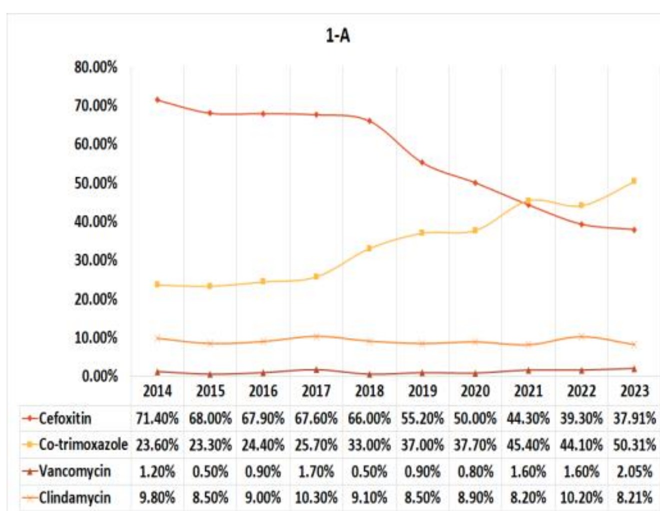


Figure 48. Resistance rates of *S. aureus* skin and soft tissue isolates, DOH-ARSP, 2023

Figure 48 shows the resistance rates of *S. aureus* isolates from skin and soft tissues. Resistance rates against oxacillin was 39.67%, clindamycin at 8.21%, co-trimoxazole at 50.31%, erythromycin at 8.95%, tetracycline at 6.57%, vancomycin at 2.05% and linezolid at 0.89%. No isolates resistant against daptomycin were reported. Compared with resistance rates of *S. aureus* isolates from all samples, resistance rates of *S. aureus* isolates from skin and soft tissues were higher for co-trimoxazole, penicillin and linezolid.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Cefoxitin	71.40%	68.00%	67.90%	67.60%	66.00%	55.20%	50.00%	44.30%	39.30%	37.91%
Co-trimoxazole	23.60%	23.30%	24.40%	25.70%	33.00%	37.00%	37.70%	45.40%	44.10%	50.31%
Vancomycin	1.20%	0.50%	0.90%	1.70%	0.50%	0.90%	0.80%	1.60%	1.60%	2.05%
Clindamycin	9.80%	8.50%	9.00%	10.30%	9.10%	8.50%	8.90%	8.20%	10.20%	8.21%

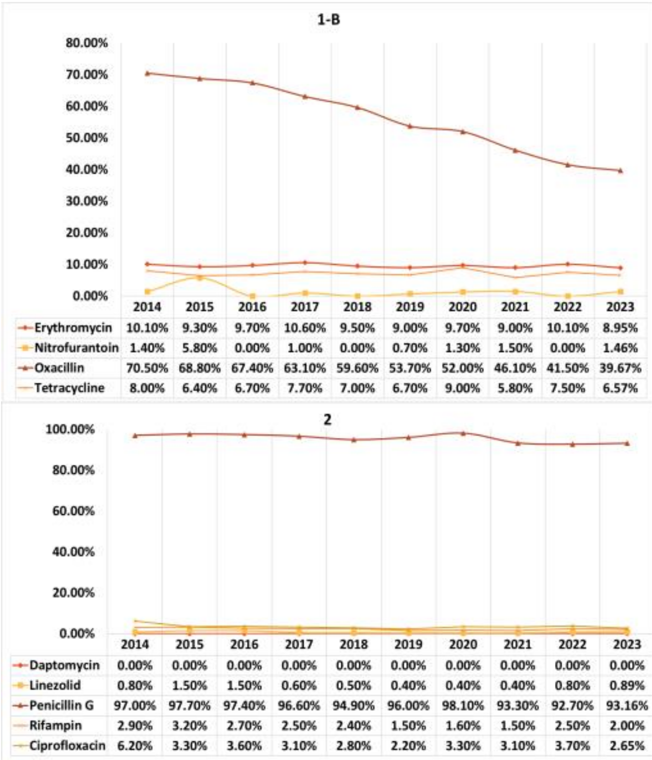


Figure 49. Yearly resistance rates of *S. aureus* skin and soft tissues isolates, DOH-ARSP, 2023

Figure 49 shows the yearly resistance rates of *S. aureus* skin and tissue isolates. Oxacillin (p=0.0000) and penicillin (p=0.0000) resistance showed decreasing rates over the last ten years while co-trimoxazole (p=0.0000) resistance was observed to have an increasing rate. Multi-year analysis showed that the differences noted across years were significant for all antibiotics except for daptomycin (p= 0.9843) and linezolid (p=0.8762).

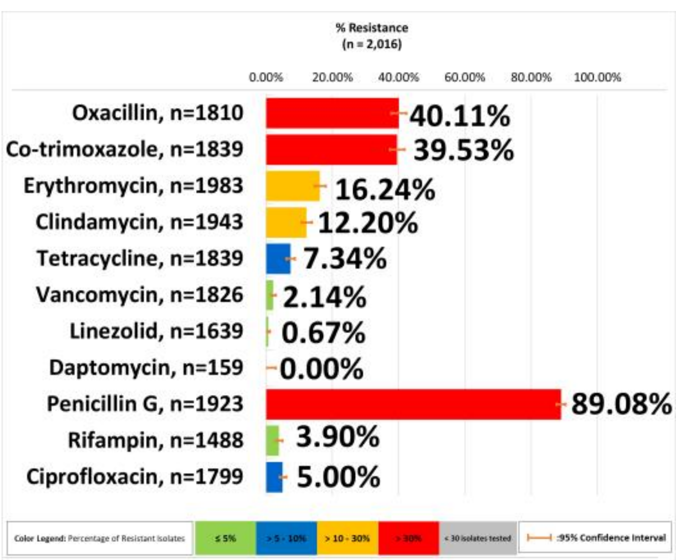


Figure 50. Resistance rates of *S. aureus* blood isolates, DOH-ARSP, 2023

The resistance rates of *S. aureus* from blood isolates are shown in **Figure 50**. Resistance against oxacillin was 40.11%, clindamycin at 12.20%, erythromycin at 16.24%, and co-trimoxazole at 39.53%. Resistance to vancomycin was at 2.14% and linezolid at 0.67% and no resistance to daptomycin was reported. Compared with resistance rates of *S. aureus* isolates from all samples, resistance rates of *S. aureus* isolates from blood were higher for erythromycin, clindamycin, vancomycin, rifampin and ciprofloxacin.

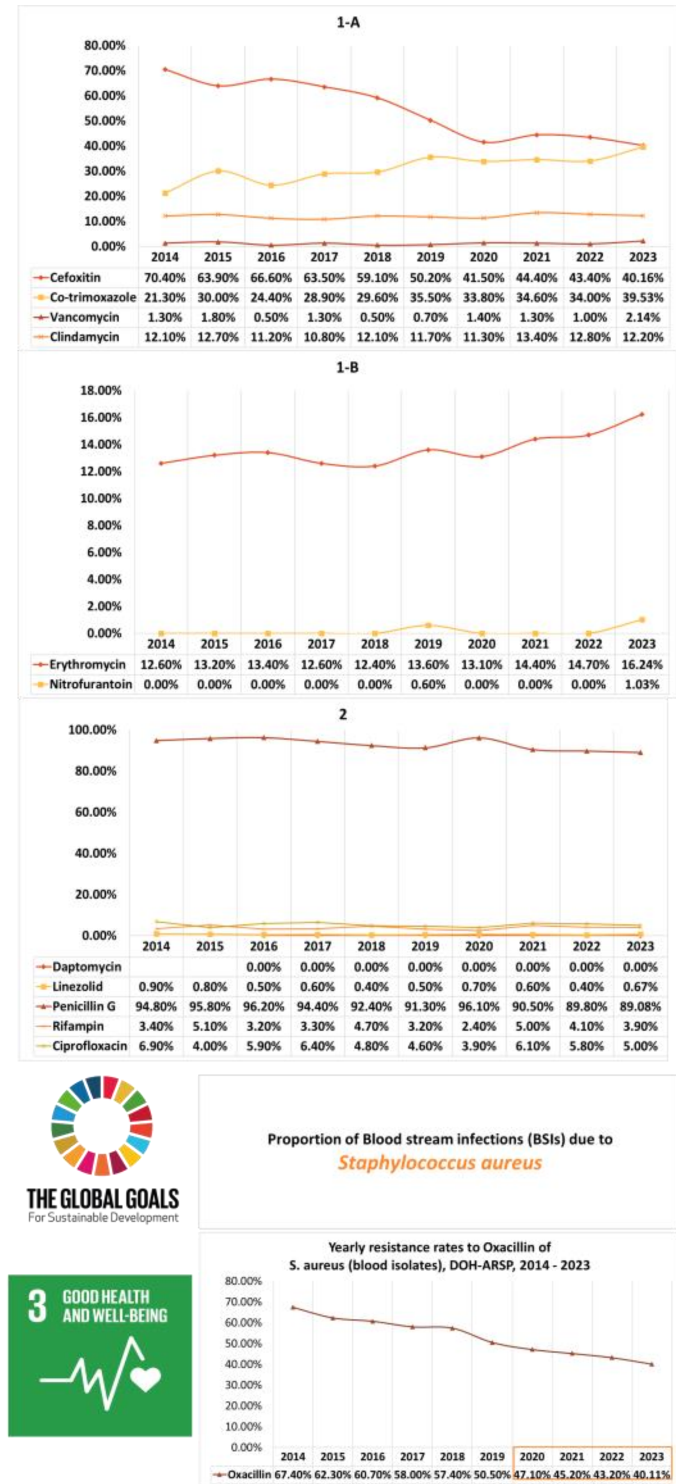


Figure 51. Yearly resistance rates of *S. aureus* blood isolates, DOH-ARSP, 2023

Figure 51 shows the yearly resistance rates of *S. aureus* blood isolates. Oxacillin (p=0.0000) and penicillin (p=0.0000) resistance showed a decreasing trend over the last ten years. Multi-year analysis showed that the differences noted across years were significant for all antibiotics except for daptomycin (p= 0.2376) and linezolid (p=0.4376).

One of the AMR indicators in the monitoring framework for the Sustainable Development Goals (SDG) linked to the health target 3.d ("strengthen the capacity of all countries, in particular developing countries, for early warning, risk reduction and management of national and global health risks" ïncluded in 2020 is the proportion of patients with bloodstream infections (BSI) caused by methicillin-resistant *S. aureus*[8,9],. As shown in **Figure 51**, the percentage of methicillin(oxacillin)-resistant *S. aureus* isolates from blood samples has been noted to decrease over the past decade. Using isolates from blood specimens as proxy for patients with BSI caused by methicillin-resistant *S. aureus*, ARSP data indicates that the Philippines is on the way to achieving the SDG target to reduce the proportion of patients with bloodstream infections (BSI) caused by methicillin-resistant *S. aureus.*

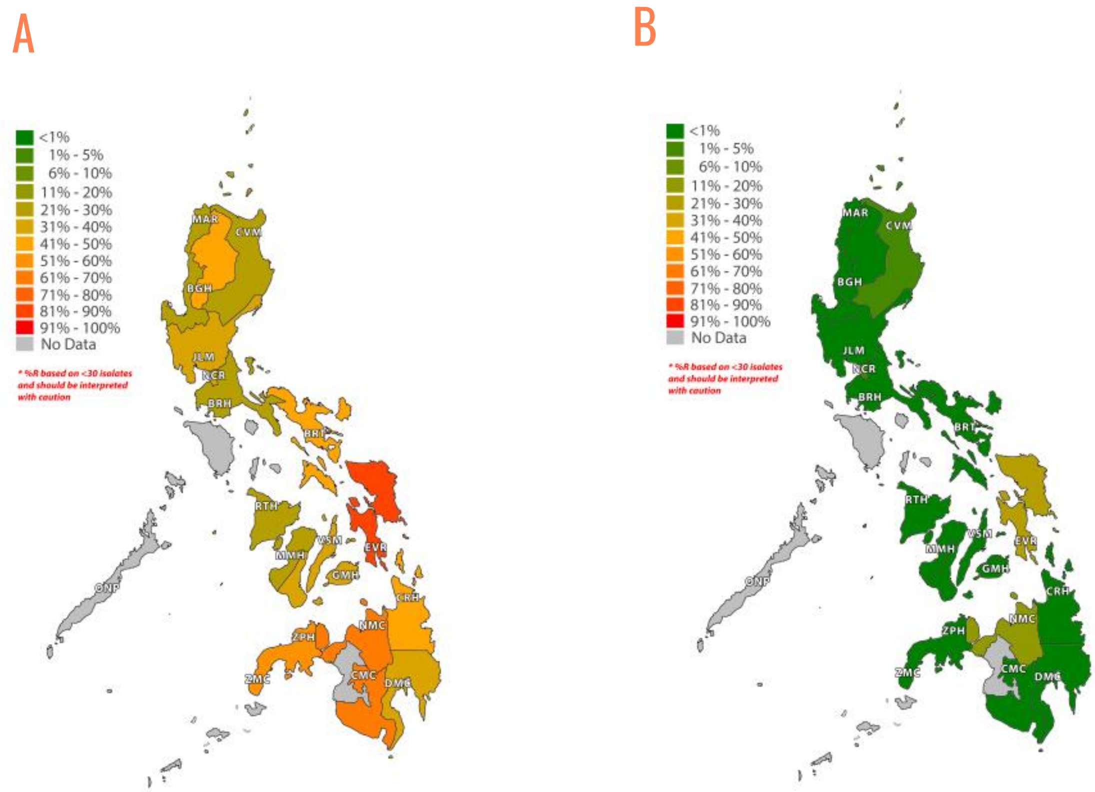


Figure 52. Geographic distribution of A) oxacillin-resistant and B) vancomycin-resistant *S. aureus* in the Philippines, DOH-ARSP, 2023

The oxacillin resistance rates of *S. aureus* across different regions in the country is shown in **Figure 52.A**. Sentinel sites in Mindanao have MRSA rates from 51-71%, while sentinel sites in the Visayas have a wide range from 11-80%. In Luzon, the sentinel sites have MRSA rates ranging from 21-50%. The geographic distribution of vancomycin-resistant isolates is shown in **Figure 52.B**. Resistance rates to most of the sentinel sites were less than 1%.

Methicillin Resistant *Staphylococcus aureus*

There were **2,448** methicillin-resistant *Staphylococcus aureus* (MRSA) isolates reported for 2023. Largest contributors for MRSA include BGH (10.97%), DMC (10.85%) and JLM (7.99%).

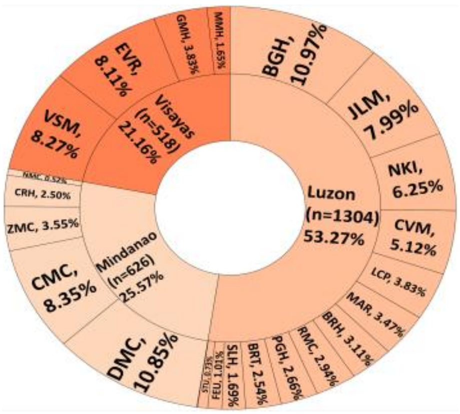
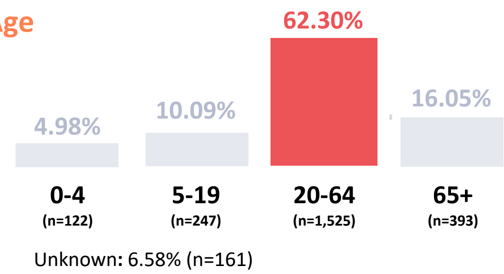


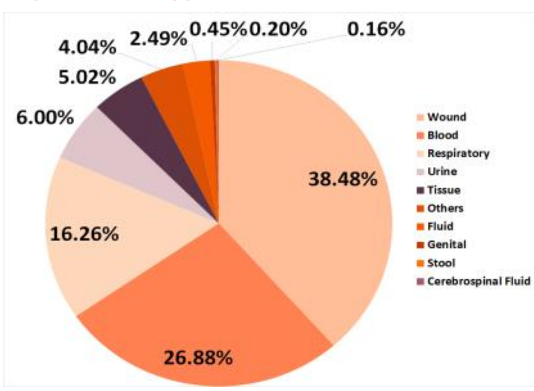
Figure 53. Isolate distribution of methicillin-resistant *S. aureus*, DOH-ARSP, 2023 (n= 2,448)

A. Sex

B. Age



C. Specimen Type



D. Clinical Service

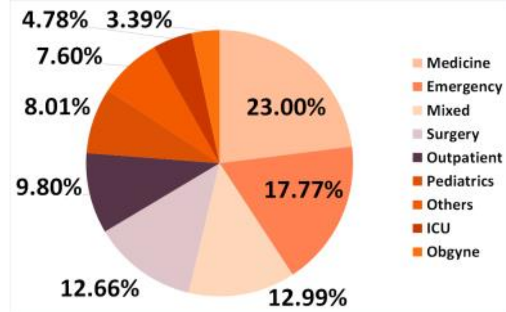


Figure 54. Patient characteristics of methicillin-resistant *S. aureus*, DOH-ARSP, 2023, (n=2,448)

Most (62.30%) of the isolates were from 20-64 years old and majority (55.35%) were from male patients.

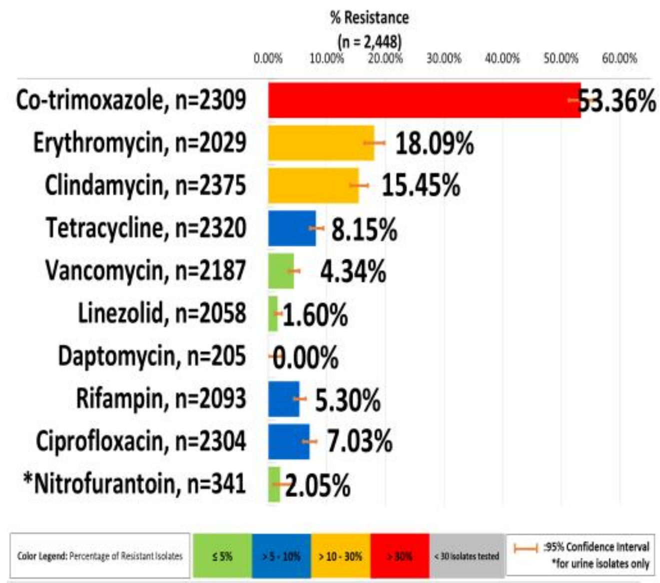
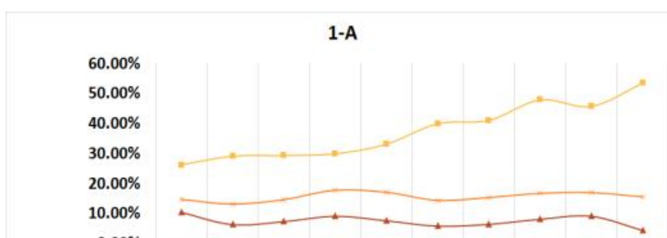


Figure 55. Resistance rates of methicillin-resistant *S. aureus* for all specimens, DOH-ARSP, 2023

Resistance rates of MRSA isolates from all specimens are shown in **Figure 55**. Resistance to vancomycin and linezolid were at 4.34% and 1.60%, respectively. Resistance to clindamycin was at 15.45% and to erythromycin at 18.09%. Resistance rates to tetracycline, rifampin, ciprofloxacin and nitrofurantoin were all less than 10%. The highest resistance for co-trimoxazole was very high at 53.36%.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Co-trimoxazole	26.10%	29.00%	29.20%	29.80%	33.00%	39.85%	40.98%	47.81%	45.65%	53.36%
Vancomycin	10.40%	6.30%	7.30%	9.10%	7.60%	5.80%	6.40%	8.10%	9.10%	4.34%
Clindamycin	14.60%	13.00%	14.50%	17.70%	17.00%	14.25%	15.24%	16.66%	16.89%	15.45%

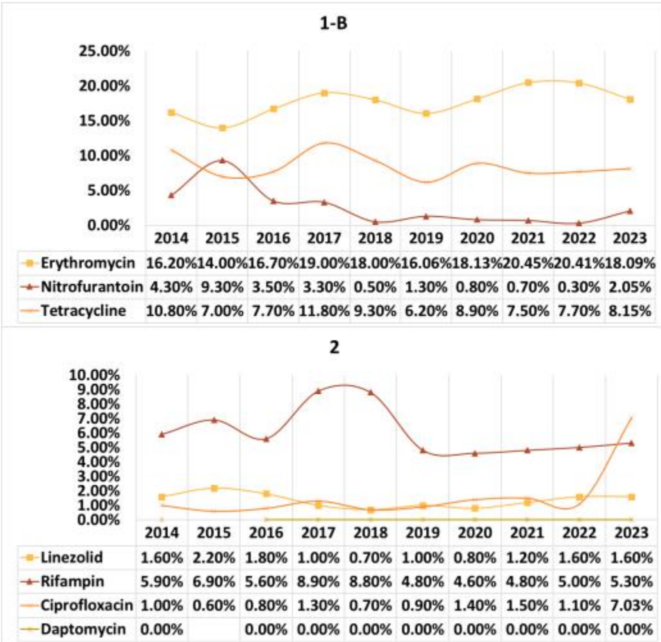


Figure 56. Yearly resistance rates of Methicillin-resistant *S. aureus*, DOH-ARSP, 2014-2023

Figure 56 shows the yearly resistance rates of methicillin-resistant *S. aureus*. It was noted that there was a relatively slow increase in the resistance rates for erythromycin (p=0.0005) while resistance to clindamycin remained relatively stable over the past decade (p=0.0376). In the past decade, co-trimoxazole showed increasing resistance rates (p=0.000).

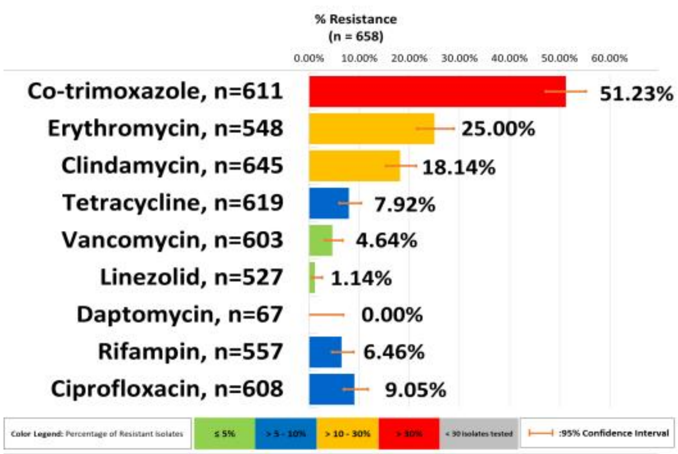


Figure 57. Resistance rates of methicillin-resistant *S. aureus* blood isolates, DOH-ARSP, 2023

Resistance rates of methicillin-resistant *S. aureus* blood isolates are shown in **Figure 57**. Co-trimoxazole resistance was at 51.23%, erythromycin at 25%, clindamycin at 18.14% and tetracycline at 7.92%. Resistance rates to vancomycin, linezolid, rifampin and ciprofloxacin were 4.64%, 1.14%, 6.46% and 9.05% respectively. No daptomycin resistant MRSA isolate from blood was observed in 2023. Compared with resistance rates of MRSA isolates for all specimens, resistance rates of MRSA from blood are higher for erythromycin, clindamycin and rifampin.

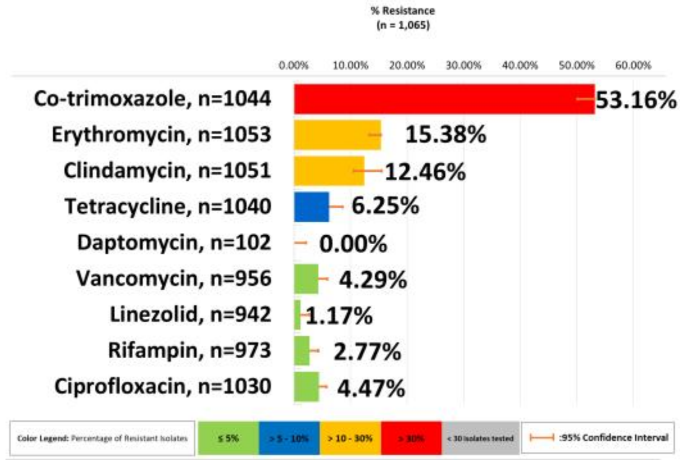


Figure 58. Resistance rates of methicillin-resistant *S. aureus* skin and soft tissue isolates, DOH-ARSP, 2023

Resistance rates of methicillin-resistant *S. aureus* skin and soft tissue isolates are shown in **Figure 58**. Resistance to erythromycin was at 15.38%, clindamycin at 12.46% and tetracycline at 6.25%. Resistance rates to rifampin and ciprofloxacin were 2.77% and 4.47% respectively while resistance rates to vancomycin and linezolid were 4.29% and 1.17% respectively. No daptomycin resistant MRSA isolate from skin and soft tissue was observed in 2023. Compared with resistance rates of MRSA isolates for all specimens, resistance rates of MRSA from skin and soft tissues are lower.

Methicillin Susceptible *Staphylococcus aureus*

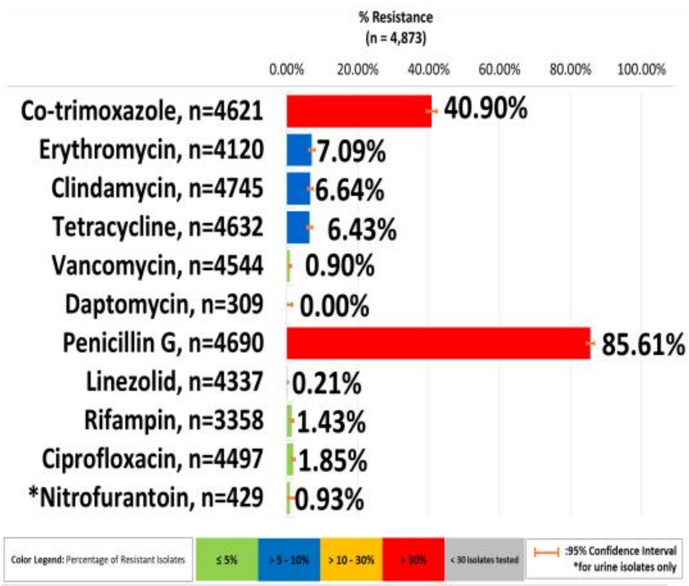


Figure 59. Resistance rates of methicillin-susceptible *S. aureus* for all specimens, DOH-ARSP, 2023

Cumulative resistance rates of methicillin susceptible *S. aureus* (MSSA) for all specimens are shown in **Figure 59**. Resistance rates for erythromycin, clindamycin and tetracycline were 7.09%, 6.64% and 6.43% respectively. Resistance to vancomycin and nitrofurantoin were both at 0.90% and 0.93% respectively. Resistance rates to linezolid, rifampin and ciprofloxacin remained below 2%. No resistant isolate against daptomycin was reported. The highest resistance was for penicillin at 85.61%. followed by co-trimoxazole at 40.90%.

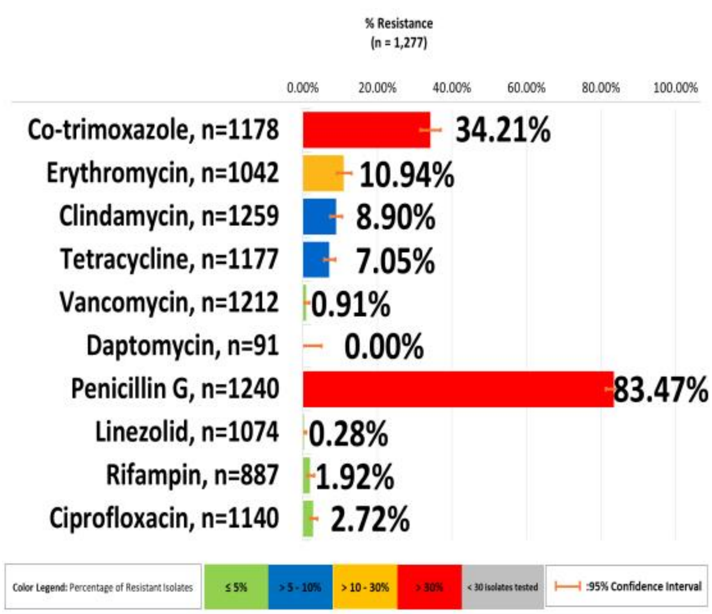


Figure 60. Resistance rates of methicillin-susceptible *S. aureus* blood isolates, DOH-ARSP, 2023

Resistance rates of methicillin susceptible *S. aureus* blood isolates are shown in **Figure 60**. The highest resistance was for penicillin at 83.47% followed by co-trimoxazole at 34.21%. Resistance rates for erythromycin, clindamycin and tetracycline were 10.94%, 8.90% and 7.05% respectively. Resistance to vancomycin and linezolid were 0.91% and 0.28% respectively. Resistance rates to rifampin and ciprofloxacin remained below 3%. No resistant isolate against daptomycin was reported.

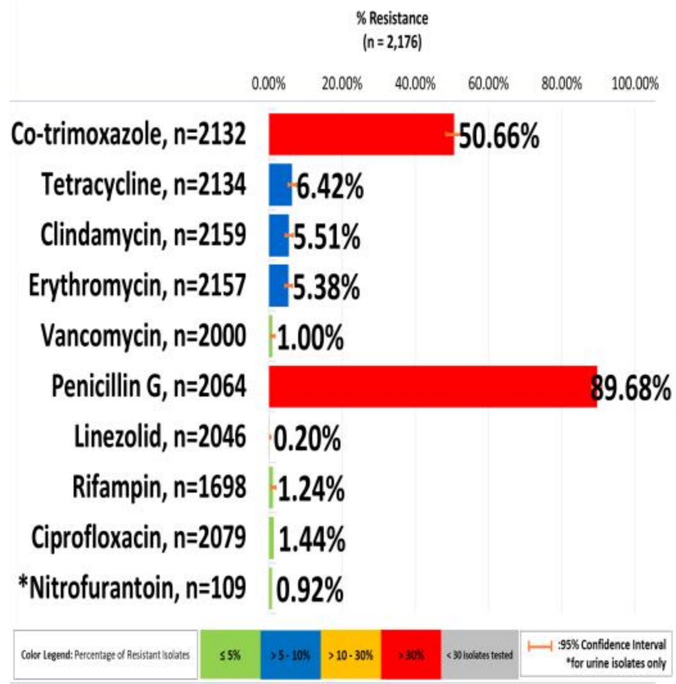


Figure 61. Resistance rates of methicillin-susceptible *S. aureus* skin and soft tissue isolates, DOH-ARSP, 2023

Cumulative resistance rates of methicillin susceptible *S. aureus* skin and soft tissue isolates are shown in **Figure 61**. The highest resistance was for penicillin at 89.68% followed by co-trimoxazole at 50.66%. Resistance rates for erythromycin and clindamycin were both at 5.38 and 5.51% respectively. Resistance rates to vancomycin, linezolid, rifampin and ciprofloxacin remained below 2%.

Enterococcus species

Enterococcus faecalis

A total of **3,220** isolates of *Enterococcus faecalis* was analysed for 2023. The PGH (16.55%) contributed most of the data on *E. faecalis* followed by DMC (15.03%) and CVM (10.25%). Luzon sentinel sites contributed the most (58.20%) data on the isolates.

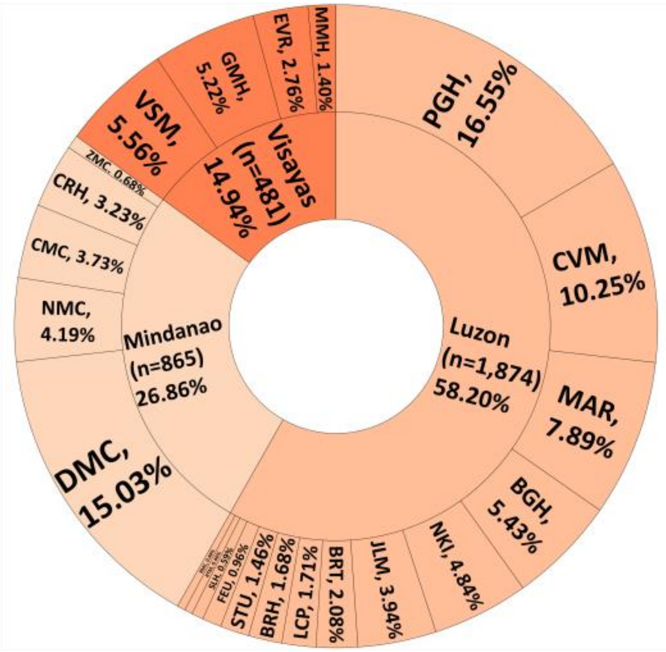
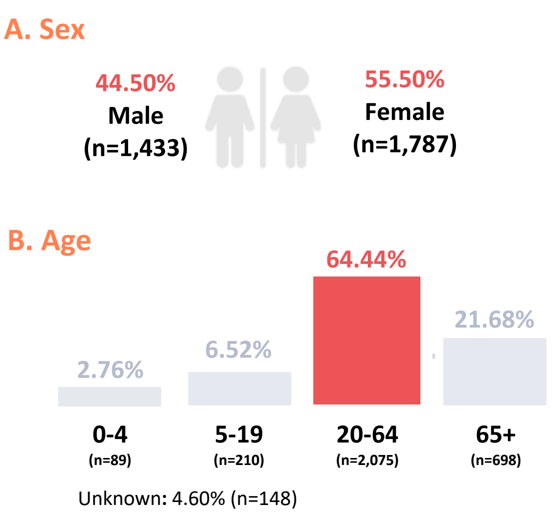


Figure 62. Isolate distribution of *E. faecalis* isolates, DOH-ARSP 2023 (n=3,220)

Most of the isolates were from the 20-64 years age range (64.44%) and most (55.50%) were from female patients (**Figure 63**). *E. faecalis* isolates were mostly (49.72%) collected from urine specimens and most (62.05%) isolates were from presumptively community acquired infections.



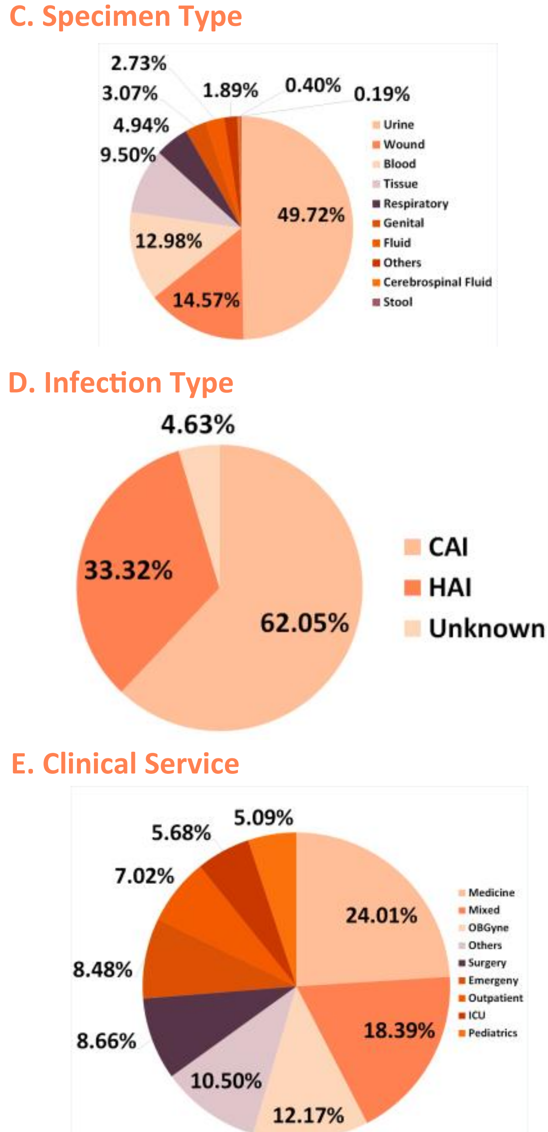


Figure 63. Patient characteristics of *E. faecalis,* DOH-ARSP, 2023 (n=3,220)

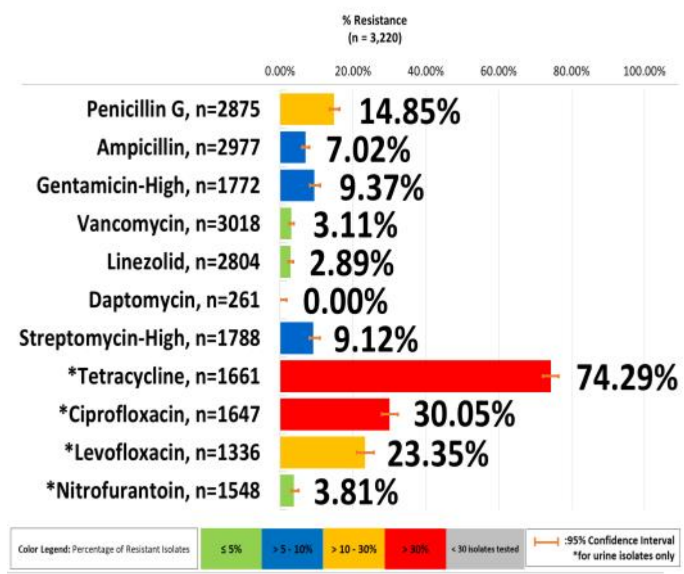


Figure 64. Resistance rates of *E. faecalis* from all specimens, DOH-ARSP, 2023

Resistance of *E. faecalis* to penicillin was at 14.85% and 7.02% to ampicillin. Resistance to vancomycin and linezolid were at 3.11% and 2.89%, respectively (Figure 64). All isolates were susceptible against daptomycin. Resistance against high-level gentamicin and high level streptomycin were at 9.37% and 9.12%, respectively. Percent resistance against ampicillin (p=0.0282) decreased from 8.53% in 2022 to 7.02% in 2023. A decrease was also noted for gentamicin-high level from 12% in 2022 to 9.37% in 2023 and streptomycin-high level (p=0.0000) from 15.59% in 2022 to 9.12% in 2023. Resistance against tetracycline notably increased from the previous year but the increase was not statistically significant. All isolates tested were susceptible to daptomycin.

There were 2 confirmed vancomycin-resistant *Enterococcus faecalis* isolates from urine specimens of 34-year old 64-year old patients from the Visayas. The isolates were both resistant to ciprofloxacin and tetracycline, but susceptible to ampicillin, daptomycin, linezolid, penicillin and streptomycin-high level gentamicin-high-level.
There were confirmed linezolid resistant *E. faecalis* isolates reported in 2023. The molecular characterization of these emerging resistant isolates are described in the succeeding section.

Molecular characterization of linezolid resistant *E. faecalis*

The WHO AWARE classification in 2023 continues to categorize linezolid as a "Reserve" antibiotic for treating vancomycin-resistant and multidrug-resistant Gram-positive organisms [1] . A 2021 global prevalence survey reported that resistance against linezolid for *E. faecalis* at 2.8% in Asia [2]. In 2022, Philippines ARSP reported 3.3% resistance rate in *E. faecalis* to this antibiotic [3].

Eleven (11) linezolid-resistant *E. faecalis* (LRE) isolates collected through ARSP in 2023 were sequenced and their genomic characteristics are shown in Table 1. Ten of the isolates were from Luzon and one from Davao. Most isolates (8 out of 11) were from presumptively community acquired, and came from the adult population. Diagnoses of the patients with LRE infections included chronic kidney disease, pneumonia, soft tissue abscess, acute rheumatic fever, pneumonia, spontaneous bacterial peritonitis and electrical injury.

Table 7. Genomic characterization of linezolid resistant *E. faecalis* isolates, DOH-ARSP, 2023

Isolate No.	Region	Isolate Source	MLST	Linezolid MIC (µg/mL)	Resistance profile	AMR genotype	Virulence Factors
1	1	Tissue HAI	-	>=8	Linezolid-Gentamicin (HL)-Streptomycin (HL)	aac(6')-Ie/aph(2'')-Ia, aph(3')-IIIa, spw, lnu (B), lsa(A), lsa(E), erm (B)	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, cylA, cylB, cylM, ebpC, efaAfs hylA, tpx
2	1	Catheter CAI	480	8	Linezolid-Gentamicin (HL)-Streptomycin (HL)	optrA, aac(6')-Ie/aph (2'')-Ia, aph(3')-IIIa, spw, fexA, lnu(B), lsa (A), lsa€, ant(6)-Ia, sat4, tet(M), tet(L), erm(B), ant(9)-Ia, dfrG, narA, narB	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, ebpA, ebpB, ebpC, efaAfs, hylA, tpx
3	1	Blood CAI	16	>=8	Linezolid-Gentamicin (HL)-Streptomycin (HL)	optrA, aac(6')-Ie/aph (2'')-Ia, aph(3')-IIIa, spw, fexA, lnu(B), lsa (A), lsa(E), sat4, tet(M), erm(B), ant(9)-Ia	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, cylA, cylB, cylL, cylM, ebpA, ebpB, ebpC, efaAfs, hylA, tpx
4	2	Tissue CAI	16	8	Linezolid-Gentamicin (HL)-Streptomycin (HL)	optrA, aac(6')-Ie/aph (2'')-Ia, aph(3')-IIIa, spw, lnu(B), lsa(A), lsa (E), sat4, tet(M), erm(B), ant(9) -Ia	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, cylA, cylB, cylL, cylM, ebpA, ebpB, ebpC, efaAfs, hylA, tpx
5	2	Urine CAI	16	32	Linezolid-Gentamicin (HL)-Streptomycin (HL)-Tetracyline	optrA, aac(6')-Ie/aph (2'')-Ia, aph(3')-IIIa, spw, fexA, lnu(B), lsa (A), lsa(E), ant(6)-Ia, sat4, tet(M), erm(B), ant(9)-Ia	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, cylA, cylB, cylL, cylM, ebpA, ebpB, ebpC, efaAfs, hylA, tpx

6	11 –	Abscess CAI	895	16	Linezolid-Gentamicin (HL)	optrA, aac(6')-Ie/aph (2'')-Ia, aph(3')-IIIa, fexA, lsa(A), ant(6)-Ia, sat4, tet(L), erm(B), ant(9)-Ia, dfrG	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, ebpA, ebpB, ebpC, efaAfs, hylA, tpx
7	NCR-	Wound CAI	-	>=8	Linezolid-Daptomycin	optrA, fexA, lsa(A), tet (M), tet(L), ant(9)-Ia,	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, ebpA, ebpB, ebpC, efaAfs, fsrB,
8	3	Tracheal Aspirate CAI	394	4	Linezolid- Streptomycin (HL)	erm(B), lsa(A), narA, narB, tet(M), tet(L), dfrG	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, ebpA, ebpB, ebpC, efaAfs, fsrB, gelE, hylA, hylB, tpx
9	3	Blood HAI	16	8	Linezolid-Gentamicin (HL)-Streptomycin (HL)	optrA, aac(6')-Ie/aph (2'')-Ia, aph(3')-IIIa, spw, fexA, lnu(B), lsa (A), lsa(E), ant(6)-Ia, sat4, tet(M), erm(B), dfrG	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, cylA, cylB, cylL, cylM, ebpA, ebpB, ebpC, efaAfs, hylA, tpx
10	3	Blood CAI	895	8	Linezolid-Gentamicin (HL)-Streptomycin (HL)	optrA, aac(6')-Ie/aph (2'')-Ia, aph(3')-IIIa, spw, fexA, lnu(B), lsa (A), lsa(E), ant(6)-Iam, sat4, tet(L), ant(9)-Ia, dfrG	ElrA, SrtA, ace, agg, cCF10, cOB1, cad, camE, ebpA, ebpB, ebpC, efaAfs, hylA, tpx
11	CAR –	Wound HAI	-	32	Linezolid-Gentamicin (HL)-Streptomycin (HL)-Daptomycin	optrA, aac(6')-Ie/aph (2'')-Ia, aph(3')-IIIa, spw, fexA, lnu(B), cfr (D), lsa(A), lsa(E), ant (6)-Ia, sat4, tet(M)	ElrA, SrtA, ace, agg, cCF10, cOB1, cameE, cylA, cylB, cylL, cylM, ebpA, ebpB, ebpC, efaAfs, hylA, tpx

All the LRE were noted to be susceptible to vancomycin. Ten (10) of the isolates were resistant to both linezolid and high level aminoglycosides, and two (2) tested intermediate to daptomycin.

Two (2) of the isolates were multi-drug resistant – one from the urine sample of a patient treated for moderate signs of dehydration from Region 2 and the other from a wound specimen of a patient with a presumptively hospital-acquired spontaneous bacterial peritonitis from CAR.

Two of the 11 isolates exhibited high MICs (32 µg/mL) to linezolid. Of the two isolates, the isolate from urine was likewise resistant against high level aminoglycosides and tetracycline while the isolate from wound specimen was resistant against high level aminoglycosides and daptomycin.

Four of the isolates were of ST 16 (4/11) which is a sequence type previously identified to be of zoonotic origin [4]. There were 2 isolates with ST 895 and one isolate each of related variants ST 480 and ST 394 which are STs known to carry a combination of optrA and fexA genes, conferring resistance to oxazolidinones and chloramphenicols, respectively [5]. ST 480 and ST 895 are also associated with linezolid resistance linked to the use of phenicols, macrolides, and streptogramins which may drive co-selection of oxazolidinones resistance [6]. Three of the isolates were non-typeable.

The optr*A* gene, which confers resistance to linezolid, was found in nine (9) isolates and were all accompanied by fex*A* gene which confers resistance against chloramphenicol. The two of the isolates did not harbor genes known to confer resistance against linezolid. Linezolid resistance among these isolates were likely due to mutations in the 23S rRNA, which is a common mechanism of linezolid resistance in *E. faecalis* isolates.

No genes directly associated with daptomycin resistance were detected among the isolates. Resistance to daptomycin can generally be attributed to: i) genes encoding regulatory systems that orchestrate cell- envelope homeostasis and stress-response, and ii) genes coding for enzymes involved in the metabolism of cell membrane phospholipids [7].

Virulence genes with identified protein functions harbored by the linezolid resistant isolates were ace (collagen adhesion precursor), agg (aggregation substance), camE (sex pheromone cAM373 precursor), and fsrB (biofilm formation).
Phylogenetic analysis showed the isolates to be non clonal (Figure 65).

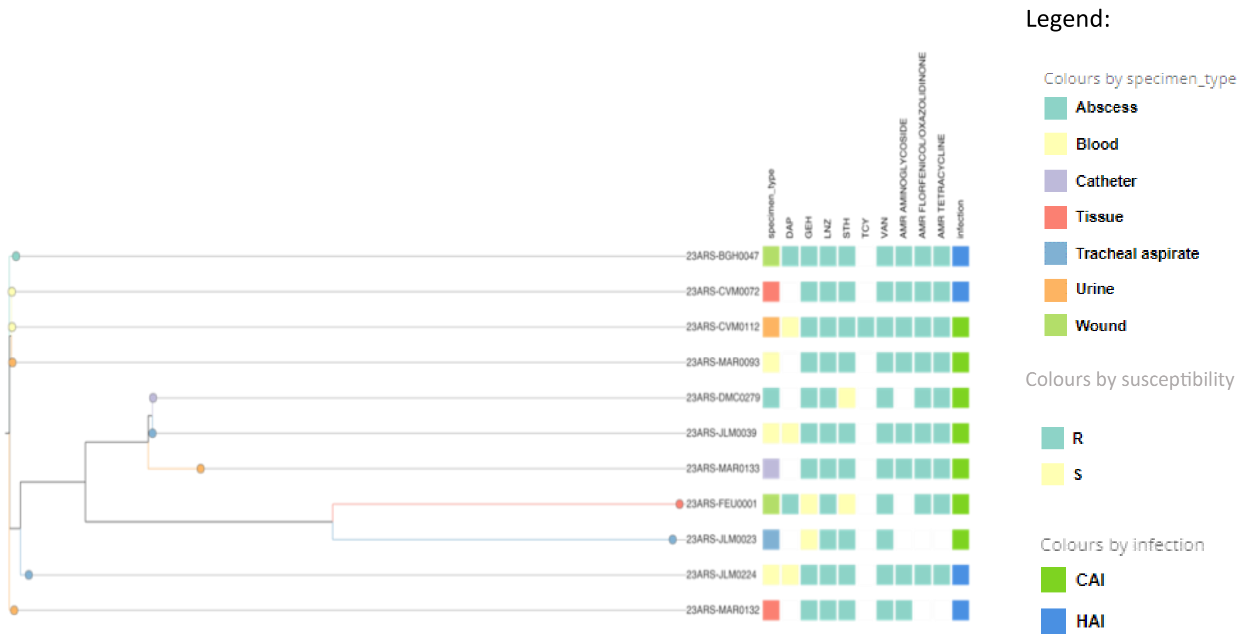


Figure 65. Phylogenetic analysis of linezolid resistant *E. faecalis,* DOH-ARSP, 2023 (https://microreact.org/project/4qHrJUrz254BtUQvcy7V3d-lre-2023)

The detection of a multi-drug resistant strain of LRE calls for a sustained surveillance of these pathogens. While resistance to linezolid and other reserve antibiotics such as daptomycin and vancomycin remains low, the emergence of resistance to these antibiotics calls for an action in order to preserve the use of these antibiotics in both humans and veterinary applications.

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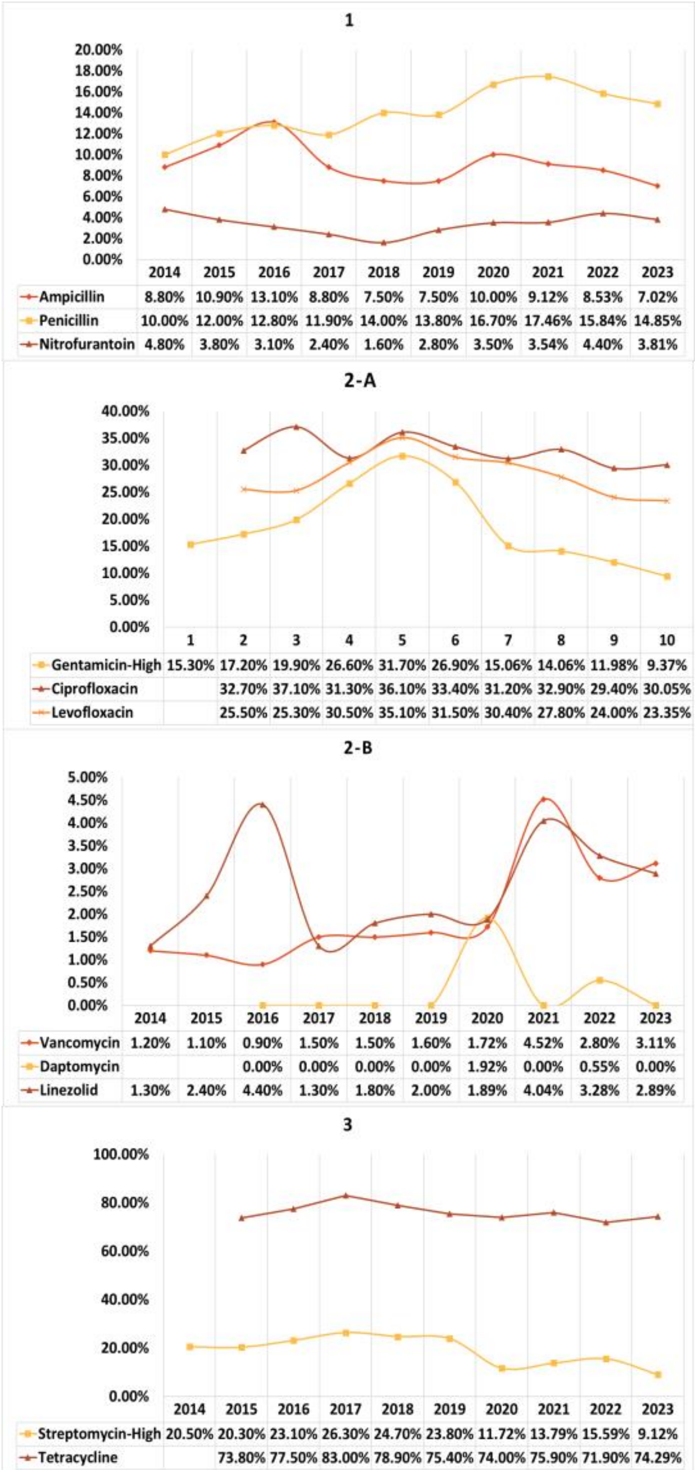


Figure 66. Yearly resistance rates of *E. faecalis*, DOH-ARSP, 2014-2023

Multi-year analysis showed an overall increase in resistance to penicillin (0=0.0000), vancomycin (p=0.0000) and linezolid (p=0.0018) and decrease for ampicillin (p=0.0000), nitrofurantoin, ciprofloxacin, levofloxacin and gentamicin-high level.

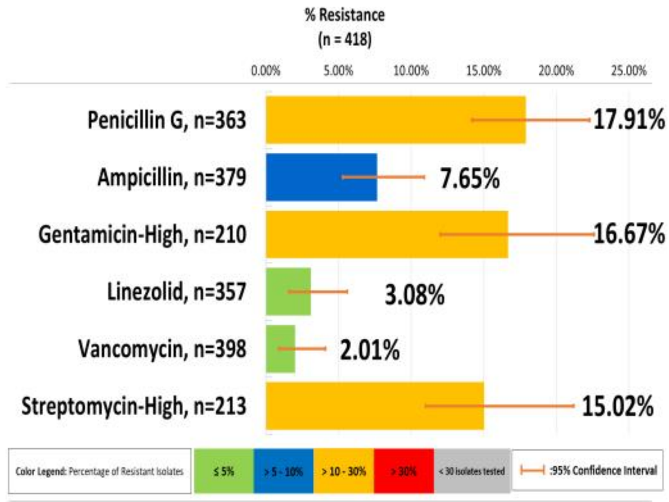
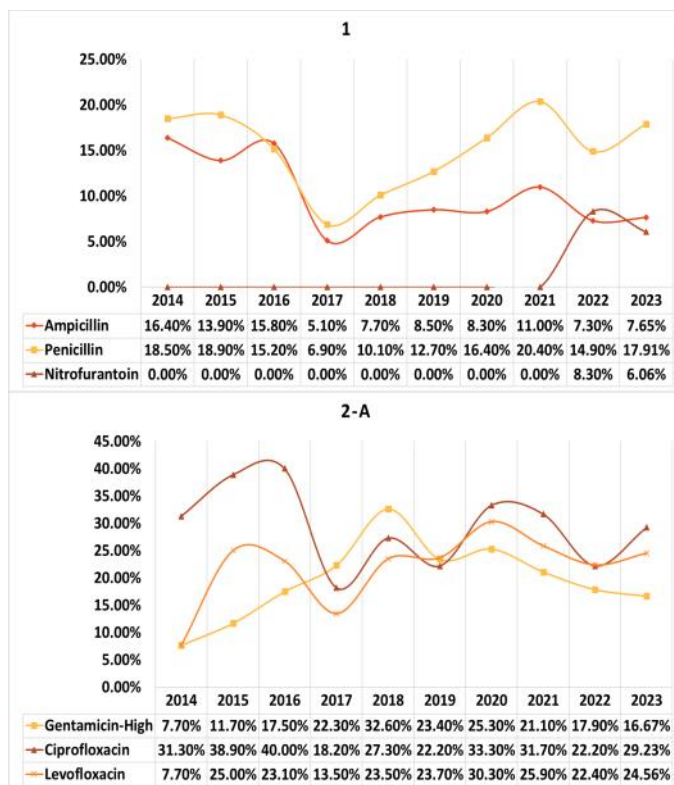


Figure 67. Resistance rates of *E. faecalis* from blood isolates, DOH-ARSP, 2023

Figure 67 shows the resistance rates of *E. faecalis* isolates from blood specimens. Resistance to penicillin was at 17.91%, ampicillin at 7.65%, vancomycin at 2.01% and linezolid at 3.08%. Resistance against high level gentamicin was at 16.67% and high level streptomycin was at 15.02%. Compared with resistance rates of *E. faecalis* isolates from all samples, resistance of *E. faecalis* from blood are higher for all tested antibiotics except for vancomycin.



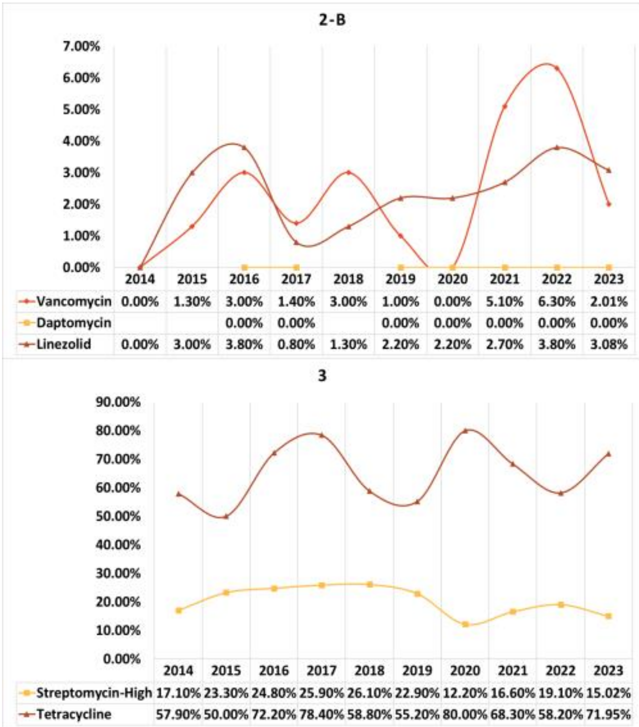


Figure 68. Yearly resistance rates of *E. faecalis* blood isolates, DOH-ARSP, 2014-2023

Multiple year analysis showed increase in the resistance rates for gentamicin- high level (p=0.0000), linezolid and vancomycin and decrease for ampicillin, penicillin and streptomycin-high level.

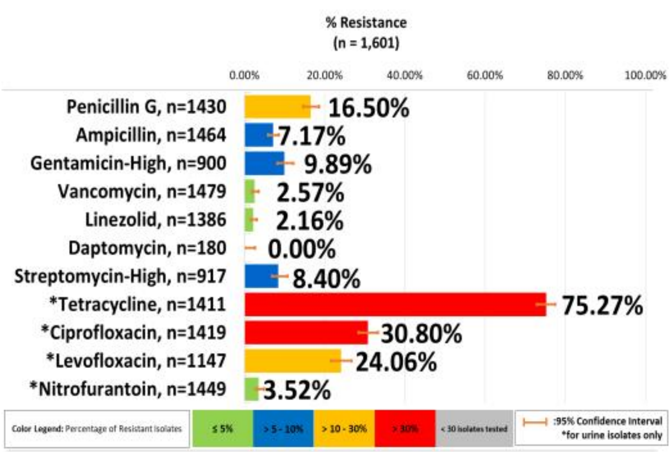


Figure 69. Resistance rates of *E. faecalis* from urine isolates, DOH-ARSP, 2023

Figure 69 shows the resistance rates of *E. faecalis* isolates from urine specimens. Among the antibiotics indicated for urinary infection due to *E. faecalis,* resistance for tetracycline and ciprofloxacin were very high at 75.27% and 30.80%, respectively. Resistance to levofloxacin was at 24.06 and to nitrofurantoin was at 3.52%. Resistance to penicillin was at 16.50%, ampicillin at 7.17%, vancomycin at 2.57%, and linezolid at 2.16%. Resistance against high level gentamicin and high level streptomycin were at 9.89% and 8.40%, respectively. Compared with resistance rates of *E. faecalis* isolates from all samples, those from urine are slightly higher or similar to overall resistance rates from all specimens.

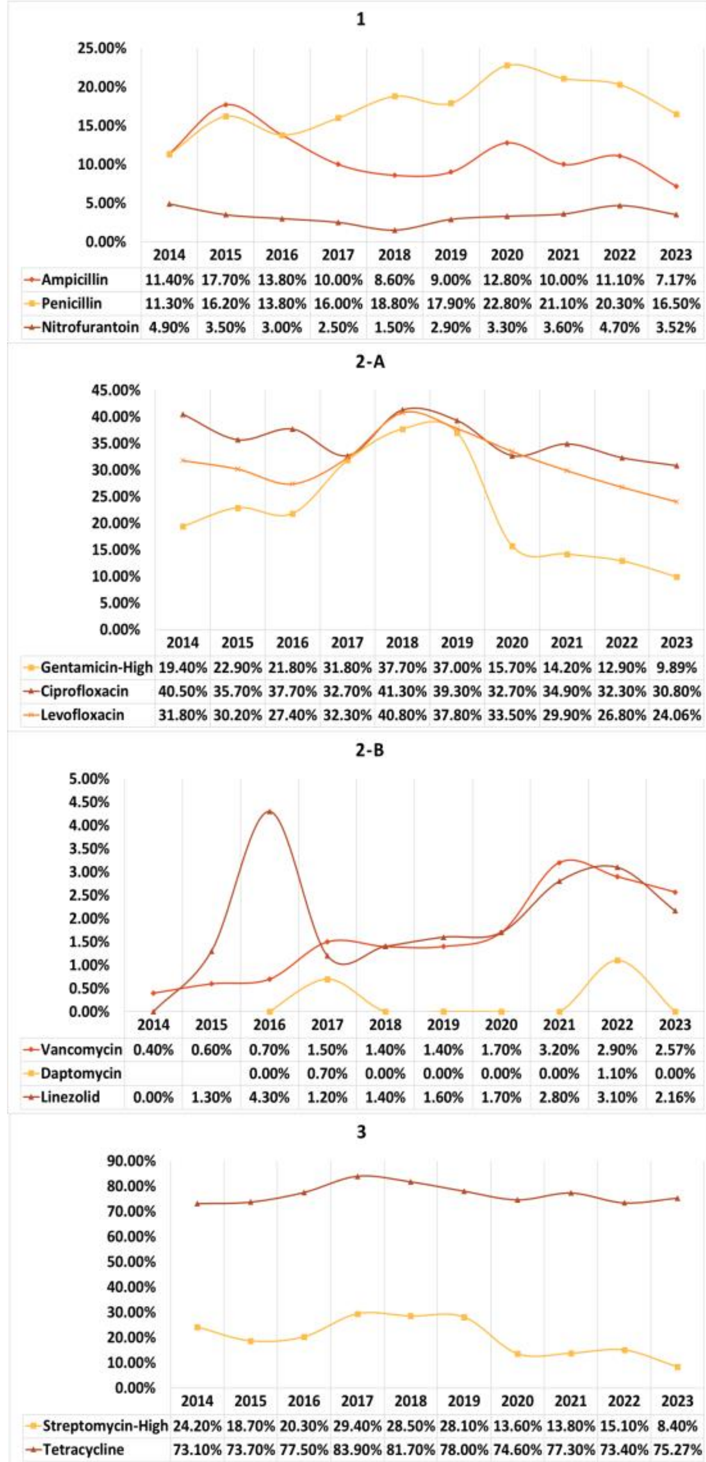


Figure 70. Yearly resistance rates of *E. faecalis* urine isolates, DOH-ARSP, 2014-2023

Multiple year analysis showed an overall decrease in resistance to nitrofurantoin, ciprofloxacin, and levofloxacin, ampicillin (p=0.0000), streptomycin- high level (p=0.0000) and gentamicin- high level (p=0.0000) and overall increase for tetracycline, penicillin (0=0.0000), vancomycin (p=0.0000) and linezolid (p=0.0018).

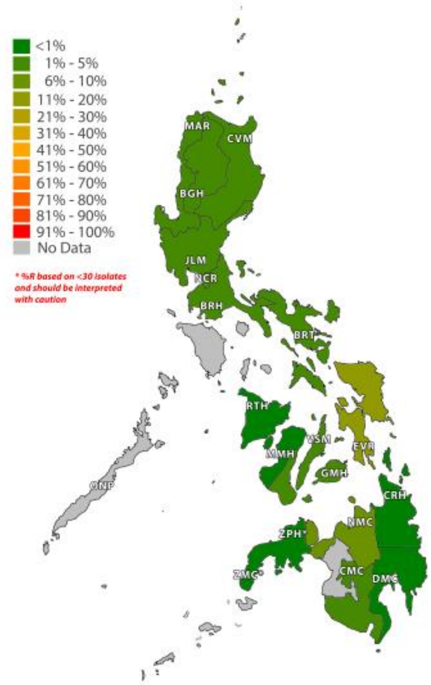


Figure 71. Geographic distribution of vancomycin-resistant *E. faecalis* in the Philippines, DOH-ARSP, 2023

Figure 71 shows the distribution of vancomycin resistant *E. faecalis* in the Philippines. Rates are at 11-20% at EVR and LCP, 6-10% at FEU, NMC, VSM, range of 1-5% at CMC, BRT, BGH BRH, NCR, JLM, STU, PGH, CVM, and MAR. Rates are low at <1% at DMC, CRH, ZPH, ZMC, NKI, RTH, RMC, RTM, SLH, GMH and MMH.

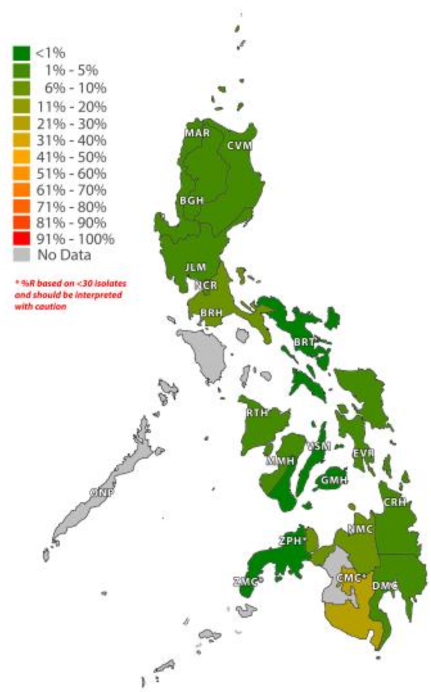


Figure 72. Geographic distribution of linezolid-resistant *E. faecalis* in the Philippines, DOH-ARSP, 2023

Figure 72 shows the distribution of linezolid resistant *E. faecalis* in the Philippines. Rates are at 11-20% at CMC, LCP, and FEU, 6-10% at BRH, EVR, NMC, SLH, NMC, and 1-5% at BGH, CRH, CVM, DMC, JLM, MAR, MMH, PGH, and STU. Rates are low at <1% at BRT, GMH, RMC, VSM and ZMC.

Enterococcus faecium

There were **2,038** *E. faecium* isolates reported for 2023. Highest contributors of data for *E. faecium* were DMC at 22.67%, followed by PGH at 21.34%, and VSM at 7.70% (Figure 73). The sentinel sites from Luzon contributed 50.34% of the data with 28.95% coming from NCR.

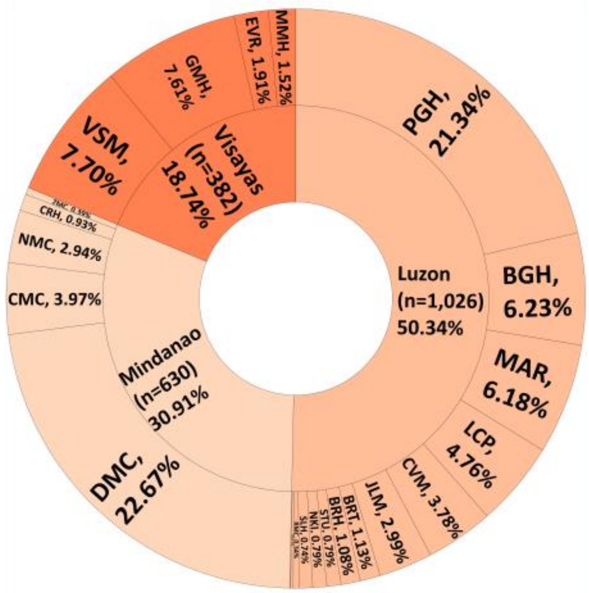
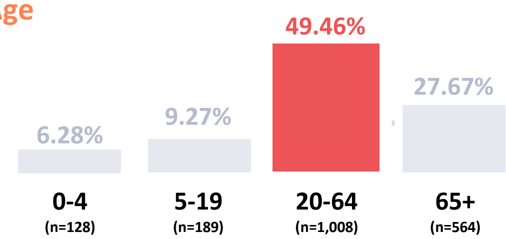


Figure 73. Isolate distribution of *E. faecium*, DOH-ARSP, 2023 (n=2,038)

A. Sex

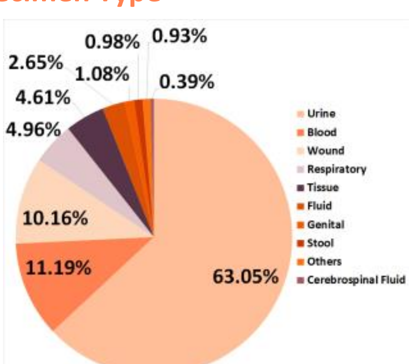
No Data: 0.20% (n=4)

B. Age

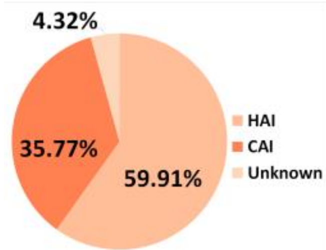


Unknown: 7.31% (n=149)

C. Specimen Type



D. Infection Type



E. Clinical Service

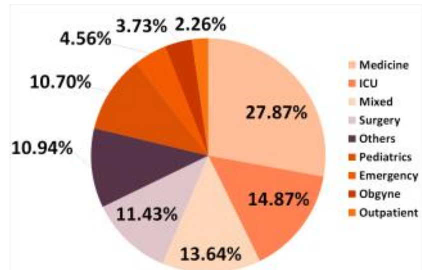


Figure 74. Patient characteristics of *E. faecium isolates*, DOH-ARSP, 2023 (n=2,038)

Many (49.46%) of the isolates were still from the adult population aged 20-64 years old and were mostly (56.53%) from female patients (Figure 74). The isolates were mostly (63.05%) isolated from urine specimens, and many were from the medicine clinical service (27.87%), ICU (14.87%) and surgery department (11.43%). Most (59.91%) of the isolates were from presumptive hospital-acquired infections.

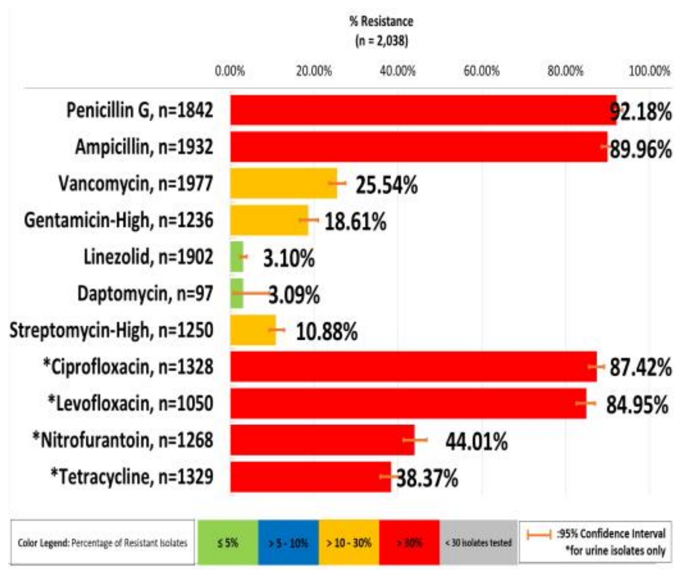
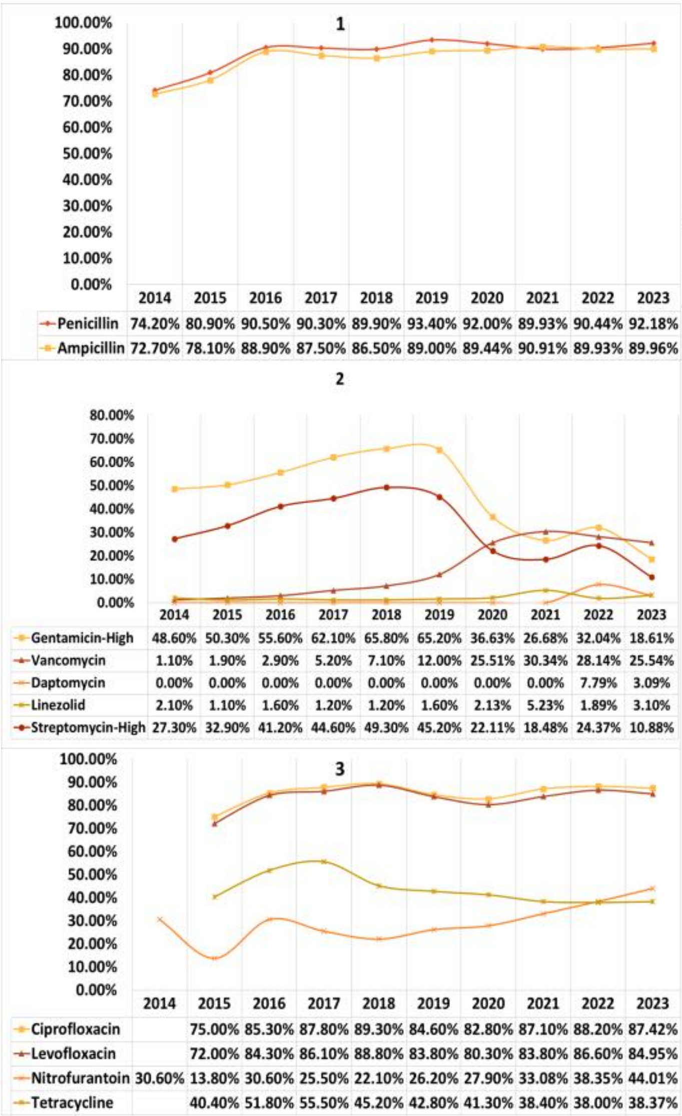


Figure 75. Resistance rates of *E. faecium* from all specimens, DOH-ARSP, 2023

Resistance rates of *E. faecium* are shown in Figure 75. Percent resistance to penicillin was the highest at 92.18%, ampicillin at 89.96%, and vancomycin at 25.54%. Resistance to daptomycin was at 3.09% and to linezolid at 3.10%. Decrease in resistance rates from the previous year were observed in high level streptomycin at 10.88% (p=0.0000), high level gentamicin at 18.61% (p=0.0000), and vancomycin at 25.54% (p=0473). An increase in resistance rate for nitrofurantoin compared to rate from previous year was likewise noted to be statistically significant



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Penicillin	74.20%	80.90%	90.50%	90.30%	89.90%	93.40%	92.00%	89.93%	90.44%	92.18%
Ampicillin	72.70%	78.10%	88.90%	87.50%	86.50%	89.00%	89.44%	90.91%	89.93%	89.96%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Gentamicin-High	48.60%	50.30%	55.60%	62.10%	65.80%	65.20%	36.63%	26.68%	32.04%	18.61%
Vancomycin	1.10%	1.90%	2.90%	5.20%	7.10%	12.00%	25.51%	30.34%	28.14%	25.54%
Daptomycin	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.79%	3.09%
Linezolid	2.10%	1.10%	1.60%	1.20%	1.20%	1.60%	2.13%	5.23%	1.89%	3.10%
Streptomycin-High	27.30%	32.90%	41.20%	44.60%	49.30%	45.20%	22.11%	18.48%	24.37%	10.88%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ciprofloxacin		75.00%	85.30%	87.80%	89.30%	84.60%	82.80%	87.10%	88.20%	87.42%
Levofloxacin		72.00%	84.30%	86.10%	88.80%	83.80%	80.30%	83.80%	86.60%	84.95%
Nitrofurantoin	30.60%	13.80%	30.60%	25.50%	22.10%	26.20%	27.90%	33.08%	38.35%	44.01%
Tetracycline		40.40%	51.80%	55.50%	45.20%	42.80%	41.30%	38.40%	38.00%	38.37%

Figure 76. Yearly resistance rates of *E. faecium*, DOH-ARSP, 2014-2023

E. faecium resistance against penicillin and ampicillin remained high in the past ten years (Figure 76). A steady increase in resistance to nitrofurantoin (p=0.0000), vancomycin (p=0.0000) and linezolid (p=0.0000) had been observed. On the other hand, resistance rates to gentamicin- high level (p=0.0000) and streptomycin- high level (p=0.0000) decreased.

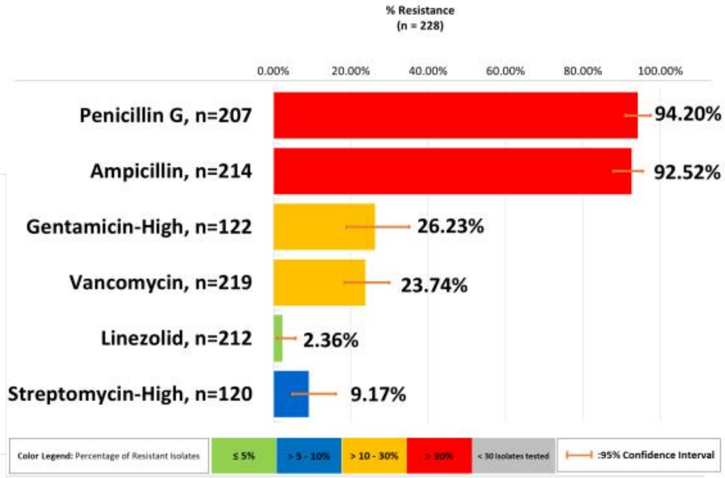
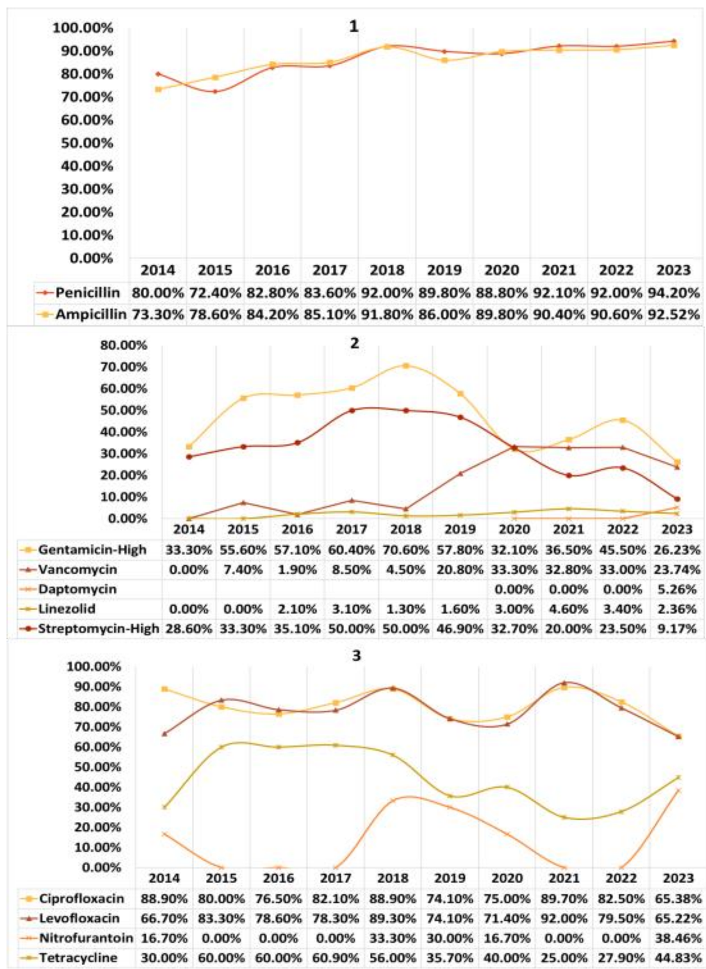


Figure 77. Resistance rates of *E. faecium* from blood isolates, DOH-ARSP, 2023

Figure 77 shows the resistance rates of *E. faecium* isolates from blood specimens. Resistance to penicillin was at 94.20%, ampicillin 92.52%, vancomycin at 23.74% and linezolid at 2.36%. Resistance against high level gentamicin was at 26.23% and high level streptomycin was at 9.17%. Compared with resistance rates of *E. faecium* isolates from all samples, resistance of isolates from blood are higher except to vancomycin, linezolid, and high level streptomycin.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Penicillin	80.00%	72.40%	82.80%	83.60%	92.00%	89.80%	88.80%	92.10%	92.00%	94.20%
Ampicillin	73.30%	78.60%	84.20%	85.10%	91.80%	86.00%	89.80%	90.40%	90.60%	92.52%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Gentamicin-High	33.30%	55.60%	57.10%	60.40%	70.60%	57.80%	32.10%	36.50%	45.50%	26.23%
Vancomycin	0.00%	7.40%	1.90%	8.50%	4.50%	20.80%	33.30%	32.80%	33.00%	23.74%
Daptomycin							0.00%	0.00%	0.00%	5.26%
Linezolid	0.00%	0.00%	2.10%	3.10%	1.30%	1.60%	3.00%	4.60%	3.40%	2.36%
Streptomycin-High	28.60%	33.30%	35.10%	50.00%	50.00%	46.90%	32.70%	20.00%	23.50%	9.17%

	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ciprofloxacin	88.90%	80.00%	76.50%	82.10%	88.90%	74.10%	75.00%	89.70%	82.50%	65.38%
Levofloxacin	66.70%	83.30%	78.60%	78.30%	89.30%	74.10%	71.40%	92.00%	79.50%	65.22%
Nitrofurantoin	16.70%	0.00%	0.00%	0.00%	33.30%	30.00%	16.70%	0.00%	0.00%	38.46%
Tetracycline	30.00%	60.00%	60.00%	60.90%	56.00%	35.70%	40.00%	25.00%	27.90%	44.83%

Figure 78. Yearly resistance rates of *E. faecium* blood isolates, DOH-ARSP, 2014-2023

Multiple year analysis revealed that the observed fluctuation resistance rates of *E. faecium* blood isolates for the following antibiotics were significant: ampicillin (p=0.0000), gentamicin- high level (p=0.0000), linezolid (p=0.0000), penicillin (0=0.0000), vancomycin (p=0.0000) and streptomycin- high level (p=0.0000).

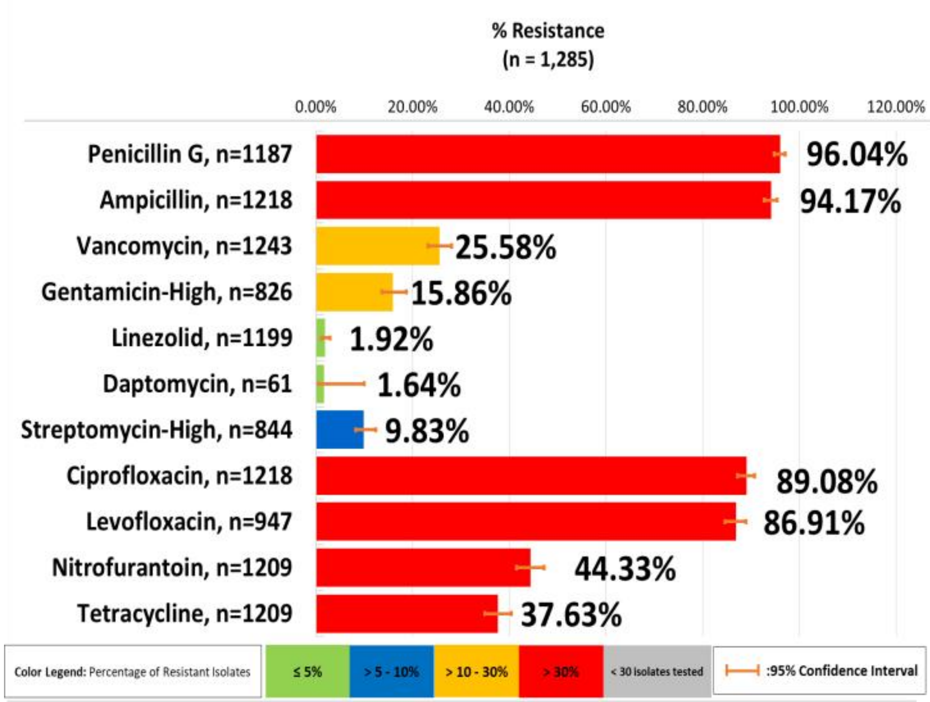
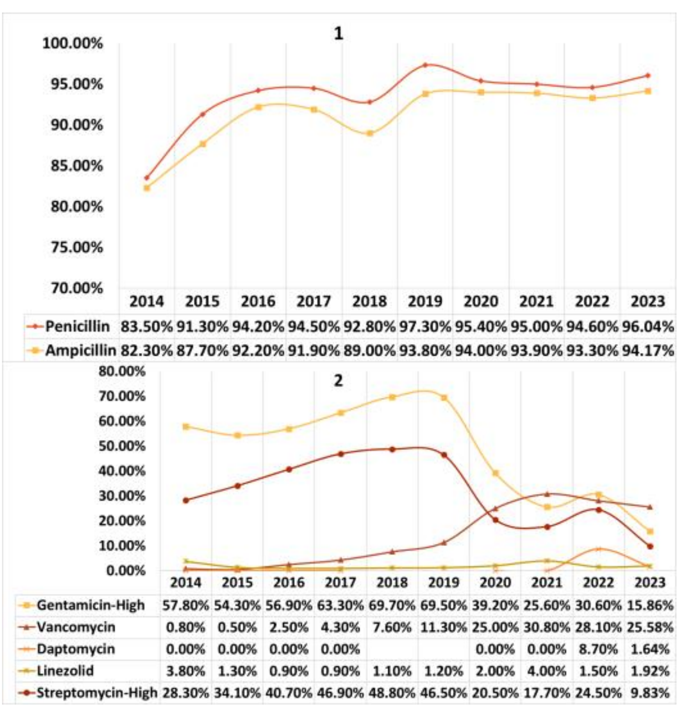


Figure 79. Resistance rates of *E. faecium* from urine isolates, DOH-ARSP, 2023

Figure 79 shows the resistance rates of *E. faecium* isolates from urine specimens. Resistance to penicillin and ampicillin were very high at 96.04% and 94.17%, respectively. Resistance to vancomycin was at 25.58%, daptomycin at 1.64% and linezolid were both at 1.92%. Resistance against high level gentamicin was at 15.86% and high level streptomycin was at 9.83%. Compared with resistance rates of *E. faecium* isolates from all samples, those from urine are higher for penicillin, ampicillin, vancomycin, ciprofloxacin, levofloxacin and nitrofurantoin. Whereas, resistance rates from urine isolates are lower than from all samples for high level gentamicin, high level streptomycin, daptomycin, linezolid.



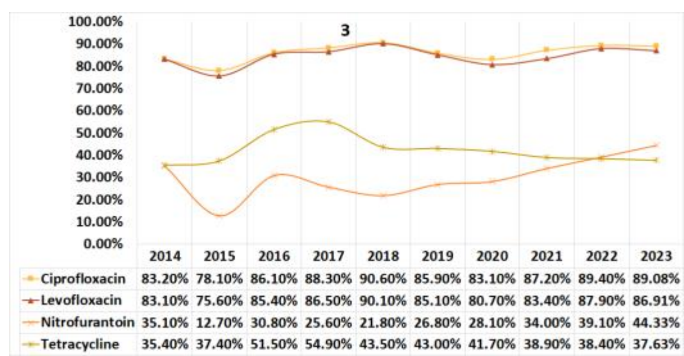


Figure 80. Yearly resistance rates of *E. faecium* urine isolates, DOH-ARSP, 2014-2023

Multiple year analysis revealed that the observed fluctuation resistance rates of *E. faecium* urine isolates for the following antibiotics were significant: ampicillin (p=0.0000), gentamicin- high level (p=0.0000), linezolid (p=0.0000), nitrofurantoin (p=0.0000), penicillin (0=0.0000), vancomycin (p=0.0000) and streptomycin- high level (p=0.0000).

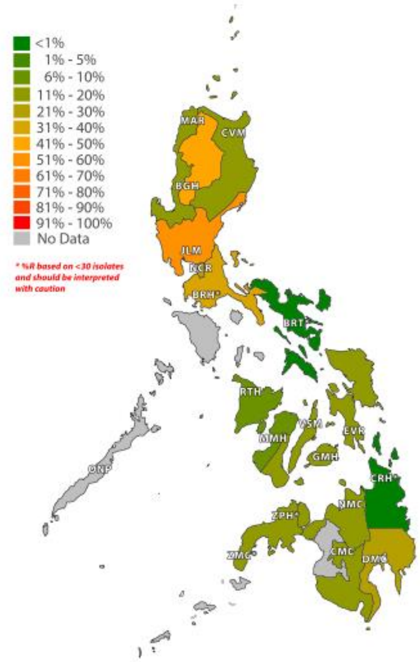


Figure 81. Geographic distribution of vancomycin-resistant *E. faecium* in the Philippines, DOH-ARSP, 2023

Figure 81 shows the geographical distribution of vancomycin-resistant *E. faecium* isolates across the country. Rates at 51-60% was observed in JLM, 41-50% at LCP, and BGH, 31-40% at BRH and SLH, 21-30% at PGH, VSM, and DMC, 11-20% at MAR, CVM, ZMC, RMC, EVR, NMC, and CMC, 6-10% at STU and MMH, and <1% at FEU, NKI, GMH, and CRH

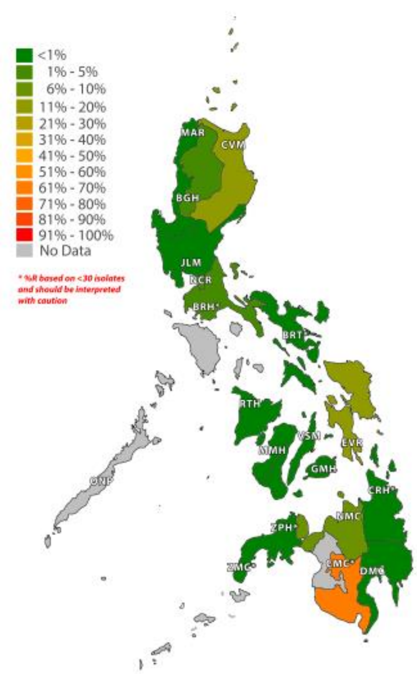


Figure 82. Geographic distribution of linezolid-resistant *E. faecium* in the Philippines, DOH-ARSP, 2023

Figure 82 shows the geographical distribution of linezolid-resistant *E. faecium* isolates across the country. Rates at 61-70% was observed in CMC, 21-30% at EVR, 6-10% at NMC and SLH, 1-5% at BRH, BGH, PGH, and CVM, and <1% at DMC, VSM, MAR, JLM, ZMC, FEU, NKI, RMC, STU, BRT, MMH, GMH, and CRH.

Escherichia coli

A total of **13,496** *E. coli* isolates were reported and analysed for 2023. PGH (15.46%) contributed most to the number of isolates followed by DMC (9.24%) and BGH (7.91%). Based on island group distribution, 58.26% were from Luzon with 30.07% from NCR sentinel sites.

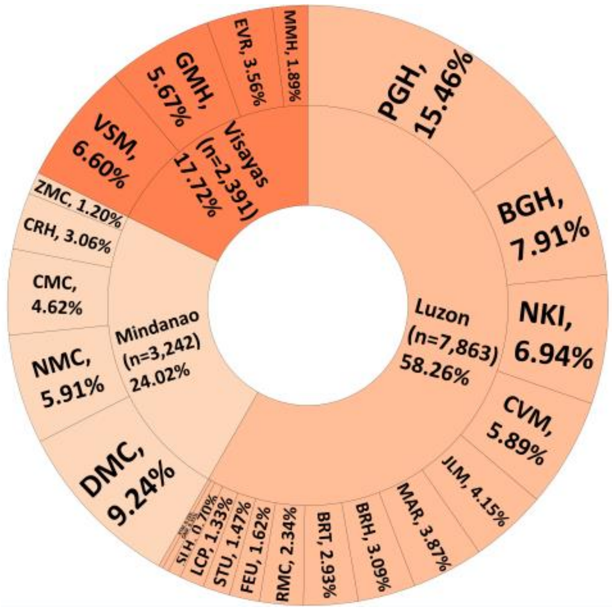


Figure 83. Isolate distribution of *E. coli*, DOH-ARSP, 2023

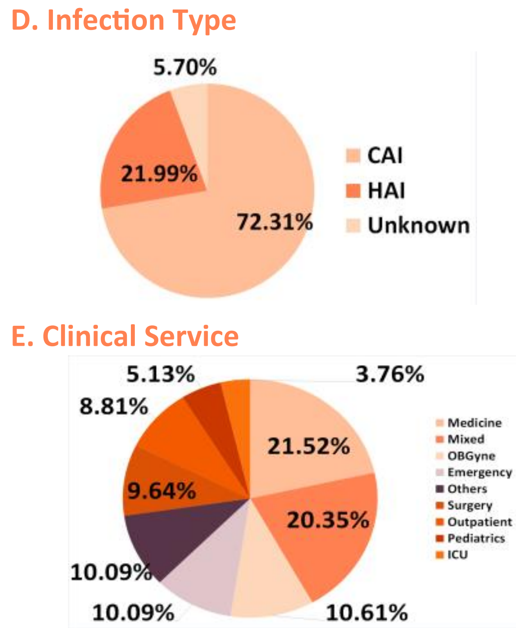
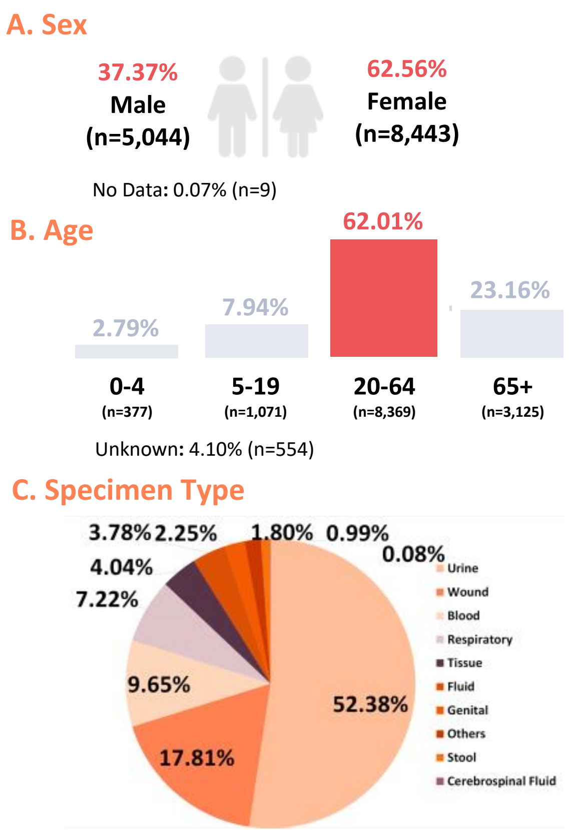


Figure 84. Patient characteristics of *E. coli* isolates, DOH-ARSP, (n= 13,496)

More than half (62.01%) of the isolates were from patients aged 20-64 years old and most (62.56%) were from female patients (**Figure 84**). Most (52.38%) *E. coli* isolates were from urine specimens and most (72.31%) were presumptive community acquired infections



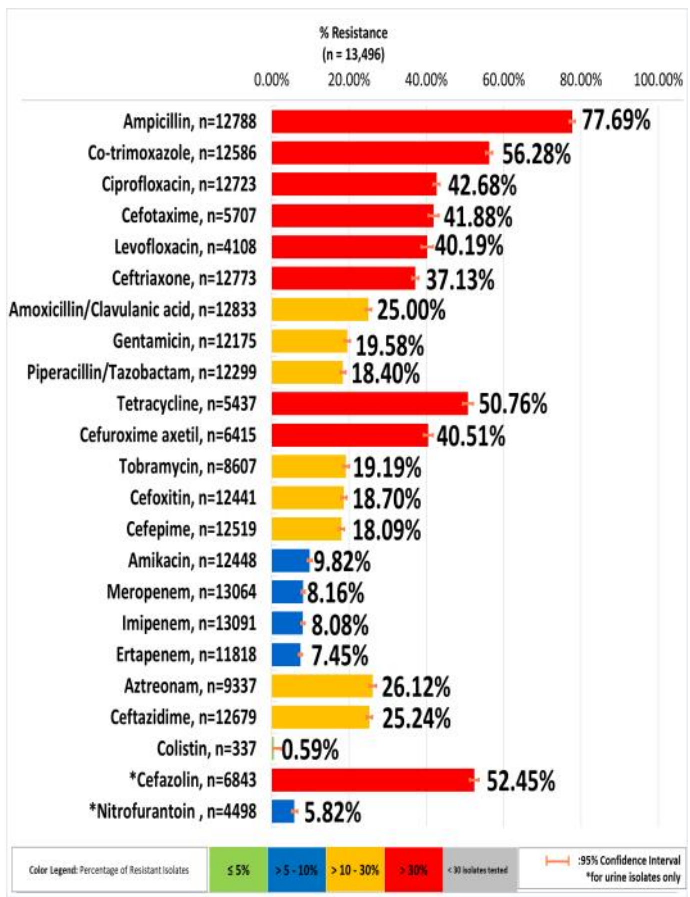


Figure 85. Resistance rates of *E. coli* isolates for all specimens, DOH-ARSP, 2023

Cumulative resistance rates of *E. coli* for 2023 is shown in **Figure 85**. Resistance rates of *E. coli* to almost all antibiotics were above 10%. Resistance to nitrofurantoin was at 5.82%, to co-trimoxazole at 56.28% and to ciprofloxacin at 42.68%. Resistance to the combination antibiotics amoxicillin-clavulanic acid was at 25.00%, to amikacin at 9.82% and piperacillin-tazobactam at 18.40%. Resistance to carbapenems are from 7-8% and 0.59% to colistin. There were significant increase in the resistance rates of the following antibiotics from 2022 compared with 2023 rates: co-trimoxazole (p=0.0000), amikacin (p=0.0000), aztreonam (p=0.0244), and colistin (p=0.0000). The noted increase in the resistance rates in 2023 for amikacin and tobramycin may be attributable to the change to more stringent breakpoints for these antibiotics for 2023. A significant decrease from 2022 to 2023 resistance rates were observed for ampicillin (p=0.0000) and ciprofloxacin (p=0.0000). Lowest resistance rates were noted for colistin (0.59%), and nitrofurantoin (5.82%).

There are sporadic reports (12 isolates) from Luzon of resistance among *E. coli to* the new combination antibiotics ceftazidime-avibactam detected through MIC. The isolates were from urine specimens of adults and elderly patients with presumptive hospital acquired infections. Most of the isolates are multi-drug resistant with some of the isolates noted to be variably susceptible to amikacin, aztreonam, nitrofurantoin and tobramycin. Expansion of susceptibility testing of Enterobacterales to include testing for the newer combination antibiotics across all laboratories are needed to guide appropriate use and to safeguard use of these antibiotics.

There were two confirmed colistin resistant *E. coli* isolates in 2023. The first isolate was from a urine specimen of a 75-year-old female from Region III. The isolate was ESBL positive and likewise resistant to ciprofloxacin, ceftriaxone, cefotaxime, cefuroxime axetil, cefazolin, co-trimoxazole and tetracycline. However, it showed susceptibility to amikacin, aztreonam, ceftazidime, ertapenem, cefoxitin and gentamicin. The second isolate was from a tissue sample of a 67-year old male from Region X. The isolate showed susceptibility to all antibiotics tested.

Molecular characterization of emerging colistin-resistant *Escherichia coli*

Introduction

Colistin is a potent antibiotic that is typically reserved as a last line of treatment for severe infections from pathogenic bacteria with high-level resistance. However, the emergence of colistin-resistant bacteria is a growing concern for public health. Given that *E. coli* is a common bacterium that can cause a range of infections, it is crucial to detect and report cases of colistin resistance in *E. coli* isolates. This information helps to monitor the spread of resistance to this important antibiotic and develop effective treatment strategies [1].

This section describes the phenotypic and genotypic characteristics of colistin-resistant *Escherichia coli (E. coli)* collected through ARSP for 2023. Continued monitoring and molecular characterization of this emerging resistant pathogen can provide insight on the potential mechanism of spread of this resistant phenotype to inform control and prevention measures.

Table 8 shows the antimicrobial resistance data for the three colistin resistant *E. coli* isolates from urine and tissue samples. The isolates have colistin MIC of 8. The isolates showed varying resistance profiles with the one of the isolate from urine sample noted to be resistant to aminoglycosides and fluoroquinolones while the second isolate also from urine was resistant to cephalosporins, beta-lactams, cotrimoxazole, and tetracycline. In contrast, the isolate from tissue sample showed susceptibility to the other antibiotics except colistin.

Table 8. Antimicrobial resistance data of *Escherichia coli* isolates, (n=3)

Sample Name	Specimen type	Colistin MIC	Antimicrobial Resistance							
			Polymixin	Carbapenem	Cephalosporins	Aminoglycoside	Fluoroquinolone	Beta-lactam	folate pathway antagonist	Tetracycline
23ARS-BRH0037	Urine	8	Colistin	None	None	Gentamicin, Tobramycin	Ciprofloxacin	None	None	None
23ARS-JLM0081	Urine	8	Colistin	None	Cefotaxime, Ceftriaxone	None	Ciprofloxacin	Co-amoxiclav, Ampicillin	Co-trimoxazole	Tetracycline
23ARS-NMC0005	Tissue	8	Colistin	None	None	None	None	None	None	None

The distinct strain types of the three *E. coli* isolates are shown in **Table 9**. Isolate 23ARS-BRH0037 is classified as MLST 93 and serotype O159:H21, categorized in phylotype A, which differentiates it from the others. Isolates 23ARS-JLM0081 and 23ARS-NMC0005 are both in phylotype B1 but differ in MLST and serotype; 23ARS-JLM0081 is MLST 224, serotype O7:H4, and 23ARS-NMC0005 is MLST 223, serotype O8:H23.

Table 9. Strain types of *Escherichia coli* isolates, (n=3)

Sample Name	MLST	Serotype	Phylotype
23ARS-BRH0037	93	O159:H21	A
23ARS-JLM0081	224	O7:H4	B1
23ARS-NMC0005	223	O8:H23	B1

Table 10. Antimicrobial resistance genes of *Escherichia coli* isolates, (n=3)

Sample Name	COLISTIN	CEPHALO-SPORIN	GENTAMICIN	QUINOLONE	BETA-LACTAM	Cotri-moxazole	TETRACY-CLINE	Plasmids
23ARS-BRH0037	mcr-1.1		aac(3)-IId					Col(MG828), IncFIB (AP001918), IncFIB (pLF82), IncFIC(FII), IncI2, p0111
23ARS-JLM0081	mcr-1.1	blaCTX-M-14		qnrS	blaTEM-1	dfrA12, sul3	tet(A)	Col440I, IncFIB (pB171), IncFII(pCoo), IncFII(pHN7A8), IncFII (pRSB107), IncHI1B (CIT), IncI1, IncI2, IncL/M, IncQ1, IncX4,
23ARS-NMC0005	mcr-1.1							IncX4

Table 10 shows the antimicrobial resistance (AMR) genes and the plasmids found in the three colistin-resistant *E. coli* isolates. All the three isolates carried the mobile colistin resistance gene mcr-1.1 and harbored multiple plasmids.

Isolate 23ARS-BRH0037 carried the aac(3)-IId gene conferring resistance to gentamicin. Isolate 23ARS-JLM0081 additionally harbored *bla*CTX-M-14, qnrS, blaTEM-1, dfrA12, sul3 and tet(A) mediating resistance to corresponding antibiotics. This is the second year of a report of an *E. coli* isolate harboring mcr-1.1 from the same sentinel site in Northern Luzon. With the noted similar plasmids being carried by the isolates reported in 2022 and in 2023, this may indicate a stable and continuous transmission of these resistance elements within the bacterial population in the said locality. This stability suggests that these plasmids are potentially critical factors in the propagation of the resistance genes [2,3]. This observation indicates the need for more stringent infection and prevention and control measures to prevent the spread of this resistant isolates.The continued surveillance of colistin-resistant *E. coli* is imperative to inform prevention and control measures against the spread of this resistant isolates in the country.

Reference

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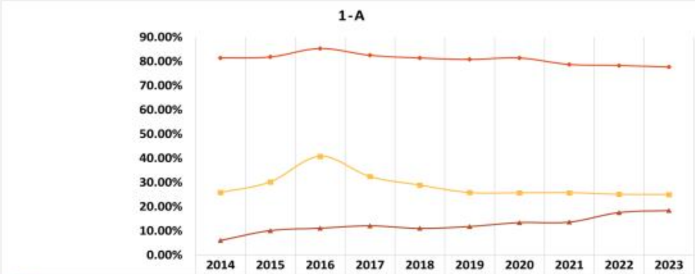
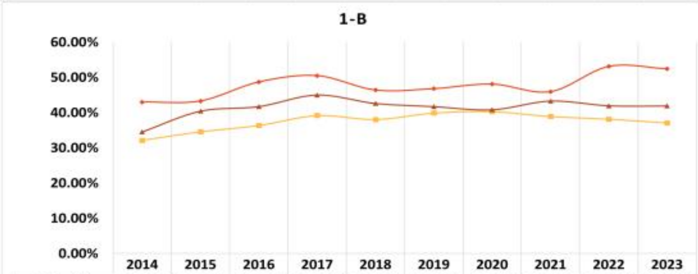
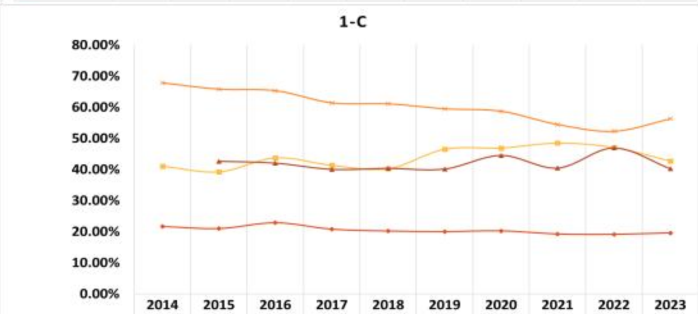


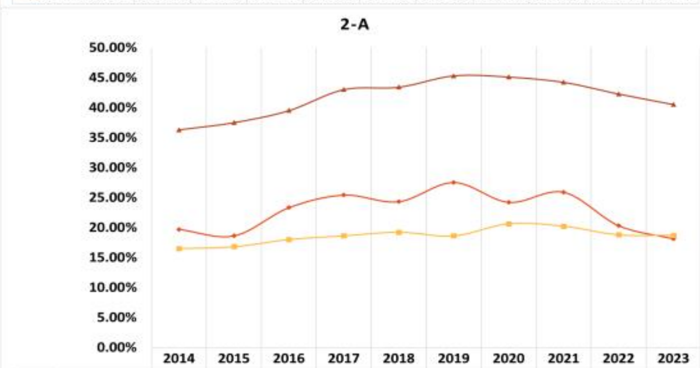
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ampicillin	81.40%	81.80%	85.30%	82.50%	81.40%	80.80%	81.39%	78.71%	78.32%	77.69%
Amoxicillin/Clavulanic acid	25.80%	30.20%	40.80%	32.40%	28.90%	25.80%	25.70%	25.75%	25.08%	25.00%
Piperacillin/Tazobactam	6.00%	10.10%	11.10%	12.10%	11.00%	11.80%	13.40%	13.61%	17.58%	18.40%



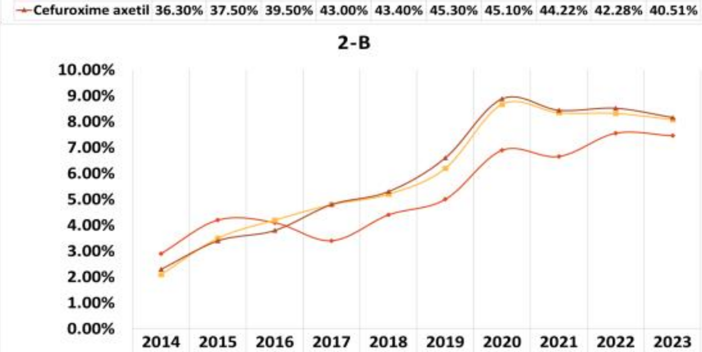
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Cefazolin	43.00%	43.30%	48.70%	50.50%	46.40%	46.80%	48.10%	45.94%	53.12%	52.45%
Ceftriaxone	32.20%	34.60%	36.40%	39.20%	38.10%	39.90%	40.31%	38.94%	38.19%	37.13%
Cefotaxime	34.50%	40.40%	41.70%	45.00%	42.60%	41.70%	40.80%	43.28%	41.95%	41.88%



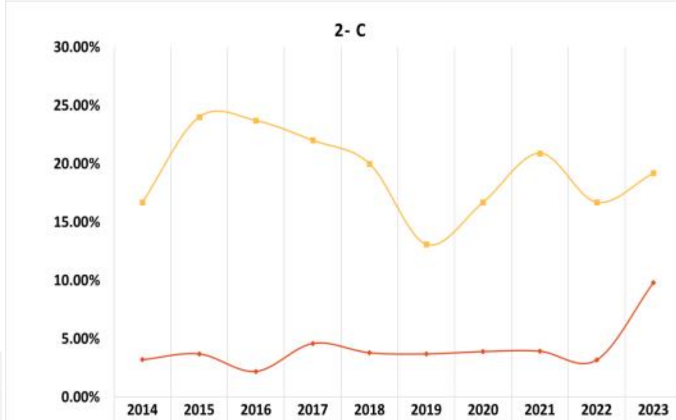
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Gentamicin	21.70%	21.00%	22.90%	20.80%	20.20%	20.00%	20.25%	19.24%	19.14%	19.58%
Ciprofloxacin	41.00%	39.20%	43.70%	41.30%	40.20%	46.50%	46.87%	48.46%	47.03%	42.68%
Levofloxacin		42.60%	42.00%	40.00%	40.30%	40.10%	44.50%	40.40%	46.90%	40.19%
Co-trimoxazole	67.80%	65.80%	65.30%	61.40%	61.10%	59.50%	58.71%	54.46%	52.27%	56.28%



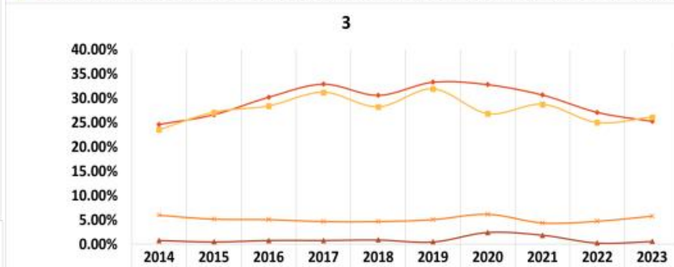
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Cefepime	19.70%	18.60%	23.30%	25.40%	24.30%	27.50%	24.20%	25.88%	20.32%	18.09%
Cefoxitin	16.50%	16.80%	18.00%	18.60%	19.20%	18.60%	20.60%	20.20%	18.77%	18.70%
Cefuroxime axetil	36.30%	37.50%	39.50%	43.00%	43.40%	45.30%	45.10%	44.22%	42.28%	40.51%



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ertapenem	2.90%	4.20%	4.10%	3.40%	4.40%	5.00%	6.90%	6.66%	7.56%	7.45%
Imipenem	2.10%	3.50%	4.20%	4.80%	5.20%	6.20%	8.67%	8.34%	8.32%	8.08%
Meropenem	2.30%	3.40%	3.80%	4.80%	5.30%	6.60%	8.88%	8.44%	8.52%	8.16%



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Amikacin	3.20%	3.70%	2.20%	4.60%	3.80%	3.70%	3.90%	3.93%	3.18%	9.82%
Tobramycin	16.70%	24.00%	23.70%	22.00%	20.00%	13.10%	16.70%	20.90%	16.70%	19.19%



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ceftazidime	24.60%	26.60%	30.20%	32.90%	30.60%	33.30%	32.80%	30.66%	27.08%	25.24%
Aztreonam	23.50%	27.10%	28.40%	31.20%	28.20%	31.90%	26.80%	28.72%	24.97%	26.12%
Colistin	0.80%	0.50%	0.80%	0.80%	0.90%	0.50%	2.40%	1.85%	0.28%	0.59%
Nitrofurantoin	6.00%	5.20%	5.10%	4.70%	4.70%	5.10%	6.20%	4.42%	4.77%	5.82%

Figure 86. Yearly resistance rates of *E. coli* isolates for all specimens, DOH-ARSP, 2023

The yearly resistance rates of *E. coli* is shown in Figure 86. There had been a decrease in the resistance rates to cotrimoxazole (p= 0.0000) and amoxicillin/clavulanic acid (p=0.0000) over the past ten years while resistance to nitrofurantoin (p=0.3681) remained stable.

There was an overall increase in *E. coli* resistance rates to ciprofloxacin (p=0.0000), ceftriaxone (p=0.0000) and cefotaxime (p=0.0000) in the past decade with rates remaining in the 35-45% range.

Overall resistance to colistin remained below 1% in the past decade (p=0.0000) while resistance to all the carbapenems have continuously increased (p=0.0000). It is noted, however, that the resistance to carbapenems among eco seemed to remain relatively stable in the past 4 years. This may indicate an effect of the collective efforts on safeguarding use of these antibiotics through effective AMS programs among the sentinel sites.

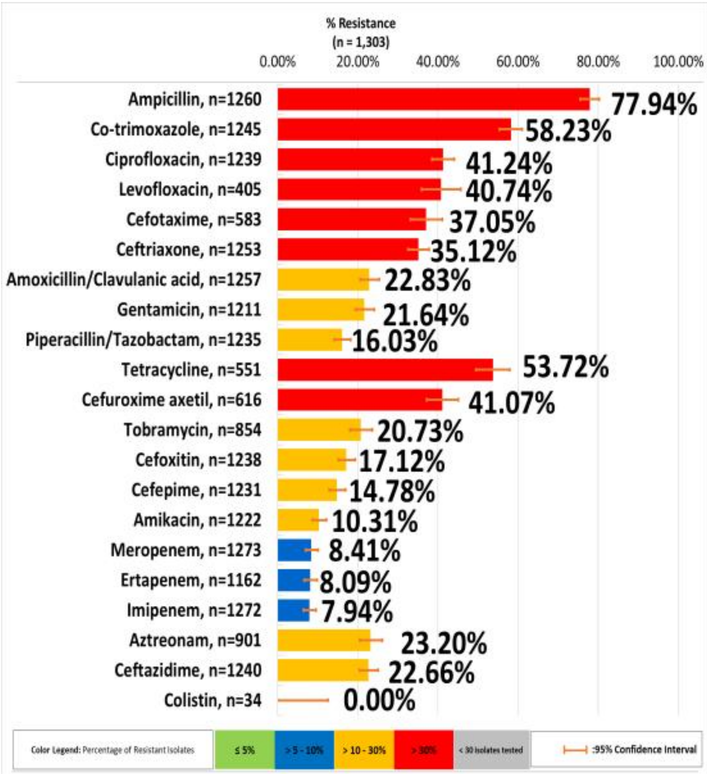


Figure 87. Resistance rates of *E. coli* blood isolates, DOH-ARSP, 2023

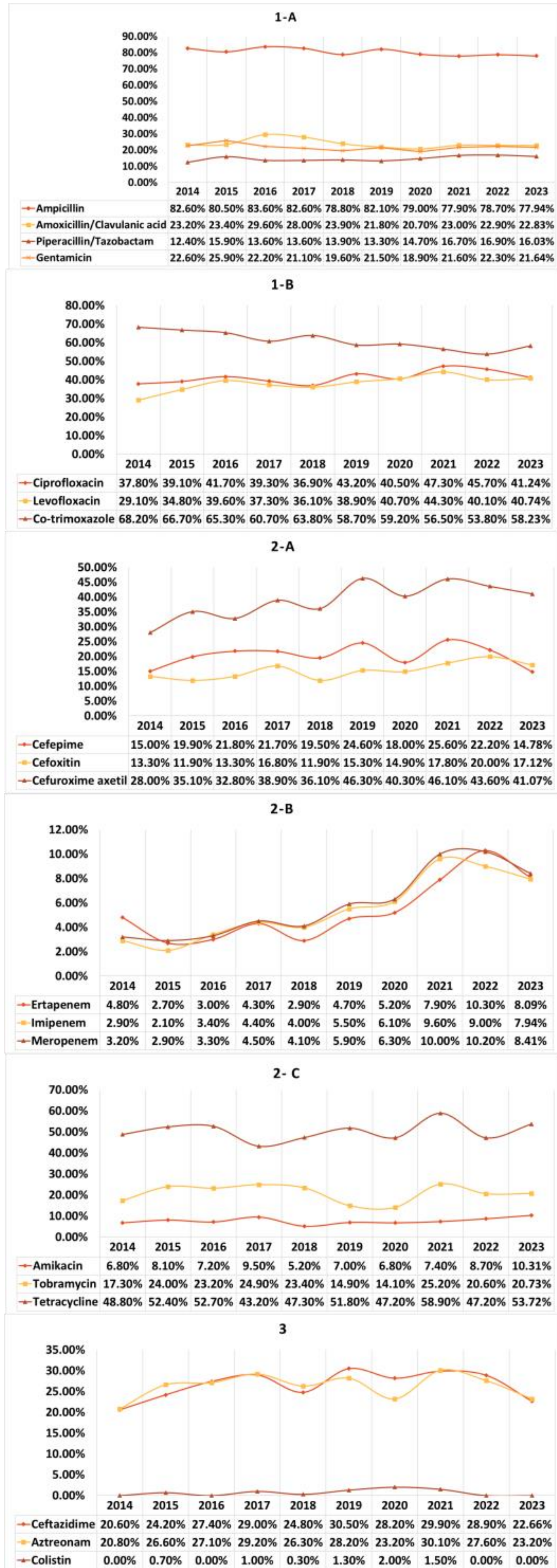


Figure 87 shows the resistance rates of *E. coli* isolates from blood specimens. Resistance rates of *E. coli* to almost all antibiotics were above 10%. Resistance to ampicillin was 77.94% followed by co-trimoxazole at 58.23%. Resistance rates to levofloxacin, ciprofloxacin, cefotaxime, ceftriaxone, tetracycline and cefuroxime were in the 35-55% range. Resistance to piperacillin-tazobactam is relatively lower at 16.03% and to the carbapenems: meropenem was 8.41%, 8.09% and 7.94% for both ertapenem and imipenem. Compared with resistance rates for all specimens, relatively higher resistance rates were seen for most antibiotics among blood isolates except for cefotaxime, ceftriaxone, amoxicillin- clavulanic, piperacillin-tazobactam, cefoxitin, cefepime and colistin which showed lower rates.

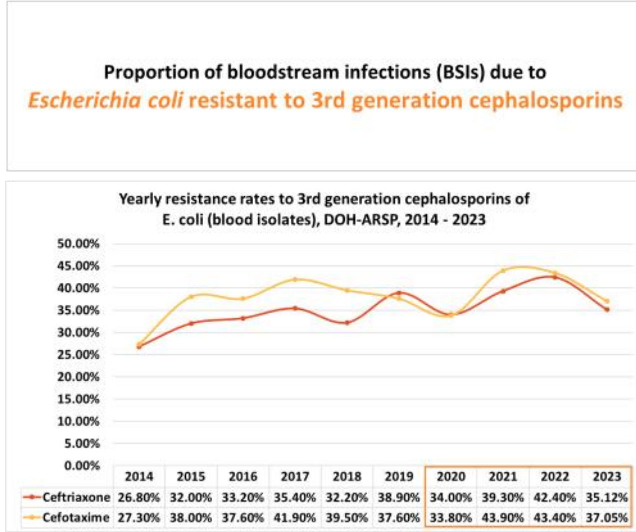


Figure 88. Yearly resistance rates of *E. coli* blood isolates, DOH-ARSP, 2023

The yearly resistance rates of *E. coli* blood isolates are shown in **Figure 88**. Although there was an overall decrease, the resistance rates of ampicillin, cefazolin, and amoxicillin-clavulanic acid, has remained high over the past decade (p=0.0000). Resistance to piperacillin-tazobactam (p=0.0000), the carbapenems (p=0.00000), and colistin (p=0.0000) has increased over the past decade.

One of the AMR indicators in the monitoring framework for the Sustainable Development Goals (SDG) linked to the health target 3.d ("strengthen the capacity of all countries, in particular developing countries, for early warning, risk reduction and management of national and global health risks'' ïncluded in 2020 is the proportion of patients with bloodstream infections (BSI) caused by *E.coli* resistant to 3rd generation cephalosporin[7,8]. As shown in **Figure 88**, among *E. coli* from blood specimens, the percentage of resistance to ceftriaxone and cefotaxime have increased from 2020 to the 2023 values. Using *E.coli* isolates from blood specimens as proxy for patients with BSI caused by *E.coli* resistant to 3rd generation cephalosporin, ARSP data indicates that, for this indicator, the Philippines may have to continue to look into possible interventions in order to achieve this SDG target

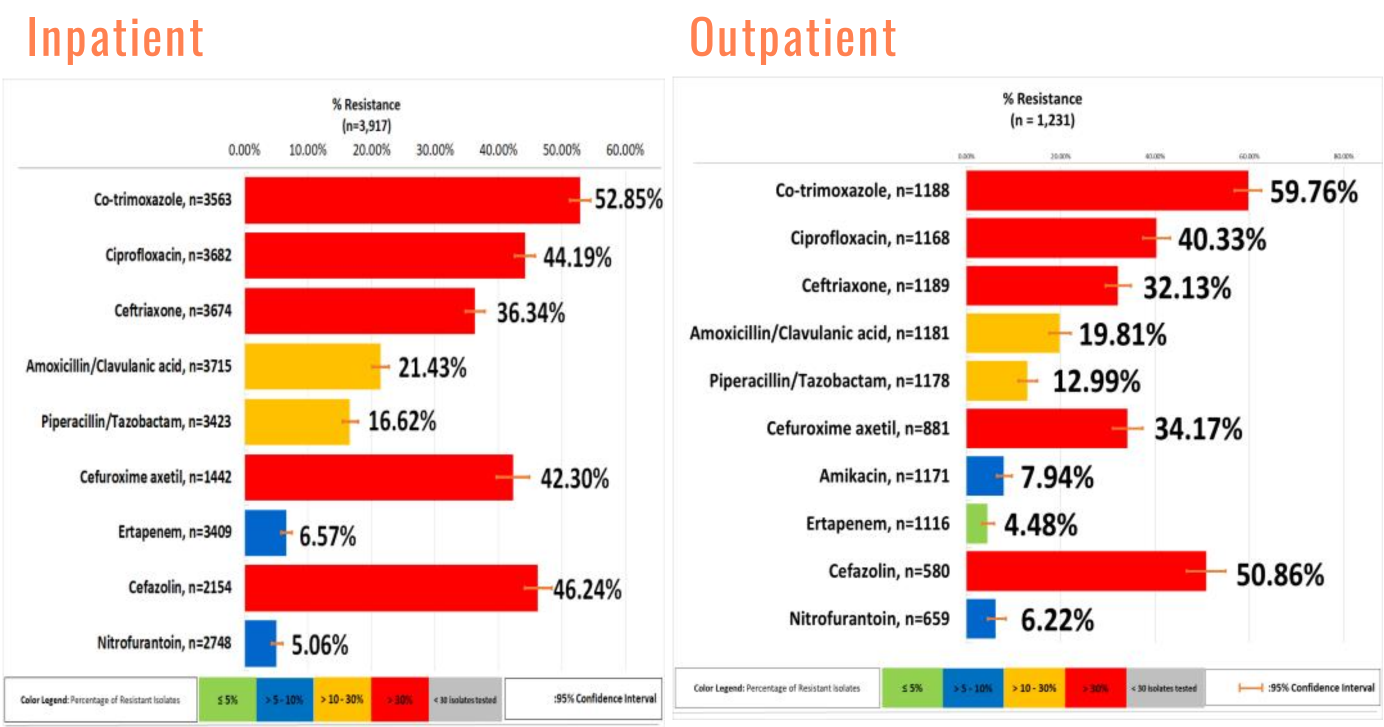
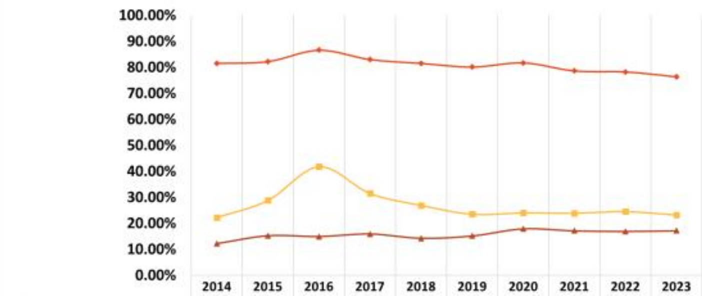


Figure 89. Resistance rates of *E. coli* urine isolates from in-patients and out-patients, DOH-ARSP, 2023

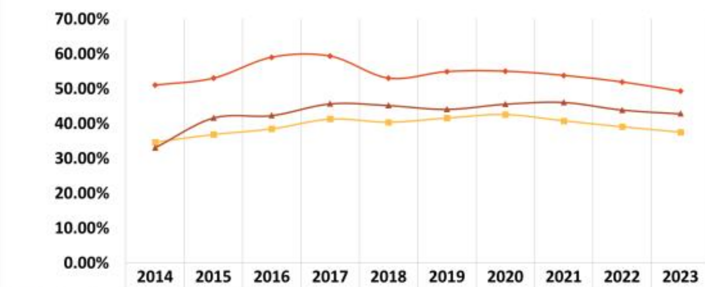
Resistance rates of in-patient and out-patient *E. coli* urine isolates against commonly used antibiotics are shown in **Figure 89**. Among urinary *E. coli* isolates from out-patients, resistance to co-trimoxazole, cefazolin, and ciprofloxacin are very high at 59.76%, 50.86%, and 40.33%, respectively. Resistance to nitrofurantoin was at 6.22%. Among urinary *E. coli* isolates from in-patients, resistance to co-trimoxazole, ciprofloxacin, ceftriaxone, cefuroxime axetil and cefazolin were above 30%. Resistance to amoxicillin-clavulanic acid and piperacillin-tazobactam were at 21.43% and 16.62%, respectively. Resistance to ertapenem and nitrofurantoin were below 10%.

1-A



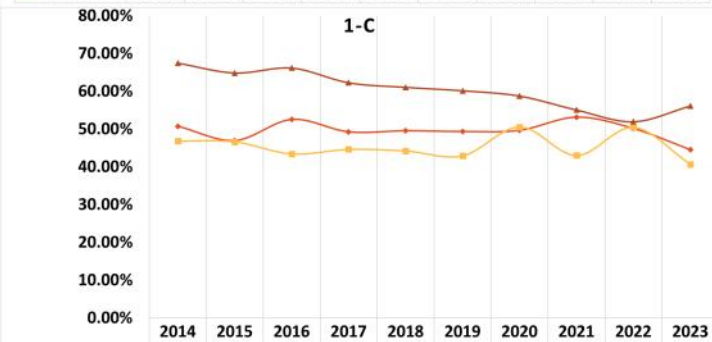
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ampicillin	81.50%	82.20%	86.60%	83.00%	81.50%	80.10%	81.70%	78.60%	78.20%	76.31%
Amoxicillin/Clavulanic acid	22.20%	28.80%	41.80%	31.50%	26.90%	23.50%	24.00%	23.90%	24.50%	23.21%
Piperacillin/Tazobactam	12.10%	15.20%	14.90%	15.90%	14.20%	15.10%	17.90%	17.10%	16.90%	17.12%

1-B



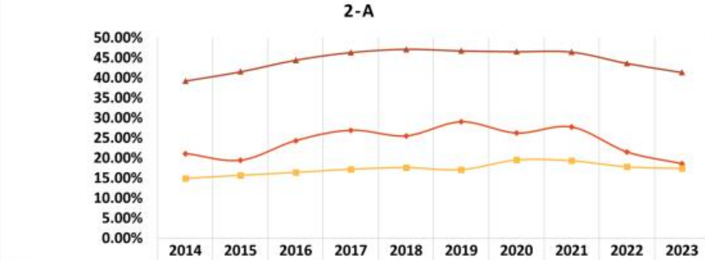
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Cefazolin	51.00%	53.00%	59.00%	59.30%	53.00%	54.90%	55.00%	53.80%	51.90%	49.27%
Ceftriaxone	34.70%	36.90%	38.50%	41.30%	40.40%	41.60%	42.60%	40.80%	39.10%	37.56%
Cefotaxime	33.00%	41.60%	42.30%	45.70%	45.20%	44.10%	45.60%	46.10%	43.90%	42.80%

1-C



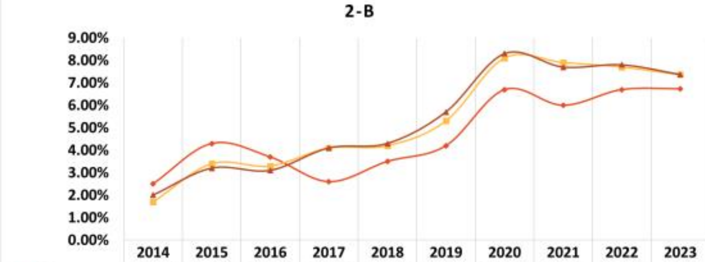
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ciprofloxacin	50.70%	46.90%	52.50%	49.20%	49.50%	49.30%	49.60%	53.10%	50.10%	44.47%
Levofloxacin	46.80%	46.60%	43.40%	44.60%	44.20%	42.90%	50.50%	43.00%	50.40%	40.66%
Co-trimoxazole	67.40%	64.80%	66.10%	62.20%	61.00%	60.10%	58.70%	55.00%	51.90%	56.06%

2-A



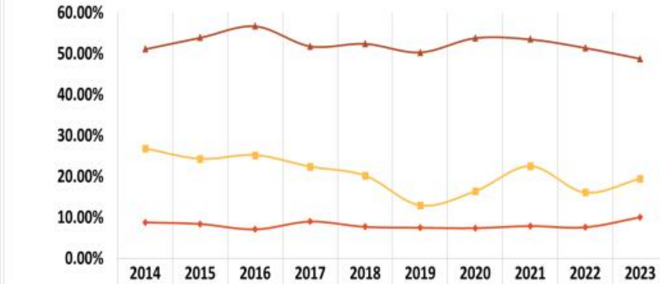
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Cefepime	21.10%	19.40%	24.30%	26.90%	25.50%	29.00%	26.20%	27.70%	21.50%	18.52%
Cefoxitin	14.90%	15.70%	16.40%	17.20%	17.60%	17.10%	19.50%	19.30%	17.80%	17.37%
Cefuroxime axetil	39.20%	41.50%	44.40%	46.30%	47.10%	46.70%	46.50%	46.40%	43.60%	41.31%

2-B



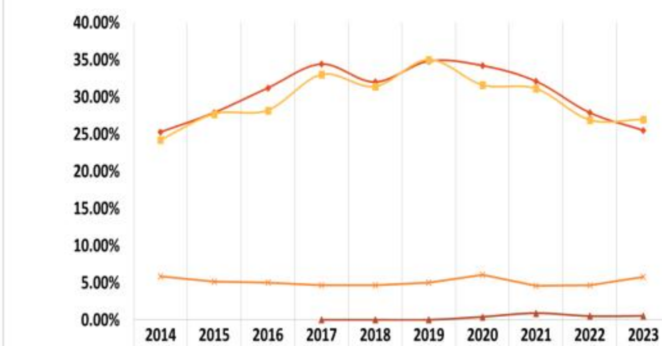
	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ertapenem	2.50%	4.30%	3.70%	2.60%	3.50%	4.20%	6.70%	6.00%	6.70%	6.74%
Imipenem	1.70%	3.40%	3.30%	4.10%	4.20%	5.30%	8.10%	7.90%	7.70%	7.36%
Meropenem	2.00%	3.20%	3.10%	4.10%	4.30%	5.70%	8.30%	7.70%	7.80%	7.37%

2- C



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Amikacin	8.80%	8.40%	7.10%	9.00%	7.70%	7.50%	7.40%	7.90%	7.60%	10.05%
Tobramycin	26.80%	24.30%	25.20%	22.40%	20.20%	13.00%	16.40%	22.50%	16.10%	19.46%
Tetracycline	51.10%	53.90%	56.70%	51.80%	52.40%	50.30%	53.80%	53.50%	51.40%	48.75%

3



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Ceftazidime	25.30%	27.90%	31.20%	34.40%	32.00%	34.80%	34.20%	32.10%	27.90%	25.53%
Aztreonam	24.20%	27.70%	28.20%	33.00%	31.40%	35.00%	31.60%	31.10%	26.90%	26.96%
Colistin				0.00%	0.00%	0.00%	0.40%	0.90%	0.50%	0.53%
Nitrofurantoin	5.90%	5.20%	5.00%	4.70%	4.70%	5.00%	6.10%	4.60%	4.70%	5.81%

Figure 90. Yearly resistance rates of *E. coli* urine isolates, DOH-ARSP, 2023

Figure 90 shows the yearly resistance rates of all *E. coli* urine isolates. There had been a decrease in the resistance rates to nitrofurantoin (p=0.8308), co-trimoxazole (p=0.0000), and ciprofloxacin (p=0.0000) over the past ten years.

There was an overall increase in *E. coli* resistance rates to amoxicillin/clavulanic acid (p=0.0000), ceftriaxone (p=0.0000), cefotaxime (p= 0.5412) in the past decade but both remained in the 35-45% range. Overall resistance to colistin remained within less than 1% in the past decade while resistance to all the carbapenems have continuously increased (p=0.0000).

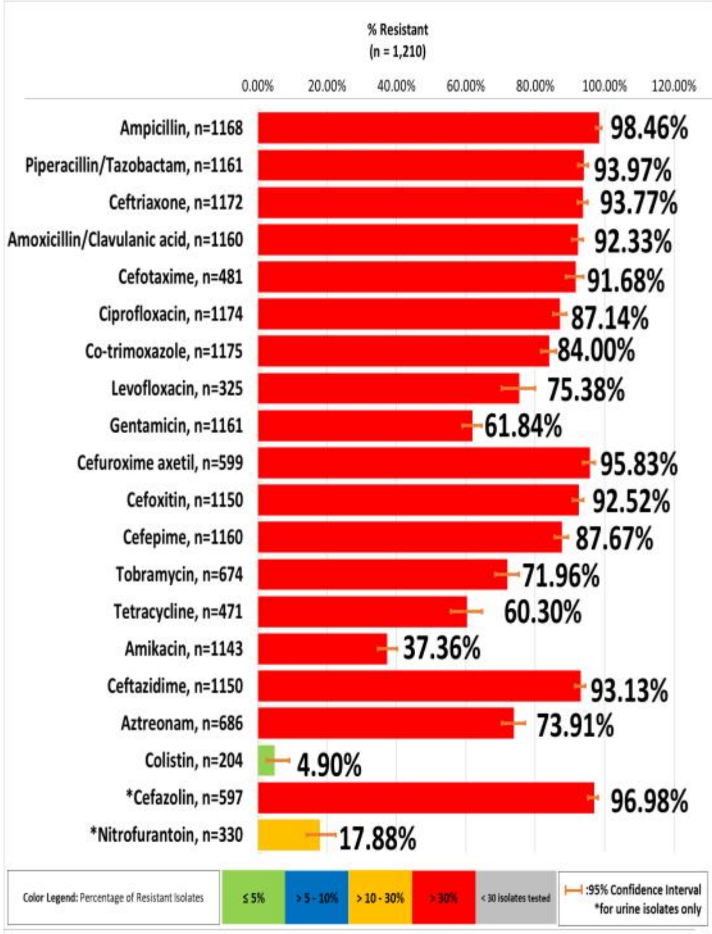


Figure 91. Resistance rates of carbapenem-resistant *E. coli* isolates, DOH-ARSP, 2023

Figure 91 shows the percent resistance of carbapenem-resistant *E. coli* isolates for 2023. Among these isolates, resistance to most antibiotics were high ranging from 50-90%. Resistance rate for amikacin was 37.36% and 4.90% for colistin.

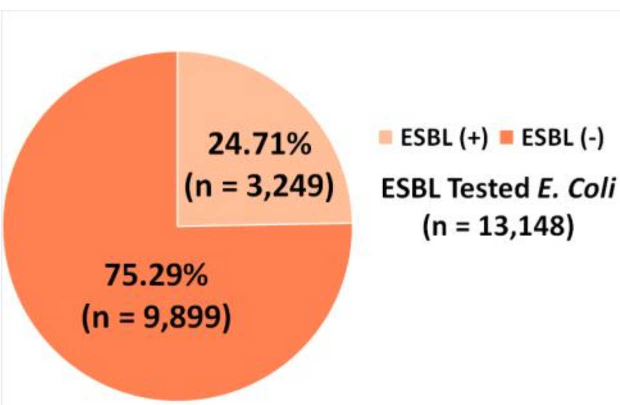
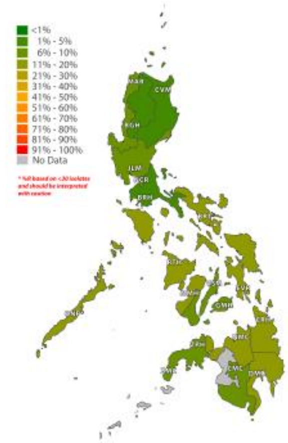


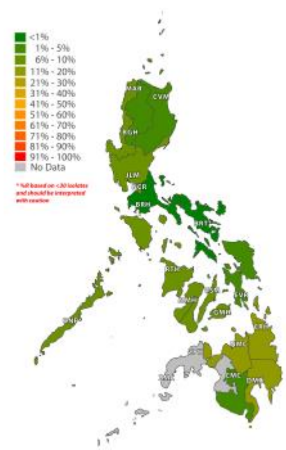
Figure 92. Percentage of ESBL positive and negative isolates among ESBL tested *E. coli*, DOH-ARSP, 2023

From the subset of 2023 *E. coli* isolates screened phenotypically for ESBL production (n= 13,148), positivity rate was at 24.71% (**Figure 92**). The ESBL positivity rate was determined by the total number of ESBL positive isolates over the total number of isolates tested for ESBL production.

Imipinem



Ertapenem



Meropenem

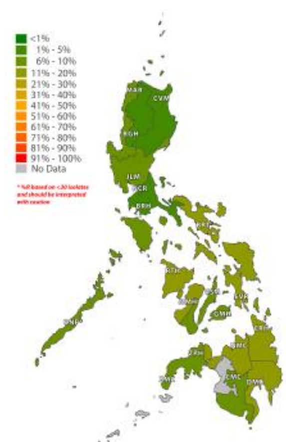


Figure 93. Resistance maps of *E. coli* for (A) imipenem, (B) ertapenem (C) meropenem

Figure 93 shows the carbapenem resistance rates of *E. coli* across regions represented by sentinel sites. The carbapenem resistance of *E. coli* isolates for imipenem across regions were mostly 11-20%. Ertapenem resistance was observed to be less than 1% for most of the regions while meropenem resistance ranges from 6-40%.

Klebsiella pneumoniae

A total of **16,164** *K. pneumoniae* isolates were reported in 2023. PGH (15.63%) contributed most to the number of isolates followed by VSM (10.39%) and GMH (7.97%). Based on island group distribution, more than half (52.75%) of the isolates were from Luzon with 24.81% coming from NCR sentinel sites, 26.81% from Visayas and 20.44% from Mindanao.

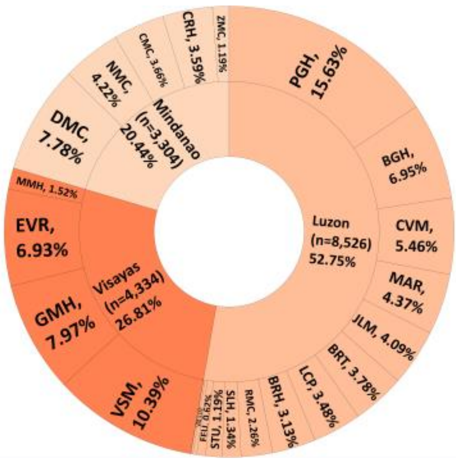


Figure 94. Isolate distribution of *K. pneumoniae*, DOH-ARSP, 2023 (n=16,164)

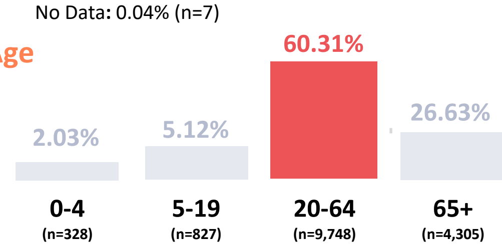
A. Sex

54.66% **Male (n=8,836)**

45.29% **Female (n=7,321)**

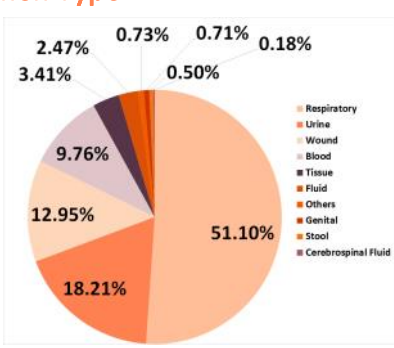
No Data: 0.04% (n=7)

B. Age

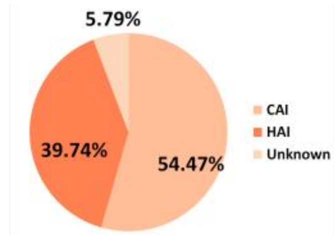


Unknown: 5.91% (n=956)

C. Specimen Type



D. Infection Type



E. Clinical Service

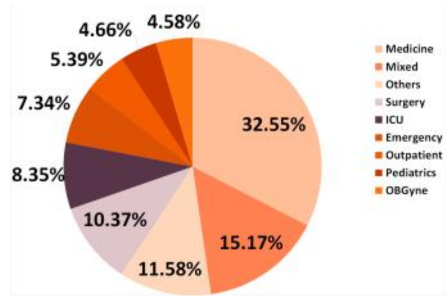


Figure 95. Patient characteristics of *K. pneumoniae* isolates, DOH-ARSP, 2023 (n=16,164)

More than half (60.31%) of the isolates were from the 20-64 years age group and most (54.66%) were from male patients. Most (51.10%) of the isolates were collected from respiratory specimens, urine (18.21%) and wound specimens (12.95%). Most (54.47%) of the isolates were from presumptive community acquired infections (**Figure 95**).

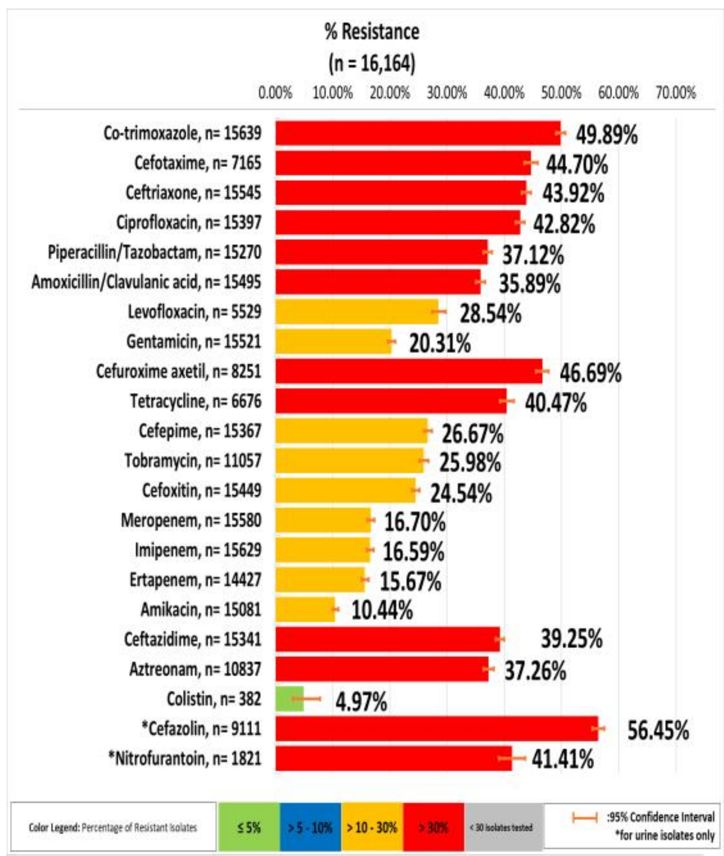


Figure 96. Resistance rates of *K. pneumoniae* isolates for all specimens, DOH-ARSP, 2023

Cumulative resistance rates of *K. pneumoniae* from all specimens are shown in Figure 96. As known to be commonly resistant to multiple antibiotics, *K.pneumoniae* antimicrobial rates to most antibiotics were above 30%. Resistance to amoxicillin-clavulanic acid was 35.89% and piperacillin-tazobactam was 37.12%. Resistance to meropenem, imipenem and ertapenem were 16.70%, 16.59% and 15.67%, respectively. There were increase in the resistance rates of the following antibiotics from 2022 compared with 2023 rates: amikacin (p= 0.0000), co-trimoxazole (p=0.0000), imipenem (p=0.0296), ertapenem (p= 0.0000), cefazolin (p=0.0043), nitrofurantoin (p= 0.0000) and piperacillin-tazobactam (p=0.0000). It must be noted that for 2023, there has been a change in the zone diameter and MIC breakpoints for amikacin which could explain the increase in the %R for amikacin for 2023. For 2023, there was a decrease in the resistance rates for colistin (p=0.0207).

There are sporadic reports (22 isolates) from Luzon of resistance among *K. pneumoniae* to the new combination antibiotics ceftazidime-avibactam detected through MIC. The isolates were mostly from respiratory specimens of adult patients with presumptive hospital acquired infections. Most of the isolates are MDR but are susceptible to aztreonam and amikacin. Two (2) of these isolates appear to be extensively drug resistant. Expansion of susceptibility testing of Enterobacterales to include testing for the newer combination antibiotics across all laboratories are needed to guide appropriate use and to safeguard use of these antibiotics.

Molecular characterization of emerging colistin-resistant *Klebsiella pneumoniae*

Introduction

Klebsiella pneumoniae (Kpn) can cause various infections, such as pneumonia, urinary tract infections (UTIs), bloodstream, and wound infections. In healthcare settings, it can be particularly problematic due to its tendency to develop resistance to multiple antibiotics, making treatment more difficult (1).

Colistin is a polymyxin that is considered last line treatment for multi-drug resistant Gram-negative bacteria but can potentially cause nephrotoxicity when administered at higher doses or for prolonged durations (2). Colistin-resistant Kpn infections represent a significant threat to public health because treatment options for these infections often become severely limited, increasing the risk of treatment failure and mortality (3). One of the most concerning mechanisms of colistin resistance is the acquisition of plasmid-mediated resistance genes, such as *mcr-1* and its variants.

These genes encode enzymes that modify lipid A, a component of the bacterial outer membrane, reducing the binding affinity of colistin and conferring resistance to the antibiotic (4). Plasmids carrying *mcr* genes can spread horizontally between bacterial strains and species, contributing to the global dissemination of colistin resistance.

This report describes the phenotypic and genotypic characteristics of colistin-resistant Kpn isolates collected through ARSP in 2023.

Patient Demographics and Clinical Characteristics

In 2023, a total of 25 colistin-resistant Kpn isolates were identified and were primarily isolated from respiratory (n=15), urine (n=5), blood (n=4) and wound (n=1) specimens. The age range of patients is from 4 days to 82 years old, with 5 patients from the ICU. Among these isolates, 19 were categorized presumptive hospital acquired infections while 6 were identified as presumptive community acquired infections while 6 were identified as community acquired infections.

Table 11. Patient Demographics and Clinical Characteristics of Colistin-resistant Kpn

Isolate	Hospital	Age	Specimen type	Ward	Infection Type
23ARS-BGH0073	BGH	57	Tracheal aspirate	MED	CAI
23ARS-BRH0097	BRH	18	Sputum	PED	HAI
23ARS-BRT0027	BRT	21	Urine	OBG	CAI
23ARS-BRT0036	BRT	19	Sputum	SUR	HAI
23ARS-CRH0046	CRH	17d	Blood	PED	HAI
23ARS-CRH0077	CRH	41	Wound	MED	CAI
23ARS-CRH0145	CRH	82	Tracheal aspirate	MED	HAI
23ARS-CVM0021	CVM	4d	Blood	NICU	HAI
23ARS-CVM0022	CVM	5d	Blood	NICU	HAI
23ARS-DMC0244	DMC	60	Tracheal aspirate	ICU	HAI
23ARS-DMC0435	DMC	43	Respiratory	SUR	HAI
23ARS-EVR0041	EVR	64	Tracheal aspirate	MCU	HAI
23ARS-GMH0009	GMH	5d	Blood	NUR	HAI
23ARS-GMH0055	GMH	67	Sputum	MED	HAI
23ARS-JLM0044	JLM	9	Urine	PED	HAI
23ARS-JLM0086	JLM	59	Tracheal aspirate	ICU	HAI
23ARS-JLM0175	JLM	43	Tracheal aspirate	MIX	HAI
23ARS-NMC0001	NMC	78	Urine	UNK	CAI
23ARS-SLH0114	SLH	34	Urine	UNK	HAI
23ARS-VSM0248	VSM	54	Tracheal aspirate	ICU	HAI
23ARS-VSM0265	VSM	26	Sputum	MED	HAI
23ARS-VSM0341	VSM	19	Sputum	MIX	HAI
23ARS-VSM0346	VSM	30	Urine	OUT	CAI
23ARS-VSM0363	VSM	67	Sputum	MED	HAI
23ARS-VSM0436	VSM	8d	Tracheal aspirate	PED	CAI

Antimicrobial Resistance

Antimicrobial susceptibility testing (AST) of colistin-resistant Kpn isolates were performed based on current Clinical Laboratory Standards Institute (CLSI) guidelines while colistin minimum inhibitory concentrations (MICs) were determined using broth microdilution. The antimicrobial resistance patterns of the 25 colistin-resistant Kpn are summarized in **Table 12**. Colistin-resistant Kpn revealed diverse AMR profiles with 6 isolates exhibiting susceptibility to all tested antibiotics except colistin. Among the 25 isolates, 10 were ESBL-producing Kpn while 8 were carbapenem-resistant.

Table 12. Antimicrobial resistance patterns of colistin-resistant Kpn

ISOLATE	FOX	TZP	AMC	3rd gen ceph: CRO, CTX, CAZ	4th gen: FEP	Carbapenems: IMP, MER	AMK	GEN	TOB	CIP	SXT	TCY
23ARS-BGH0073	R	R	R	R	R	R	R	R	R	R	R	S
23ARS-BRH0097	S	SDD	R	R	R	S	S	R	R	R	S	R
23ARS-BRT0027	S	S	S	S	S	S	S	S	S	S	S	S
23ARS-BRT0036	S	S	S	S	S	S	S	S	S	S	S	S
23ARS-CRH0046	R	R	R	R	SDD	R	R	R	R	R	S	S
23ARS-CRH0077	S	S	S	R	S	S	S	S	S	R	R	R
23ARS-CRH0145	R	R	R	R	R	R	S	S	R	R	R	R
23ARS-CVM0021	S	S	S	R	S	S	R	R	R	S	R	S
23ARS-CVM0022	S	SDD	R	R	R	S	R	R	R	R	R	S
23ARS-DMC0244	S	R	R	R	R	S	R	R	R	R	R	R
23ARS-DMC0435	S	S	S	S	S	S	S	S	S	S	S	S
23ARS-EVR0041	R	R	R	R	R	R	S	R	R	R	R	R
23ARS-GMH0009	R	R	R	R	SDD	R	S	S	R	R	R	R
23ARS-GMH0055	S	S	S	S	S	S	S	S	S	S	S	S
23ARS-JLM0044	R	R	R	R	R	R	S	R	R	R	R	S
23ARS-JLM0086	S	S	S	S	S	S	S	S	S	S	S	S
23ARS-JLM0175	S	R	R	R	R	S	S	R	R	R	R	R
23ARS-NMC0001	S	S	S	R	S	S	S	S	S	R	S	R
23ARS-SLH0114	R	R	R	R	R	R	S	S	R	R	R	S
23ARS-VSM0248	R	R	R	R	R	R	S	R	R	R	R	S
23ARS-VSM0265	R	SDD	R	S	S	S	S	S	S	R	S	R
23ARS-VSM0341	S	S	S	S	S	S	S	S	S	S	S	S
23ARS-VSM0346	S	S	S	R	S	S	S	S	S	R	R	S
23ARS-VSM0363	S	S	S	R	S	S	S	S	S	R	R	R
23ARS-VSM0436	S	S	S	R	S	S	S	S	S	R	S	R

Legend: FOX= cefoxitin, TZP= piperacillin-tazobactam, AMC = amoxicillin-clavulanate, CRO = ceftriaxone, CTX= cefotaxime, CAZ= ceftazidime, IMP= imipenem, MEM= meropenem, AMK= amikacin, GEN= gentamicin, TOB= tobramycin, CIP= ciprofloxacin, SXT = trimethoprim-sulfamethoxazole, TCY= tetracycline, R= Resistant, SDD= Susceptible

Whole genome sequencing

Out of the 25 colistin-resistant Kpn isolates, 23 high quality genomes proceeded with bioinformatics analysis. *In silico* species identification revealed *Klebsiella pneumoniae* (n=5), *Klebsiella quasipneumoniae subsp quasipneumoniae* (n=2), *Klebsiella quasipneumoniae subsp. similipneumoniae* (n=11), and *Klebsiella variicola subsp variicola* (n=5). There were 17 distinct sequence types (STs) detected, reflecting the genetic diversity within the study population.

The different AMR genes detected by WGS are summarized in **Table 13**. ESBL was mostly mediated by *bla*CTX-M-15 (n=10) while carbapenem resistance was mediated by *bla*KPC-2 (n=1), *bla*NDM-1 (n=4), and *bla*NDM-7 (n=3). Analysis showed absence of known chromosomal mutation targets nor mobile genetic elements conferring resistance to colistin resistance in 20 of the *Klebsiella pneumoniae* isolates. The noted absence of known mechanisms conferring colistin resistance among these isolates suggests the possibility of the presence of other alternative mechanisms for resistance to colistin among these isolates. Mutations in PmrB and MgrB genes were detected in some of the isolates namely: 23ARS_DMC0244, 23ARS_EVR0041, 23ARS_NMC0001, and 23ARS_SLH0114 suggesting the these to potentially mediate of colistin resistance among these isolates. Modification in these PmrB and MgrB, along with PmrA, PhoP, and PhoQ, can alter the structure of lipopolysaccharides (LPS) in the outer membrane, reducing the affinity of colistin for its target and which renders the bacteria resistant to the antibiotic (4,5). Further, one isolate - 23ARS_NMC0001 - harbored the mobile colistin resistance gene *mcr-1.1* . This isolate was recovered from a urine sample of a 78-year-old patient from Mindanao. The isolate belonged to ST520, a sequence type typically associated with carbapenem-susceptible Kpn strains (6). 23ARS_NMC0001 had a colistin MIC of >32 ug/mL and showed resistance to ceftriaxone, cefotaxime, ceftazidime, ciprofloxacin, and tetracycline. AMR gene prediction by WGS revealed that the isolate was an ESBL-producer, mediated by *bla*CTX-M-55. Other AMR genes detected were *aadA22, qnrS1, sul2, and tet(A).v2*. In the previous year, ESBL-producing colistin resistant Kpn strains either harbored CTX-M-15 or CTX-M-3 beta-lactamases (7). The CTX-M-55 gene has been widely reported in *Escherichia coli* of food animal origin in China (8).

Table 13. AMR genes detected from Colistin-resistant Kpn

Isolate	Species identification	ST	Col_ acquired	Col_ mutations	Bla acquired	Bla ESBL	Bla Carb	AGly	Flq	Sul	Tmt	Tet
23ARS-BRH0097	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST903	-	-	-	-	-	-	-	-	-	-
23ARS-BRT0027	*Klebsiella variicola subsp. variicola*	ST2994-1LV	-	-	-	-	-	-	-	-	-	-
23ARS-BRT0036	*Klebsiella variicola subsp. variicola*	ST1881	-	-	-	-	-	-	-	-	-	-
23ARS-CRH0046	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST1308	-	-	-	-	NDM-1	aac(6')-Ib; rmtF	qnrS1	-	-	-
23ARS-CRH0077	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST1344-2LV	-	-	-	CTX-M-15	-	aadA2^; strA.v1* strB.v1*	qnrS1	sul1;sul2	dfrA12	tet(A).v1
23ARS-CRH0145	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST1344-2LV	-	-	OXA-1	CTX-M-15	NDM-1	aac(6')-Ib-cr.v2; aadA2^; aadA5; strA.v1*; strB.v1*	qnrS1	sul1;sul2	dfrA12; dfrA17	tet(A).v1
23ARS-CVM0021	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST334-1LV	-	-	TEM-1D.v1^	CTX-M-3*	-	aac(3)-IId^; aadA2^; armA	-	sul1	dfrA12	-
23ARS-CVM0022	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST334-1LV	-	-	TEM-1D.v1^	CTX-M-15	-	aac(3)-IId^; aac(6')-Ib-cr.v2; aadA16*	qnrB6^	sul1	dfrA27	-
23ARS-DMC0244	*Klebsiella pneumoniae*	ST39	-	MgrB-87%	-	-	-	aac(6')-Ib-cr.v2; aadA16*; aadA2*;aph3-Ia.v1^; armA; strA.v1^; strB.v1	qnrB1.v2^	sul1;sul2	dfrA12;dfrA14.v2*;dfrA27;dfrA7	tet(A).v1
23ARS-DMC0435	*Klebsiella variicola subsp. variicola*	ST1790-2LV	-	-	-	-	-	-	-	-	-	-

23ARS-EVR0041	*Klebsiella pneumoniae*	ST147-1LV	-	MgrB-49%	OXA-1;TEM-1D.v1^	CTX-M-15	KPC-2;NDM-7	aac(3)IIa.v1^ aac(6')-Ib-cr.v2; strA.v1^; strB.v1	qnrB1.v2^	sul2	dfrA14.v2*	-
23ARS-GMH0009	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST1822	-	-	LAP-2;OXA-10	SHV-12	NDM-1	aac(6')-Ib3^; aadA*; aph(3')-Ia; strA.v1;	qnrA1; qnrS1	sul1;sul2	dfrA14.v2*	tet(A).v1
23ARS-GMH0055	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST1308	-	-	-	-	-	-	-	-	-	-
23ARS-JLM0044	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST749-3LV	-	-	OXA-1;TEM-1D.v1^	CTX-M-15	NDM-7	aac(3)-IIa.v1^; aac(6')-Ib-cr.v2; strA.v1^; strB.v1	qnrB1.v2^	sul2	dfrA14.v2*	-
23ARS-JLM0086	*Klebsiella variicola subsp. variicola*	ST4185-1LV	-	-	-	-	-	-	-	-	-	-
23ARS-JLM0175	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST903	-	-	TEM-1D.v1^	CTX-M-15	-	aac(3)-IId^; aac(6')-Ib-cr.v2; aadA16*	qnrB6^	sul1	dfrA27	tet(A).v1
23ARS-NMC0001	*Klebsiella pneumoniae*	ST520	mcr-1.1^	PmrB-34%	-	CTX-M-55	-	aadA22^	qnrS1	sul2	-	tet(A).v2
23ARS-SLH0114	*Klebsiella pneumoniae*	ST147	-	MgrB-17%	-	CTX-M-15	NDM-1	aac(6')-Ib-cr.v2;aph(3')-VI	qnrS1	sul1	dfrA27	-
23ARS-VSM0248	*Klebsiella pneumoniae*	ST147	-	MgrB-0%	OXA-1	CTX-M-15	NDM-7	aac(3)-IIa.v1^; aac(6')-Ib-cr.v2	qnrB1.v2^	-	dfrA14.v2*	-
23ARS-VSM0265	*Klebsiella quasipneumoniae subsp. similipneumoniae*	ST4490-1LV	-	-	DHA-1^	-	-	-	qnrB4	sul1	dfrA17	tet(D)
23ARS-VSM0341	*Klebsiella variicola subsp. variicola*	ST5703	-	-	-	-	-	-	-	-	-	-
23ARS-VSM0346	*Klebsiella quasipneumoniae subsp. quasipneumoniae*	ST2010	-	-	-	CTX-M-15	-	aadA2^; aph3-Ia.v1^ ;strA.v1*; strB.v1*	qnrS1	sul1;sul2	dfrA12	-
23ARS-VSM0363	*Klebsiella quasipneumoniae subsp. quasipneumoniae*	ST2010	-	-	-	CTX-M-15	-	aadA2^; aph3-Ia.v1^; strA.v1*;strB.v1*	qnrS1	sul1;sul2	dfrA12	tet(A).v1

Legend: Col= Colistin, Bla= Beta-lactamase, ESBL= Extended-spectrum beta-lactamase, Carb= Carbapenemase, AGly= Aminoglycosides, Flq= Fluoroquinolone, Sul= Sulfonamides, Tmt= Trimethoprim, Tet= Tetracycline

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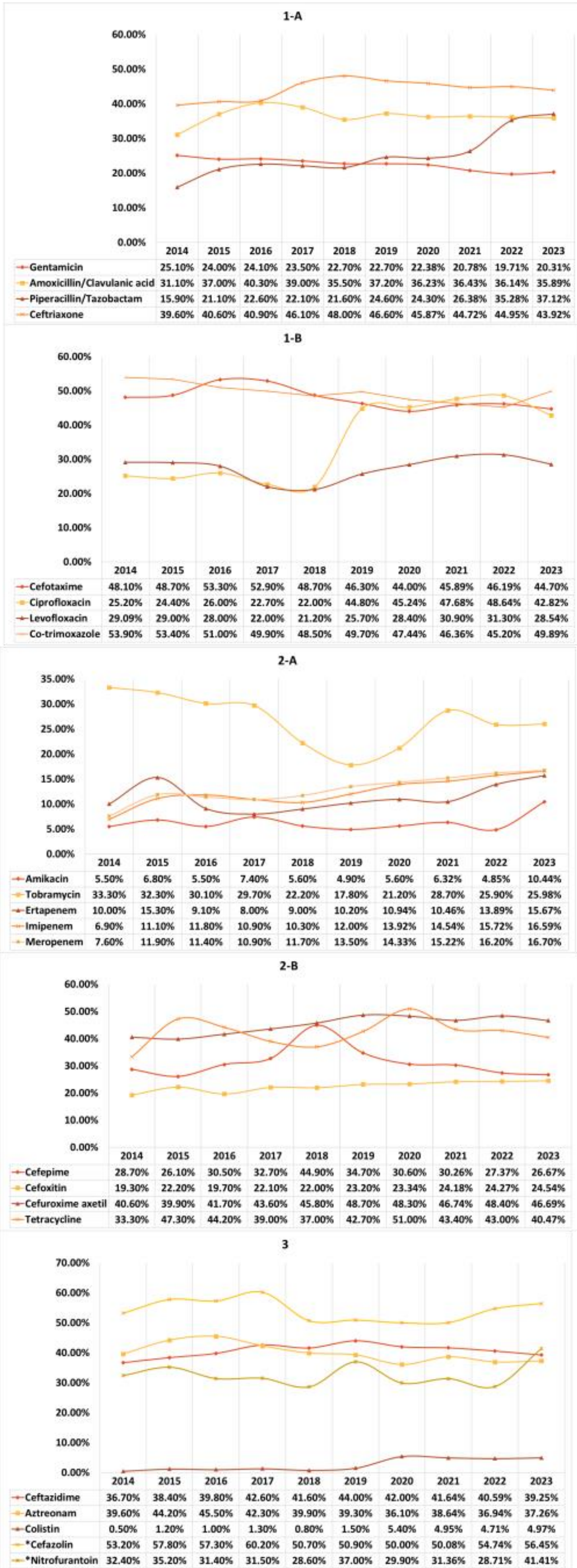


Figure 97. Yearly resistance rates of *K. pneumoniae*, DOH-ARSP, 2023

Figure 97 shows the yearly resistance rates of *K. pneumoniae*. The multiple year analysis revealed that the observed increase in percent resistance rates for almost all antibiotics tested including piperacillin-tazobactam (p=0.0000), imipenem (p=0.0000), meropenem (p=0.0000) and ertapenem (p=0.0000) were all statistically significant. On the other hand, the relatively stable resistance rates over the ten years for amoxicillin clavulanic acid (p=0.4621) was found to be not significant

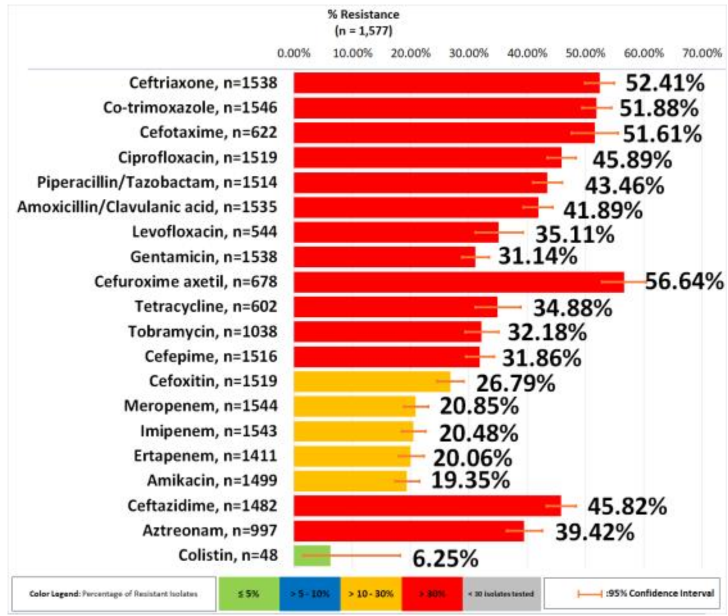
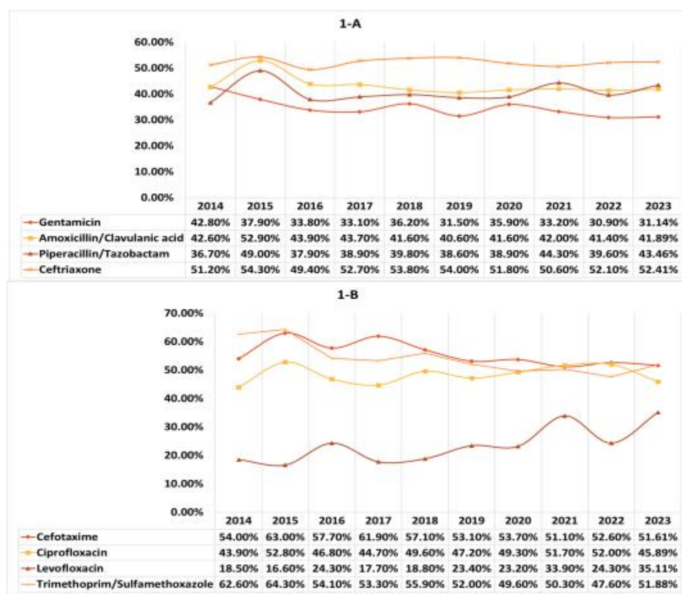


Figure 98. Resistant rates of *K. pneumoniae* blood isolates, DOH-ARSP, 2023

Figure 98 shows the percent resistance rates of *K. pneumoniae* isolates from blood specimens. Resistance rates for most antibiotics were above 30%. Resistance to amoxicillin-clavulanic acid was at 41.89% and 43.46% for piperacillin-tazobactam. Resistance to meropenem, imipenem and ertapenem were 20.85%, 20.48% and 20.06% respectively. Colistin resistance among blood isolates was 6.25%. Compared with overall resistance rates, relatively higher rates were seen for *K. pneumoniae* blood isolates for most antibiotics except for tetracycline (34.88%).



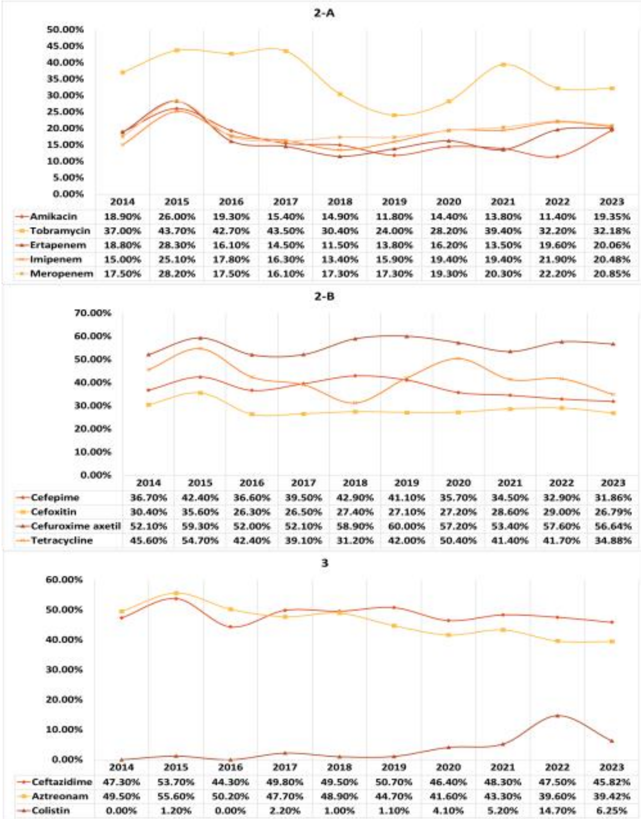


Figure 99. Yearly resistance rates of *K. pneumoniae* blood isolates, DOH-ARSP, 2014-2023

Figure 99 shows the yearly resistance rates of *K. pneumoniae* blood isolates. The multiple year analysis revealed that the observed increase in percent resistance rates for almost all antibiotics tested including piperacillin-tazobactam (p=0.0000), imipenem (p=0.0000), meropenem (p=0.0000) and ertapenem (p=0.0000) were all statistically significant. While, the relatively stable resistance rates over the ten years for amoxicillin clavulanic acid (p=0.5476) was found to be not significant.

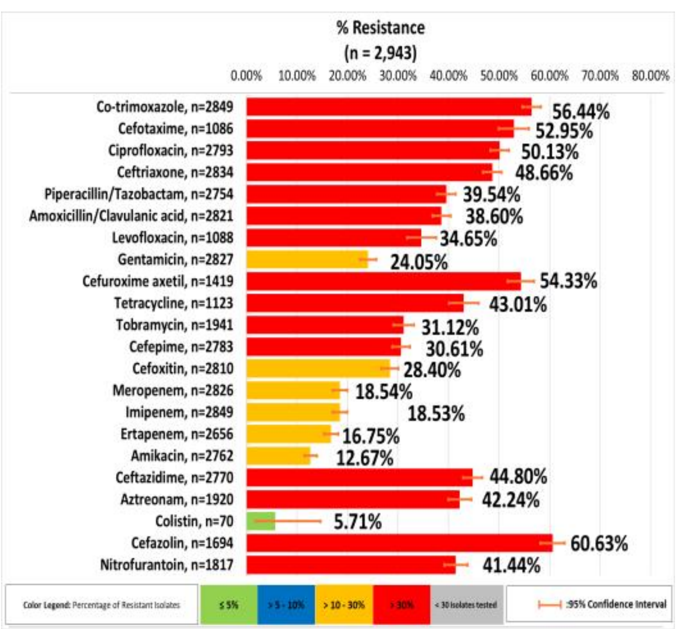


Figure 100. Resistance rates of *K. pneumoniae* urine isolates, DOH-ARSP, 2023

Figure 100 shows the percent resistance of *K. pneumoniae* isolates from urine specimens. Resistance to combination antibiotics amoxicillin- clavulanic acid and piperacillin-tazobactam were 38.60% and 39.54%. Compared with overall resistance rates from all samples, relatively higher rates were noted for *K. pneumoniae* urine isolates for most antibiotics.

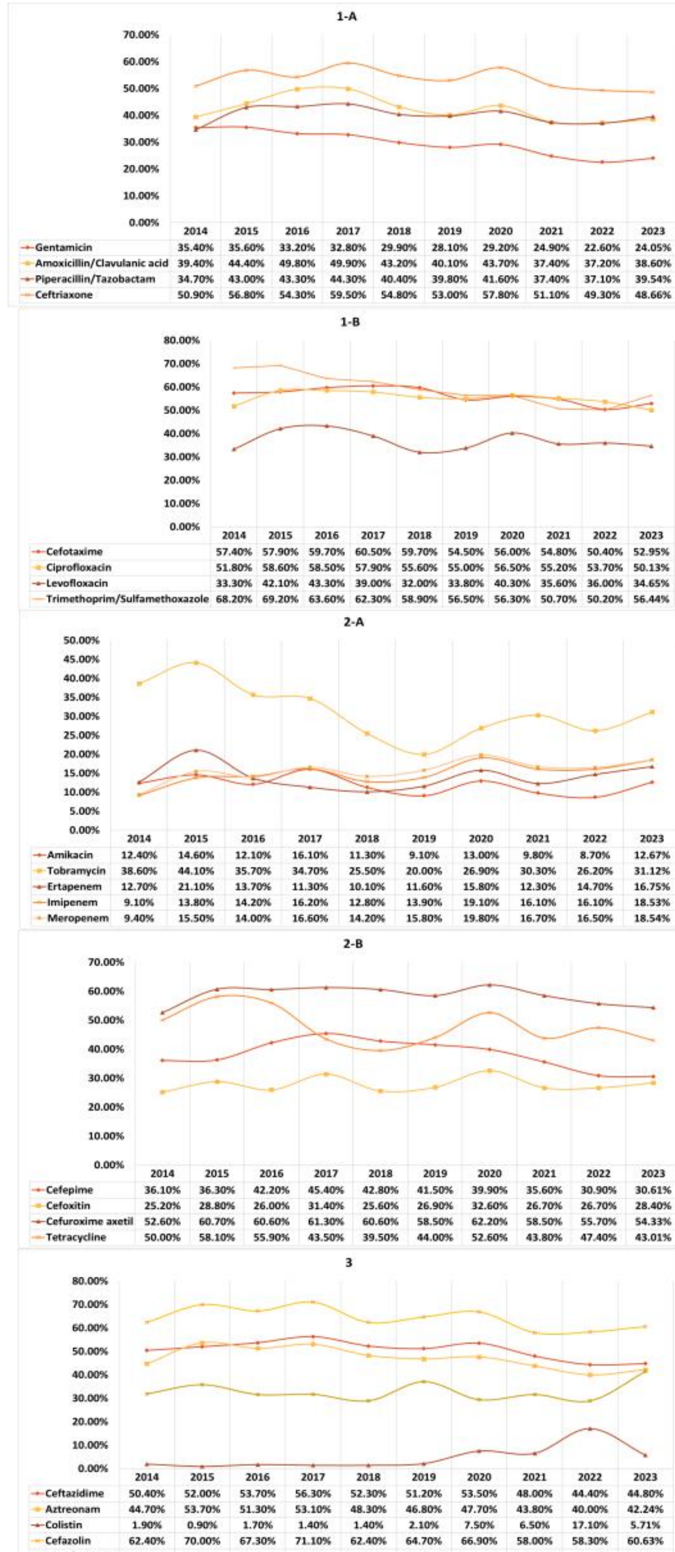


Figure 101. Yearly resistance rates of *K. pneumoniae* urine isolates, DOH-ARSP, 2014-2023

Figure 101 shows the yearly resistance rates of *K. pneumoniae* urine isolates. The multiple year analysis revealed that the observed increase in percent resistance rates for almost all antibiotics tested including piperacillin-tazobactam (p=0.0000), imipenem (p=0.0000), meropenem (p=0.0000), ertapenem (p=0.0000) and nitrofurantoin (p=0.0000) were all statistically significant. While, the relatively stable resistance rates over the ten years for amoxicillin clavulanic acid (p=0.0743) was found to be not statistically significant.

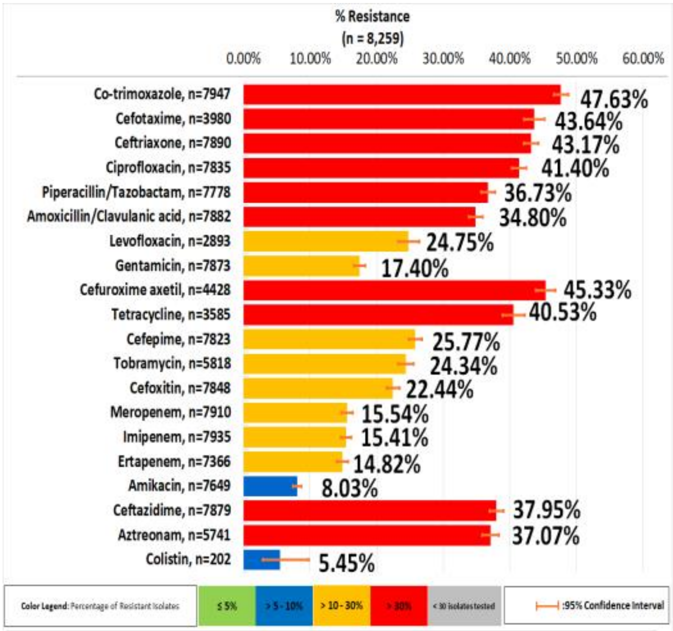


Figure 102. Resistance rates of *K. pneumoniae* respiratory isolates, DOH-ARSP, 2023

The resistance rates of *K. pneumoniae* respiratory isolates were shown in **Figure 102**. Resistance to combination antibiotics amoxicillin- clavulanic acid and piperacillin-tazobactam were 34.80% and 36.73% respectively. Resistance to carbapenems ranged from 14% to almost 16% while colistin resistance was at 5.45%. Compared with overall resistance rates from all samples, relatively lower rates were seen from *K. pneumoniae* respiratory isolates for most antibiotics.

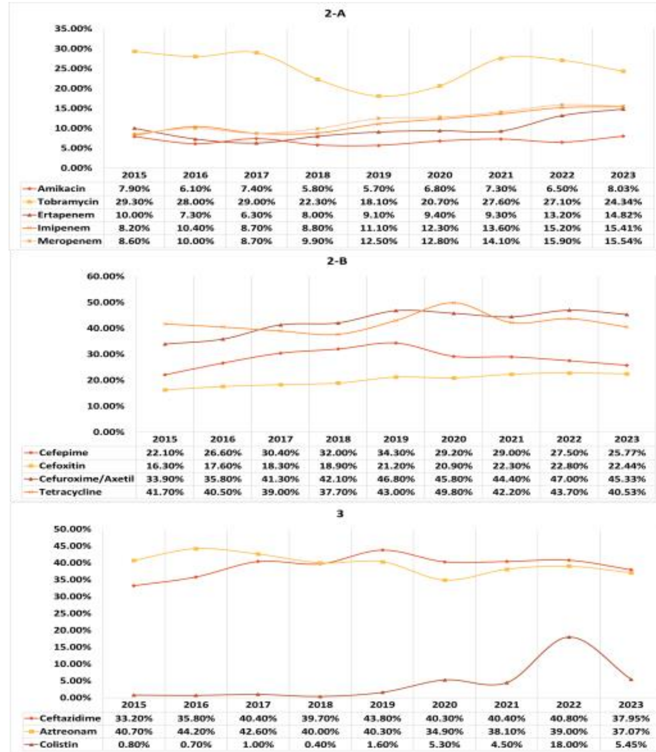


Figure 103. Yearly resistance rates of *K. pneumoniae* respiratory isolates, DOH-ARSP, 2014-2023

The yearly resistance rates of *K. pneumoniae* respiratory isolates were shown in **Figure 103**. Cefoxitin and the three carbapenem antibiotics tested, imipenem, meropenem and ertapenem, showed increasing resistance rates over the last ten years. Multiple year analysis showed that the differences in resistance rates across all tested antibiotics were all statistically significant except for amoxicillin-clavulanic acid (p=0.8645).

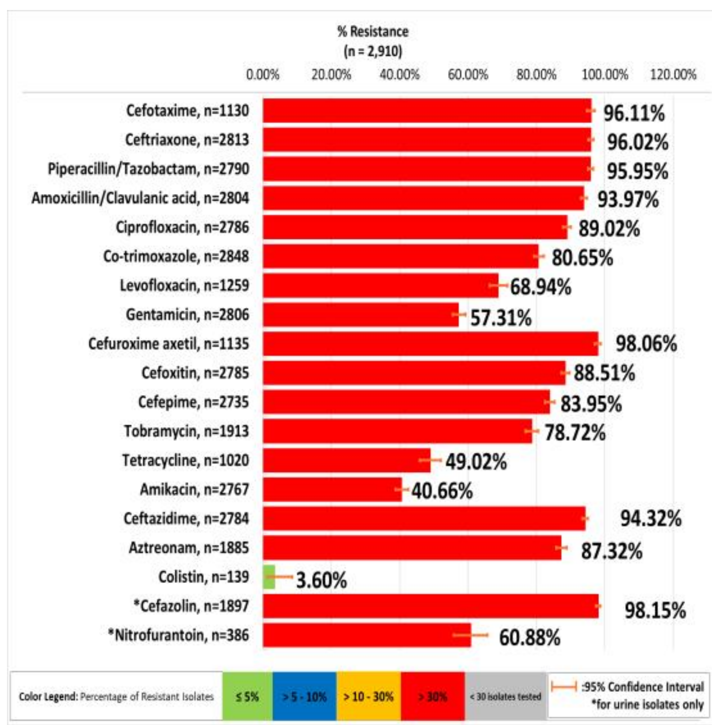


Figure 104. Resistance rates of carbapenem-resistant *K. pneumoniae* isolates, DOH-ARSP, 2023

Figure 104 shows the percent resistance of carbapenem-resistant *K. pneumoniae* isolates. Among these isolates, resistance rates to most antibiotics were high ranging from 40-90% reflecting the very limited treatment options for these resistance phenotypes. Resistance rates to amikacin, tetracycline and colistin were 40.66%, 49.02% and 3.60% respectively.

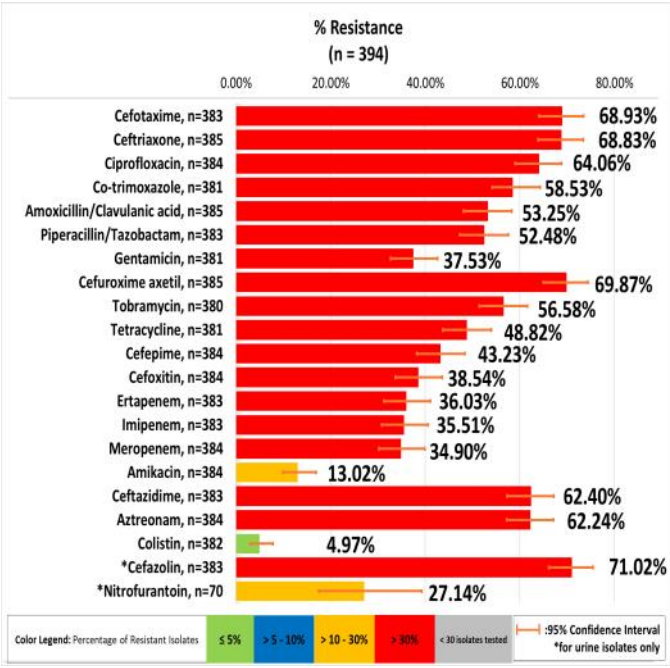


Figure 105. Resistance rates of colistin-resistant *K. pneumoniae* isolates, DOH-ARSP, 2023

The resistance rates of colistin-resistant *K. pneumoniae* isolates are shown in **Figure 105**. Among these isolates, resistance rates to most antibiotics were high ranging from 30-90%. Cefazolin resistance was at 71.02%, tobramycin at 56.58%, gentamicin 37.53% and ceftriaxone at 68.83%. Resistance rates to amikacin, tetracycline and colistin were 13.02%, 48.82% and 4.97% respectively.
There were confirmed colistin *K. pneumoniae* isolates for 2023. The molecular characterization of these emerging resistant isolates are described in the succeeding section

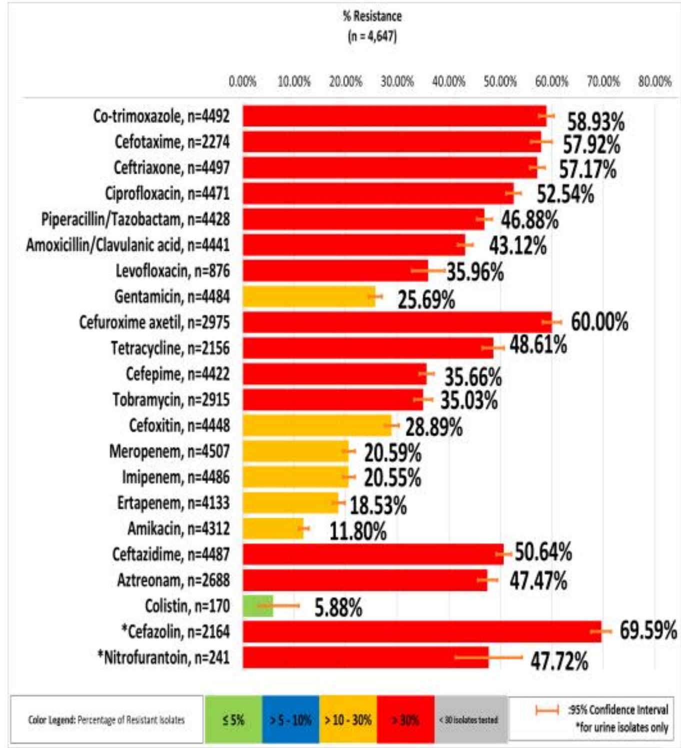


Figure 106. Resistance rates of *K. pneumoniae* Hospital Acquired Infection (HAI) isolates, DOH-ARSP, 2023

Figure 106 shows the resistance rates of *K. pneumoniae* isolates from presumptive hospital acquired infections. Resistance rates to most antibiotics were more than 30%. Resistance to carbapenems ranged from 18.53% to 20.59%. Resistance to colistin was 5.88%.

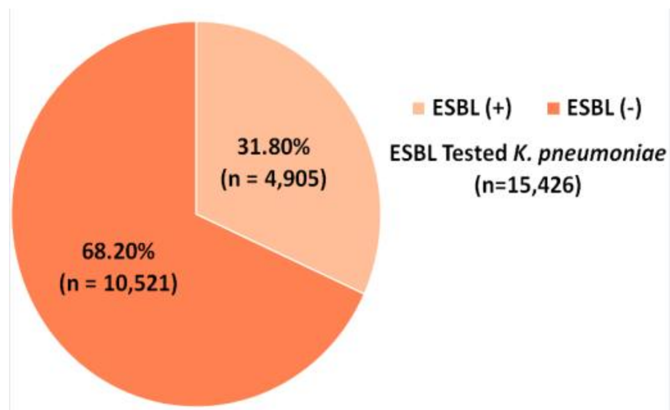


Figure 107. Percentage of ESBL positive and negative isolates among ESBL tested *K. pneumoniae*, DOH-ARSP, 2023

From the subset of 2023 *K. pneumoniae* isolates screened phenotypically for ESBL production, (n=15,426), ESBL positivity rate was at 31.80% (**Figure 107**). The ESBL positivity rate was determined by the total number of ESBL positive isolates over the total number of isolates tested for ESBL production.

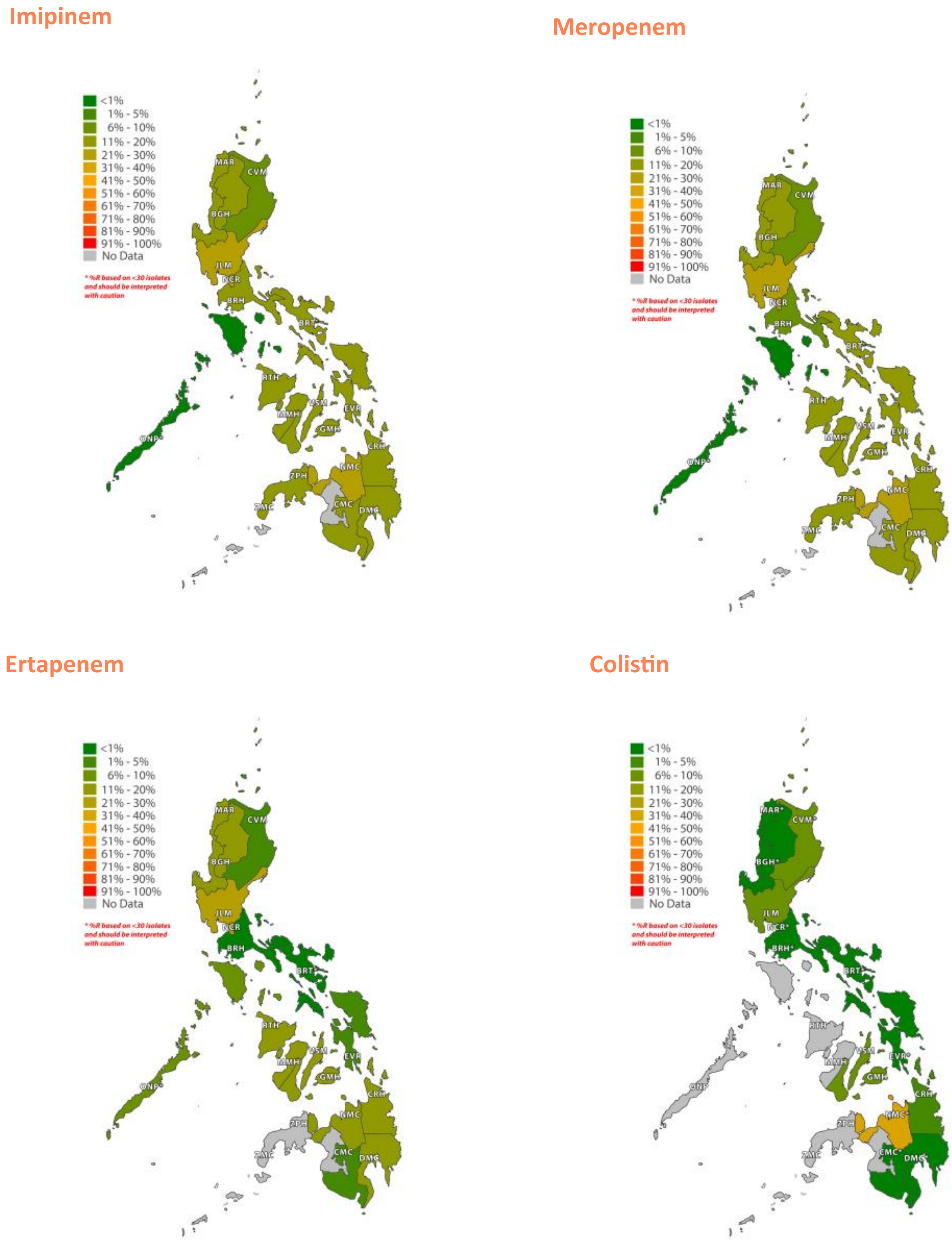


Figure 108. Resistance maps of *K. pneumoniae* for (A) Imipenem (B) Ertapenem (C) Meropenem and (D) Colistin, DOH-ARSP, 2023

Figure 108 shows the geographical distribution of carbapenem and colistin resistance across the regions in the country. The carbapenem resistance of *K. pneumoniae* isolates from Luzon and Visayas sentinel sites ranged from 1-30%, while the rates for Mindanao sentinel sites ranged from 21-40%. Confirmed colistin resistant isolates have been reported from almost all of the sentinel sites except for ONP.

Pseudomonas aeruginosa

A total of **9,680** *Pseudomonas aeruginosa* isolates for 2023. Large contributors of P. aeruginosa data were PGH (13.34%), DMC (11.25%) and VSM (9.98%). Sentinel sites from Luzon contributed 57.27% of the isolates, 21.60% from Visayas and 21.13% from Mindanao.

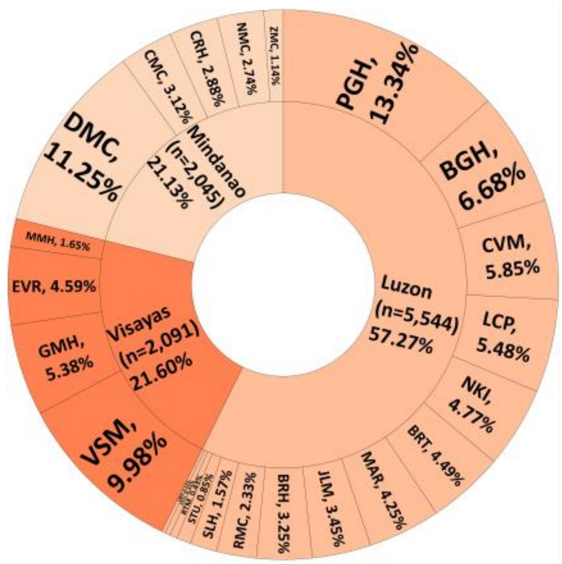


Figure 109. Isolate distribution of *P. aeruginosa*, DOH-ARSP, 2023 (n=9,680)

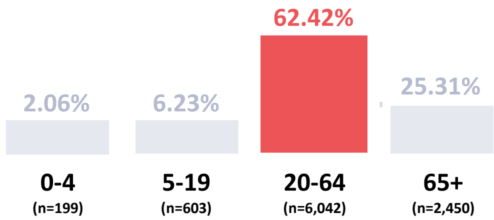
A. Sex

56.58% **Male (n=5,477)**

43.38% **Female (n=4,199)**

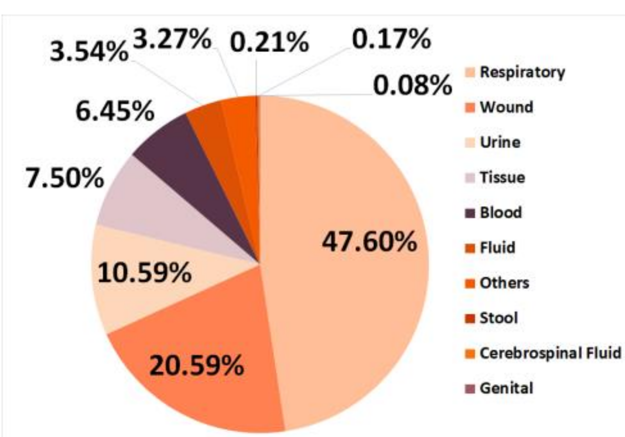
No Data: 0.04% (n=4)

B. Age

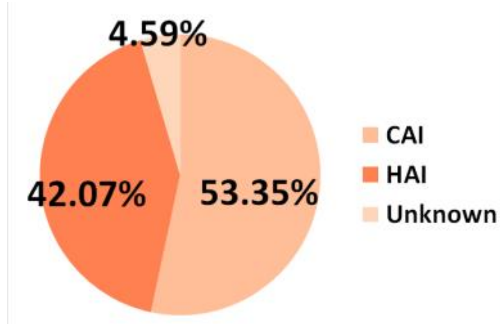


Unknown: 3.99% (n=386)

C. Specimen Type



D. Infection Type



E. Clinical Service

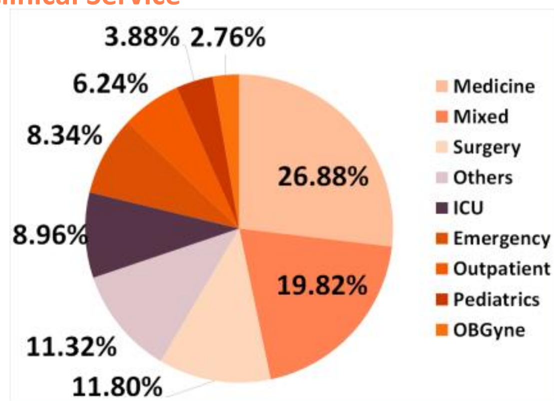


Figure 110. Patients characteristics of *P. aeruginosa* isolates, DOH-ARSP, 2023 (n=9,680)

Most (62.42%) of the isolates were from patients within 20-64 years old and most (56.58%) were from male patients. Many (47.60%) of the isolates were from respiratory specimens and wound specimens (20.59%) and most (53.35%) of the isolates were presumptive community acquired infections.

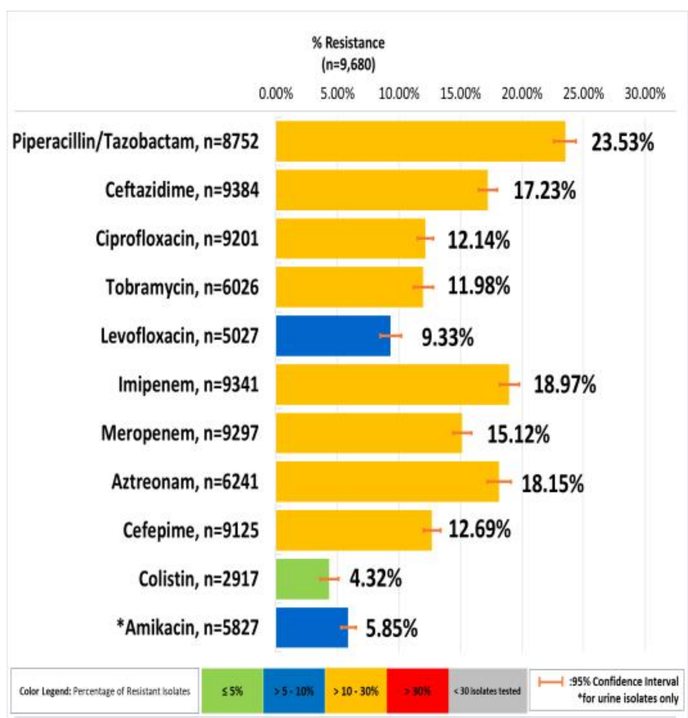


Figure 111. Resistance rates of *P. aeruginosa* for all specimens, DOH-ARSP, 2023

Figure 111 shows the cumulative resistance rates of *P. aeruginosa* isolates in 2023. Resistance to beta-lactam agents are as follows: ceftazidime was at 17.23%, cefepime at 12.69%, aztreonam at 18.15% and piperacillin-tazobactam at 23.53%. For fluoroquinolone resistance, ciprofloxacin and levofloxacin rates were 12.14% and 9.33% respectively. Resistance to imipenem was at 18.97% and to meropenem at 15.12%. There were increase in the resistance rates of the following antibiotics from 2022 compared with 2023 rates: piperacillin-tazobactam (p=0.000), imipenem (p=0.0000), and aztreonam (p=0.000). It must be noted that for 2023, there has been a change in the zone diameter and MIC breakpoints for piperacillin-tazobactam which could have resulted in the increase in the %R for this antibiotic for 2023. There was a slight decrease in the resistance rate to cefepime (p=0.000).

There are sporadic reports (10 isolates) from Luzon of resistance among *P. aeruginosa* to the newer combination antibiotics ceftazidime-avibactam detected through MIC. Many are from respiratory specimens of patients with presumptive nosocomial infections and many of the patients were less than 5 years of age. Nine out the 10 isolates are extensively drug resistant but were not tested for colistin.

There were confirmed colistin-resistant *P. aeruginosa* isolates for 2023. The molecular characterization of these emerging resistant isolates are described in the succeeding section.

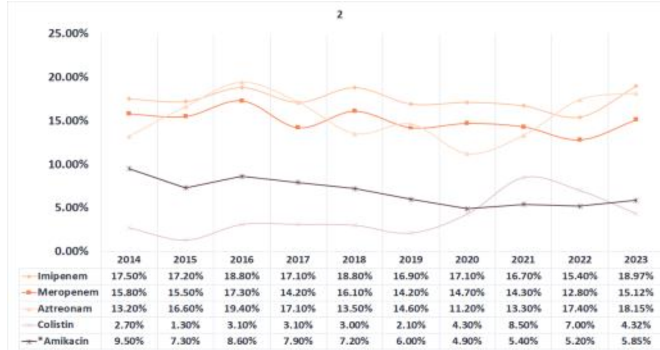


Figure 112. Yearly resistance rates of *P. aeruginosa*, DOH-ARSP, 2014-2023

Figure 112 shows the yearly resistance rates of *P. aeruginosa*. The multi-year analysis showed an increasing resistance for piperacillin-tazobactam (p=0.0013), ceftazidime (p= 0.0000) and imipenem (p=0.4011), while decreasing resistance was seen for cefepime (p=0.0000), ciprofloxacin (p=0.0000), levofloxacin (p-0.0000) and meropenem (p=0.0000).

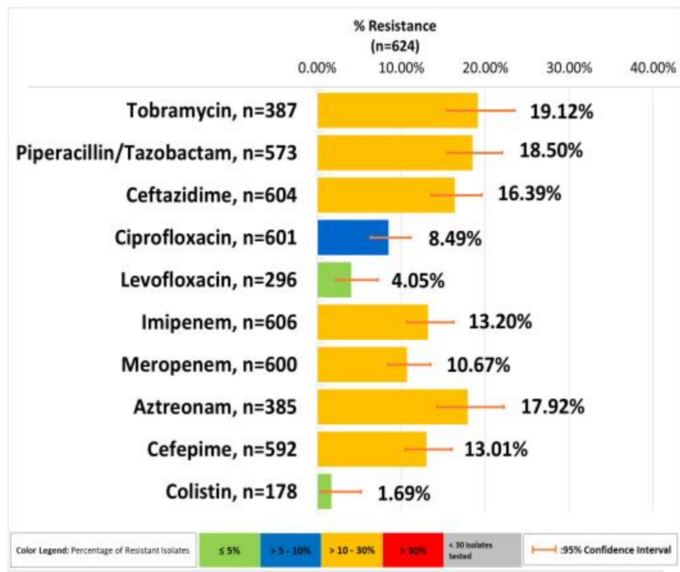


Figure 113. Resistance rates of *P. aeruginosa* blood isolates, DOH-ARSP, 2023

Figure 113 shows the antibiotic resistance rates of *P. aeruginosa* blood isolates. Resistance to ceftazidime was at 16.39%, cefepime at 13.01%, aztreonam at 17.92% and piperacillin-tazobactam at 18.50%. Resistance to fluoroquinolone were as follows: ciprofloxacin 8.49% and levofloxacin 4.05%. Resistance to meropenem is at 10.67% and to imipenem at 13.20%. Compared to cumulative rates of resistance for all isolates combined, invasive *P. aeruginosa* had relatively lower rates of resistance for almost all antibiotics except for tobramycin (19.12%).

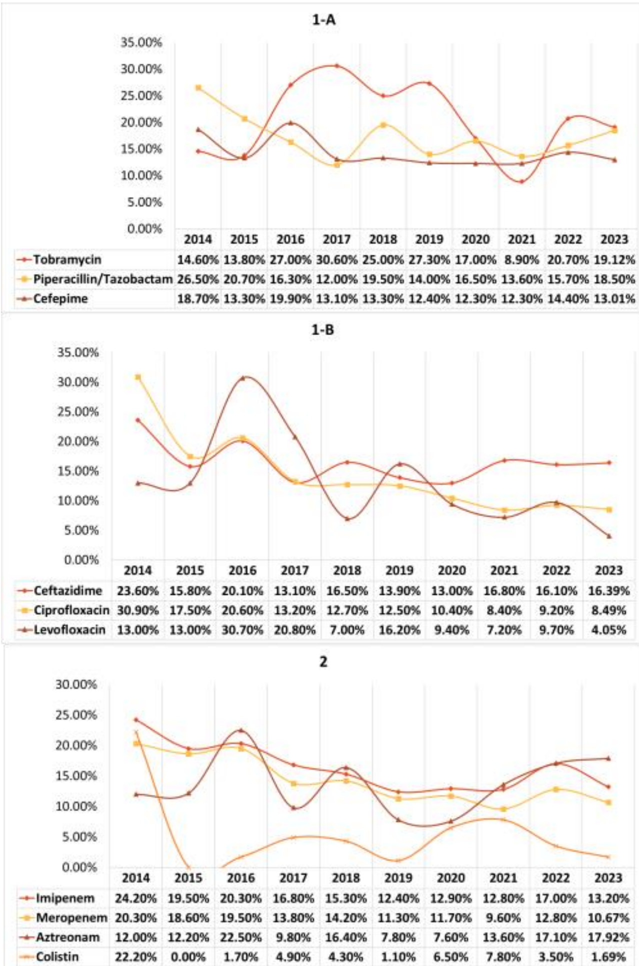


Figure 114. Yearly resistance rates of *P. aeruginosa* blood isolates, DOH-ARSP, 2014-2023

Figure 114 shows the yearly resistance rates of *P. aeruginosa* blood isolates*.* The multi-year analysis showed decreasing resistance for ceftazidime (p=0.0000), cefepime (p=0.0000), piperacillin-tazobactam (p=0.0000), ciprofloxacin (p=0.0000), levofloxacin (p=0.0000), meropenem (p=0.0000) and imipenem (p=0.5367) and increasing resistance to aztreonam (p= 0.0000).

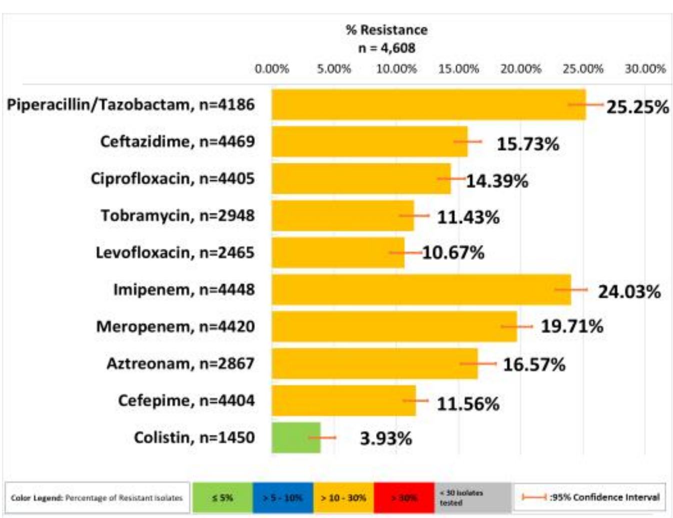


Figure 115. Resistance rates of *P. aeruginosa* respiratory isolates, DOH-ARSP, 2023

The resistance rates of *P. aeruginosa* respiratory isolates are shown in **Figure 115**. Resistance to ceftazidime was at 15.73%, cefepime at 11.56%, aztreonam at 16.57% and piperacillin-tazobactam at 25.25%. Resistance to fluoroquinolone were as follows: ciprofloxacin 14.39% and levofloxacin 10.67%. Resistance to meropenem is at 19.71% and to imipenem at 24.03%. Low resistance rates among the respiratory isolates were seen for colistin (3.93%).

Molecular Characterization of Colistin Resistant *Pseudomonas aeruginosa*

Colistin is regarded as the last-line antibiotic, which has received increasing attention for treating multidrug-resistant (MDR) and extensively resistant (XDR) *Pseudomonas aeruginosa*. Three colistin-resistant *Pseudomonas aeruginosa* isolates were collected in the year 2023 through the Antimicrobial Resistance Surveillance Program. In this report, we describe the phenotypic and genotypic characteristics of these isolates.

Table 14 shows the characteristics of the isolates. Two of the isolates showed susceptibility to other antibiotics while one of the isolates was extensively drug-resistant and was resistant to nine antibiotics including amikacin, tobramycin, ceftazidime, cefepime, aztreonam, piperacillin-tazobactam, imipenem, meropenem, and ciprofloxacin.

Whole genome sequencing revealed that the isolates were of three distinct multilocus sequencing types (MLST) - with 1 isolate each of ST 357, ST 485 and ST 3986. ST 357 was likewise reported in 2022. *P. aeruginosa* isolates from VSM and EVR were shared similar polysaccharide type O11, while the isolate from BRT was identified as serotype O4. The O antigen have been shown to be important in conferring antimicrobial resistance and critical for bacterial virulence. [1][2] None of the isolates carried the mobile colistin gene m*cr* nor were to found to show mutations in target genes conferring resistance to colistin. However, there were three efflux mechanisms detected across all isolates coming from a single efflux family *Mex (mexA, mexX, mexE)*. Efflux pumps are transport proteins involved in the extrusion of toxic substrates including antibiotics from within cells into the external environment. Previous studies have shown that efflux pumps are found in colistin resistant *P. aeruginosa* isolates[3].

The isolates harbored several resistance genes such as *blaPDC-6, blaPDC-105, blaPDC-11, blaOXA-50, blaOXA-488, blaOXA-10* and *blaVIM-2* as well as aminoglycoside resistance genes including *aph(3')-Ib, aph(3')-IIb, and aph(6)-Id*, and tetracycline resistance genes *tet(C), tmexC, tmexD* and *toprJ1*. The XDR isolate from EVR also had qnrVC1 gene which predicts ciprofloxacin resistance.

Continued genomic characterization of colistin-resistant *P. aeruginosa* is paramount to provide information on the mechanism of colistin resistance among these isolates to inform prevention and control measures.

Table 14. Characteristics of 2023 ARSP colistin- resistant *Pseudomonas aeruginosa* isolates

Laboratory Accession Number	Sentinel Site	Specimen Type	MLST	Colistin MIC (ug/ml)	Mechanism of Colistin Resistance	AMR Phenotype	AMR Genotype	Class
23ARS_BRT0039	BRT	Sputum	ST 485	4	---	COL	fosA mexA blaPDC-6 aph(3')-IIb blaOXA-50 mexE catB7 mexX	fosfomycin efflux beta-lactam aminoglycoside beta-lactam efflux phenicol efflux
23ARS_EVR0108	EVR	Wound	ST 3986	4	---	COL ATM CAZ CIP FEP IMP MER TOB TZP	mexA blaPDC-105 aph(3')-IIb catB7 blaOXA-488 fosA merE merD merA merP merT merR tmexC tmexD toprJ1 mexX mexE aph(6)-Id aph(3'')-Ib tet(C) blaVIM-2 blaOXA-10 qnrVC1 sul1	efflux beta-lactam aminoglycoside phenicol beta-lactam fosfomycin mercury mercury mercury mercury mercury mercury tetracycline tetracycline tetracycline efflux efflux aminoglycoside aminoglycoside tetracycline beta-lactam beta-lactam quinolone sulfonamide
23ARS_VSM0374	VSM	Abdomen	ST 357	4	---	COL	mexA fosA blaOXA-50 blaPDC-11 aph(3')-IIb catB7 mexX mexE	efflux fosfomycin beta-lactam beta-lactam aminoglycoside phenicol efflux efflux

References:

1 Kintz E, Scarff JM, DiGiandomenico A, Goldberg JB. Lipopolysaccharide O-antigen chain length regulation in Pseudomonas aeruginosa serogroup O11 strain PA103. J Bacteriol. 2008 Apr;190(8):2709-16. doi: 10.1128/JB.01646-07. Epub 2007 Dec 7. PMID: 18065548; PMCID: PMC2293223.

2 Cryz SJ Jr, Pitt TL, Fürer E, Germanier R. Role of lipopolysaccharide in virulence of Pseudomonas aeruginosa. Infect Immun. 1984 May;44(2):508-13. doi: 10.1128/iai.44.2.508-513.1984. PMID: 6425224; PMCID: PMC263549.

3 Abd El-Baky, RM, Masoud SM, Mohamed DS, GFM Waly N, Shafik EA, Mohareb DA, Elkady A, Elbadr MM and Hetta HF. Prevalence and Some Possible Mechanisms of Colistin Resistance Among Multidrug-Resistant and Extensively Drug-Resistant Pseudomonas aeruginosa

Figure 116. Yearly resistance rates of *P. aeruginosa* respiratory isolates, DOH-ARSP, 2014-2023

Figure 116 shows the yearly resistance rates of *P. aeruginosa* respiratory isolates. The multi-year analysis showed decreasing resistance for cefepime (p=0.0000), ciprofloxacin (p=0.0000), levofloxacin (p=0.0000) and increasing resistance to ceftazidime (p= 0.0000), piperacillin-tazobactam (p=0.0000) aztreonam (p=0.0000), meropenem (p=0.0000), and imipenem (p=0.0863)

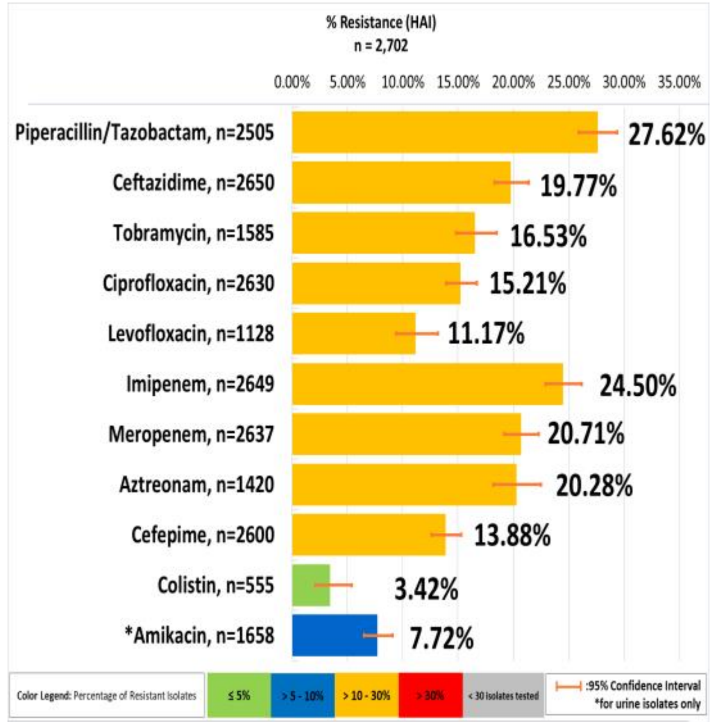


Figure 117. Resistance rates of *P. aeruginosa* Hospital Acquired Infection (HAI) isolates, DOH-ARSP, 2023

The resistance rates of *P. aeruginosa* isolates detected from presumptive hospital acquired infections are shown in **Figure 117**. Resistance to ceftazidime was at 19.77%, cefepime at 13.88%, aztreonam at 20.28% and piperacillin-tazobactam at 27.62%. Resistance to fluoroquinolone were as follows: ciprofloxacin 15.21% and levofloxacin 11.17%. Resistance to imipenem at 24.50% and to meropenem was 20.71%. Low resistance rates among the respiratory isolates were seen for colistin (7.72%).

Acinetobacter baumannii

There were **6,800** *A. baumannii* isolates reported for 2023, which was 39.63% higher than the number of isolates in 2022. Largest contributors of *A. baumannii* isolates were PGH (17.87%), VSM (9.26%) and DMC (8.76%) (Figure 118).

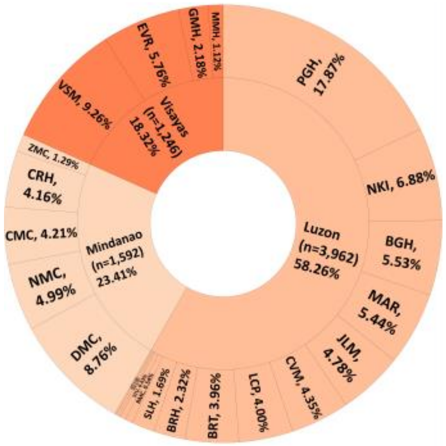


Figure 118. Isolate distribution of *A. baumannii*, DOH-ARSP, 2023, (n= 6,800)

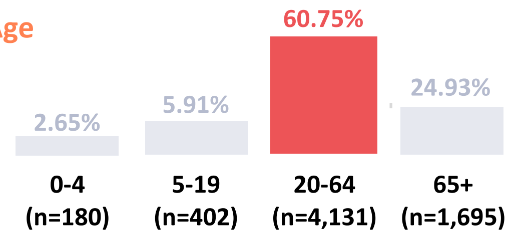
A. Sex

54.01%
Male
(n=3,673)

45.91%
Female
(n=3,122)

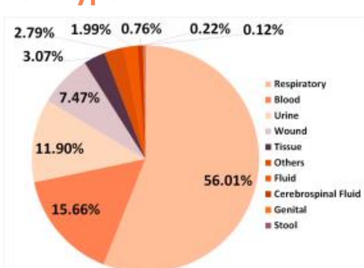
No Data: 0.07% (n=5)

B. Age

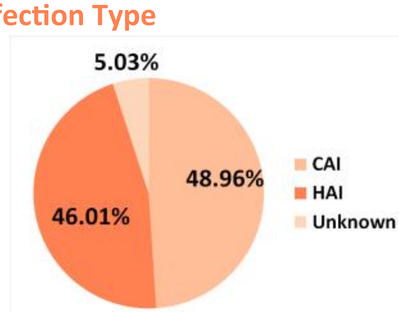


Unknown: 0.32% (n=22)

C. Specimen Type



D. Infection Type



E. Clinical Service

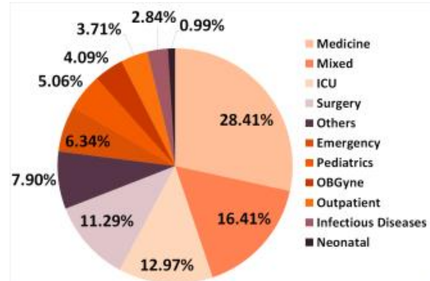


Figure 119. Patient characteristics of *A. baumannii* isolates, DOH-ARSP, 2023, (n=6,800)

Most (60.75%) of the isolates were from the 20-64 years old group and more than half (54.01%) were from male patients. Most (56.01%) of the isolates were from the respiratory samples and most (48.96%) were from presumptive community acquired infections (Figure 119).

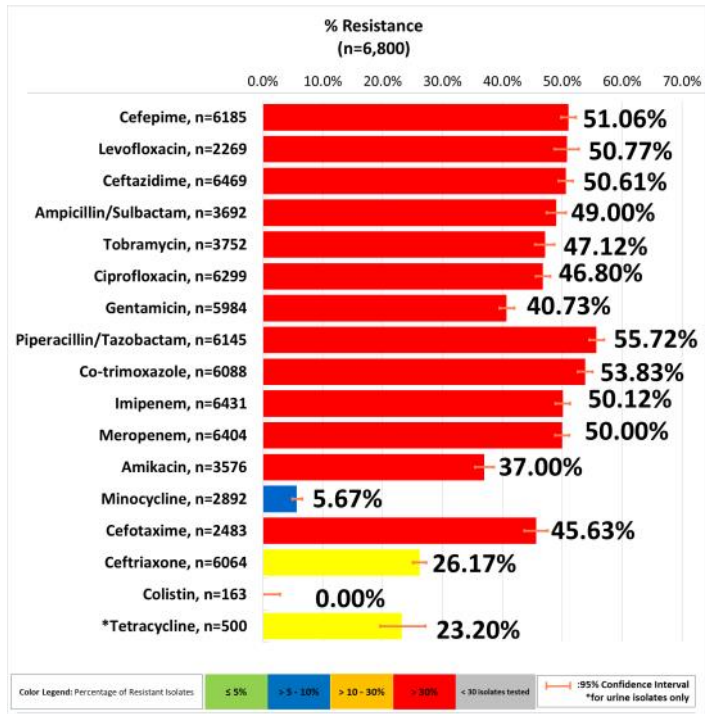


Figure 120. Resistance rates of *A. baumannii* isolates for all specimen, DOH-ARSP, 2023

Figure 120 shows the cumulative resistance rates of *A. baumannii* isolates for 2023. Many of the reported *A. baumannii* isolates were resistant to beta-lactam-beta-lactamase inhibitor combination antibiotics: ampicillin-sulbactam (49%) and piperacillin-tazobactam (55.72%), cephalosporins: cefepime (51.06%) and ceftazidime (50.61%); carbapenem: imipenem (50.12%) and meropenem (50%) and aminoglycoside tobramycin (47.12%). Lowest resistance was noted for minocycline (5.67%), ceftriaxone (26.17%) and amikacin (37%). No *A. baumannii* isolate resistant to colistin was reported in 2023.

There was a report of an *A. baumannii* isolate noted to be ceftazidime-avibactam resistant by MIC. The isolate is from a wound specimen on an adult inpatient male. The isolate appears to be extensively drug resistant but is susceptible to cotrimoxazole. Continued surveillance for emergence of resistance to the newer combination antibiotics is needed to guide appropriate use and to safeguard use of these antibiotics .

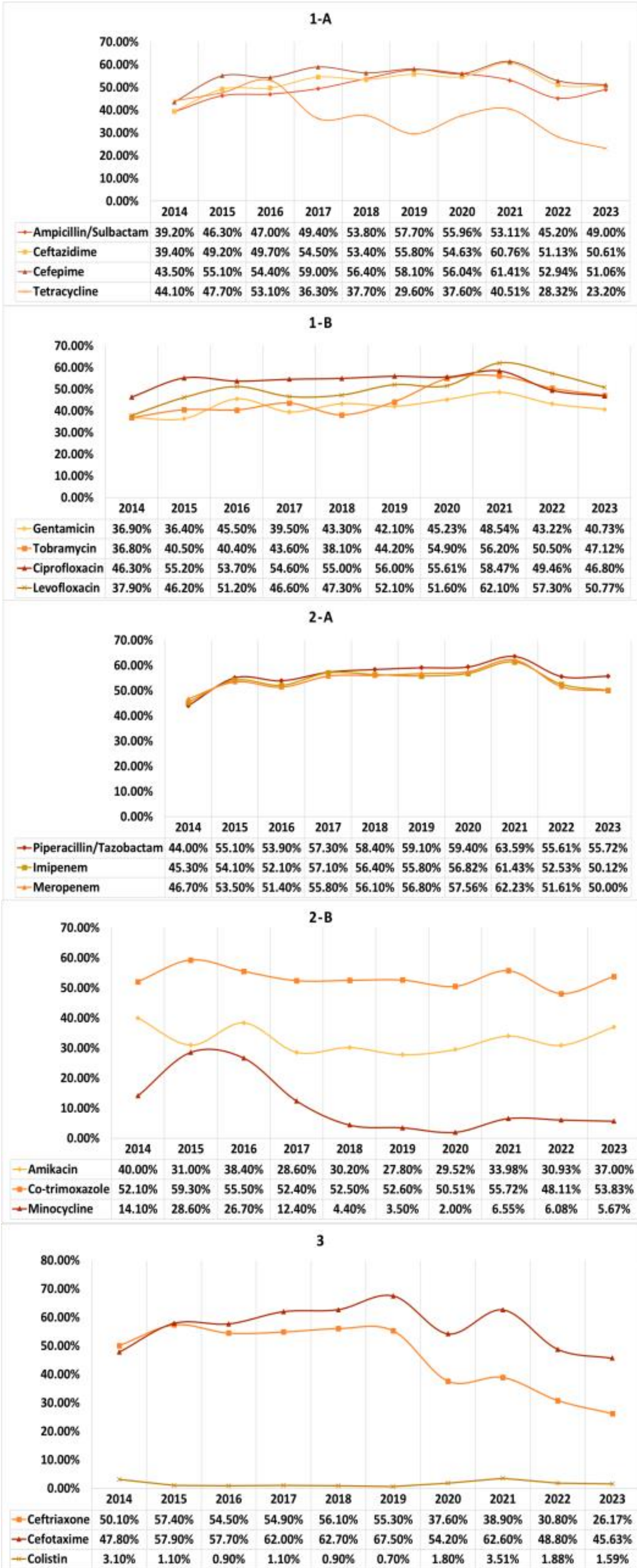


Figure 121. Yearly resistance rates of *A. baumannii* isolates, DOH-ARSP, 2023

Figure 121 shows the yearly resistance rates of *A. baumannii* isolates. There was an overall decrease in resistance rate seen for colistin (p=0.0000) and overall increase for piperacillin-tazobactam (p=0.0000), co-trimoxazole (p=0.0000) imipenem (p=0.0039), meropenem (p=0.2396) and amikacin (p=0.0001).

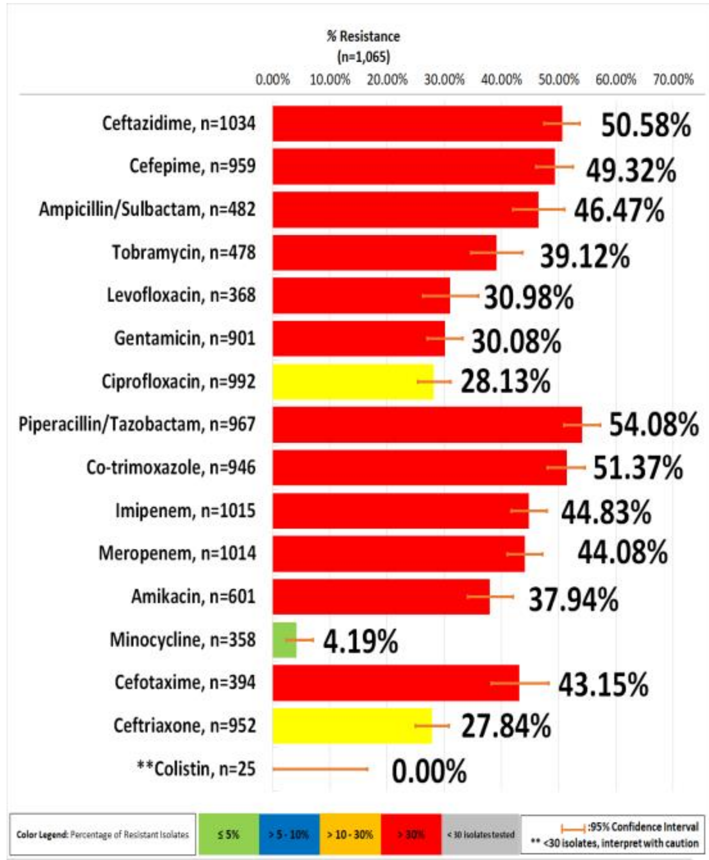


Figure 122. Resistance rates of *A. baumannii* blood isolates, DOH-ARSP, 2023

Figure 122 shows the resistance rates of *A. baumannii* isolates from blood specimens. Most of the resistance rates were above 30%. Many of the reported *A. baumannii* isolates were resistant to beta-lactam/ beta-lactamase inhibitor combination antibiotics: ampicillin-sulbactam (46.47%) and piperacillin-tazobactam (54.08%), cephalosphorins: cefepime (49.32%) and ceftazidime (50.58%); carbapenem: imipenem (44.83%) and meropenem (44.08%) and aminoglycoside: tobramycin (39.12%). Resistance to minocycline was at 4.19%, to ceftriaxone (27.84%), amikacin (37.94%) and 28.13% to ciprofloxacin. No *A. baumannii* isolate from blood specimen resistant to colistin was reported in 2023

Resistance to amikacin at 37.94% for 2023 is higher than 26.89% in 2022 (p= 0.0000). Compared to cumulative rates of resistance for all isolates combined, *A. baumannii* isolates from blood specimens had relatively lower resistance rates for all antibiotics.

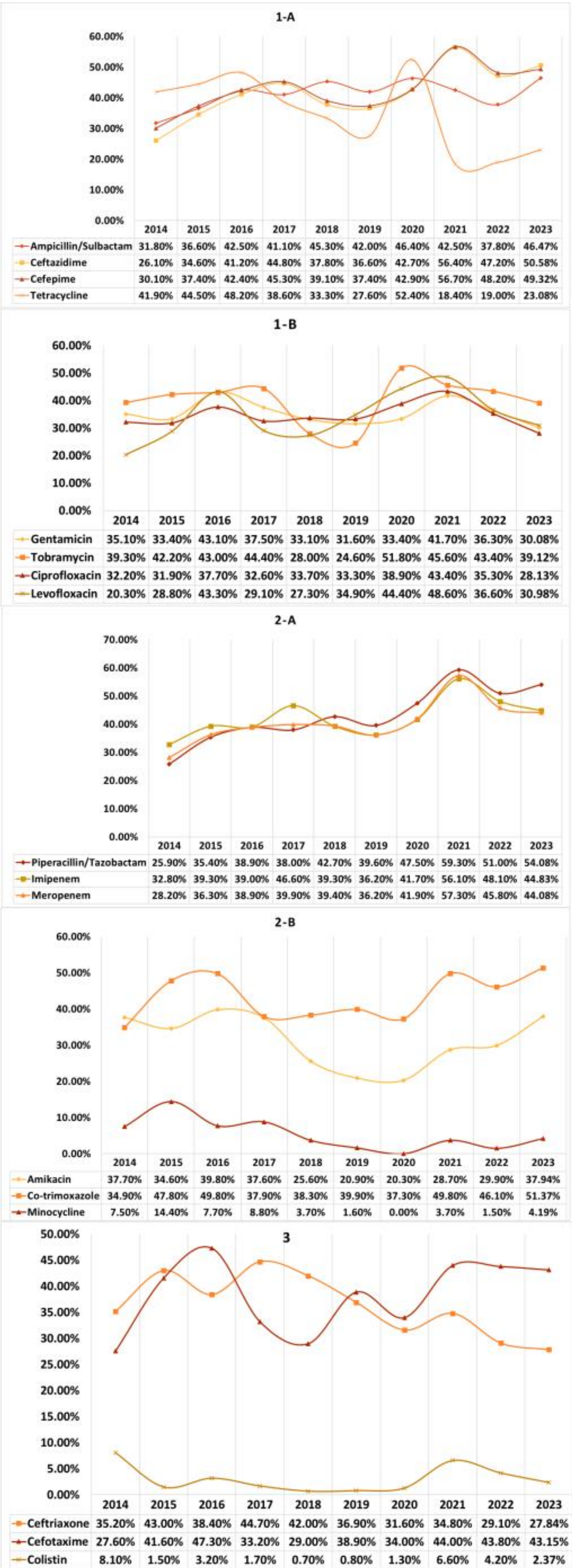


Figure 123. Yearly resistance rates of *A. baumannii* blood isolates, DOH-ARSP, 2014-2023

Figure 123 shows the yearly resistance rates of *A. baumannii* blood isolates. The decreasing resistance rates seen for piperacillin-tazobactam (p=0.0000), imipenem (p=0.0024), meropenem (p=0.0035) and colistin (p=0.0000) were found to be significant, however not significant for ampicillin-sulbactam (p=0.9265). The increasing rates observed for co-trimoxazole (p=0.0000), amikacin (p=0.0022) and minocycline (p=0.0000) were all statistically significant.

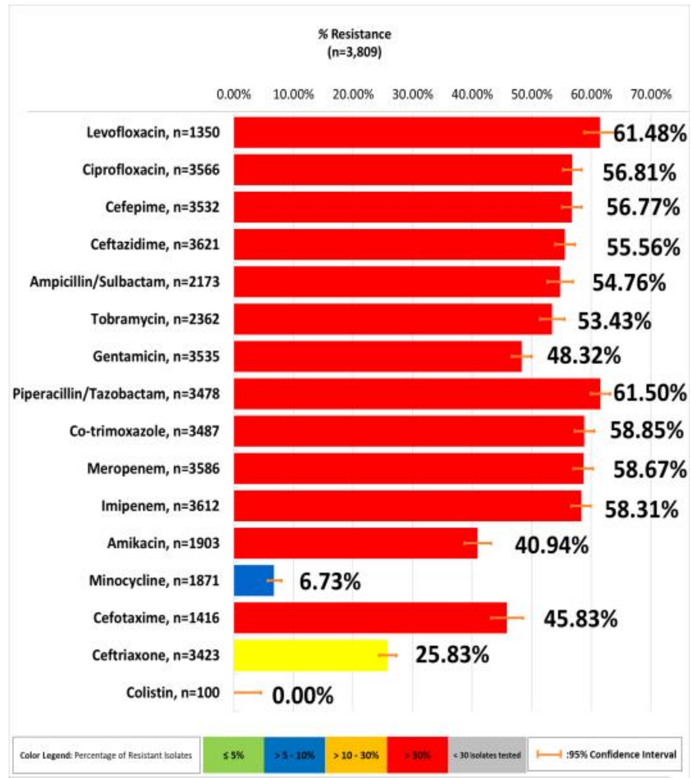


Figure 124. Resistance rates of *A. baumannii* respiratory isolates, DOH-ARSP, 2023

Figure 124 shows the resistance rates of *A. baumanni* respiratory isolates. Most antibiotics showed resistance rates of more than 30%. Resistance rate was highest for piperacillin-tazobactam (61.50%) followed by levofloxacin (61.48%). Resistance to co-trimoxazole was 58.85%, while resistance to meropenem and imipenem were 58.67% and 58.31%, respectively. No colistin resistant *A. baumannii* respiratory isolate was reported for 2023.

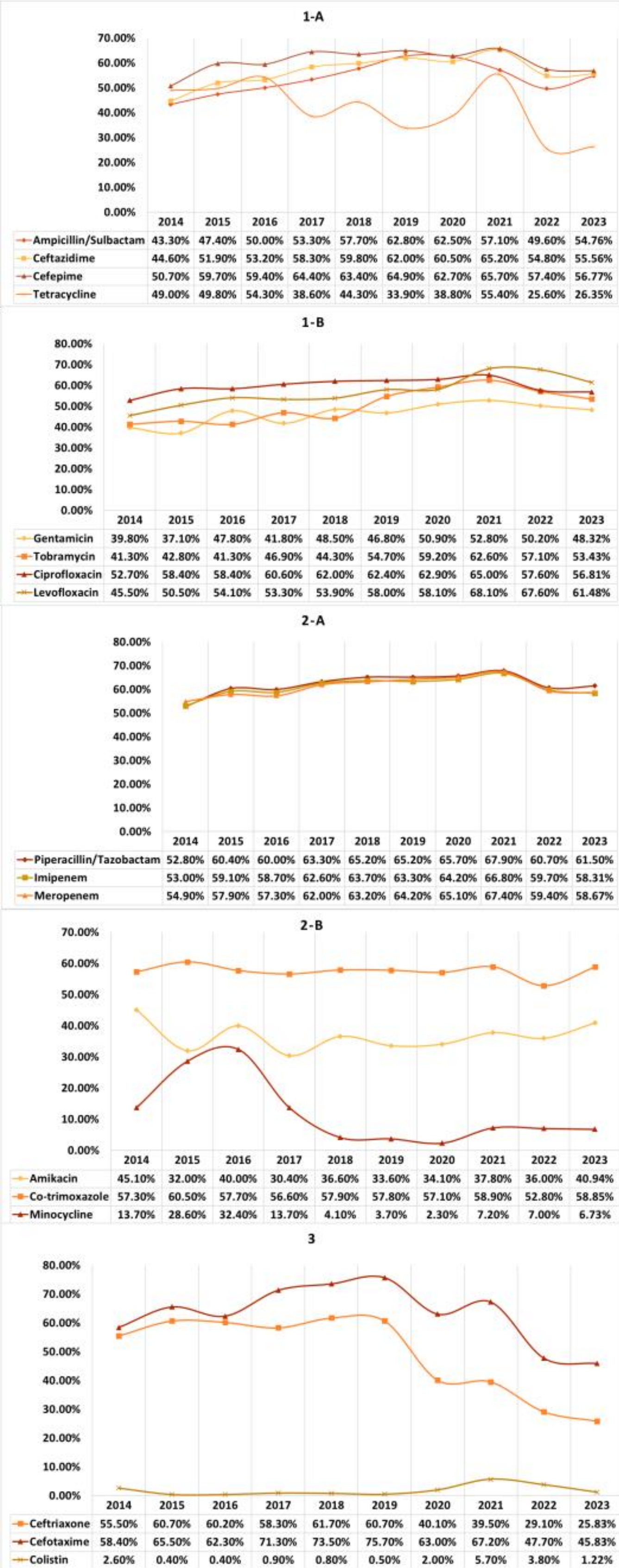


Figure 125. Yearly resistance rates of *A. baumannii* respiratory isolates, DOH-ARSP, 2014-2023

Figure 125 shows the yearly resistance rates of *A. baumannii* respiratory isolates. The decreasing resistance rates seen for piperacillin-tazobactam (p=0.0000), imipenem (p=0.0035), meropenem (p=0.0012) and colistin (p=0.0000) were found to be significant, however not significant for ampicillin-sulbactam (p=0.9204). The increasing rates observed for co-trimoxazole (p=0.0000) and amikacin (p=0.0021) were both statistically significant.

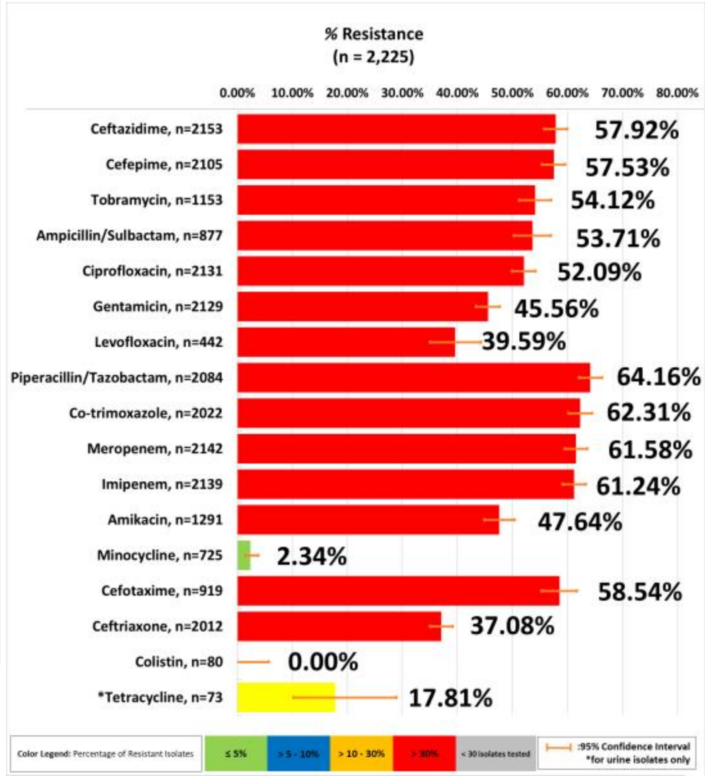
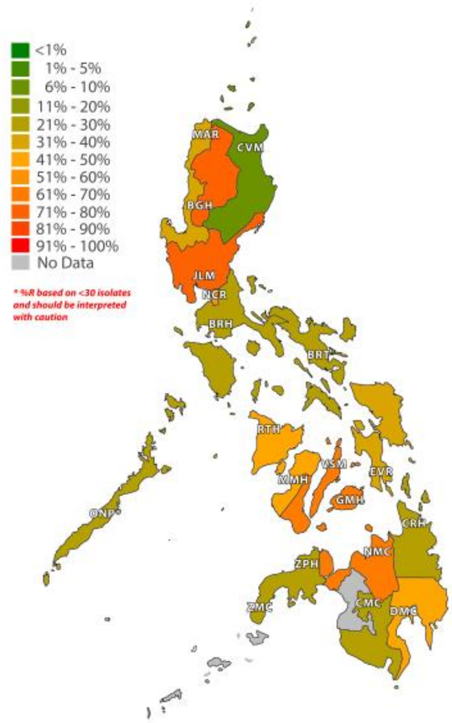


Figure 126. Resistance rates of *A. baumannii* Hospital Acquired Infection (HAI) isolates, DOH-ARSP, 2023

The resistance rates of *A. baumannii* isolates from presumptive hospital acquired infections are shown in **Figure 126**. More than 50% of all reported *A. baumannii* isolates were resistant to beta-lactam/ beta-lactamase combination antibiotics: ampicillin-sulbactam (53.71%) and piperacillin-tazobactam (64.16%), cephalosphorins: cefepime (57.53%) and ceftazidime (57.92%); carbapenem: imipenem (61.24%) and meropenem (61.58%) and aminoglycoside tobramycin (54.12%). No resistant isolate to colistin was reported for 2023.

Imipinem



Meropenem

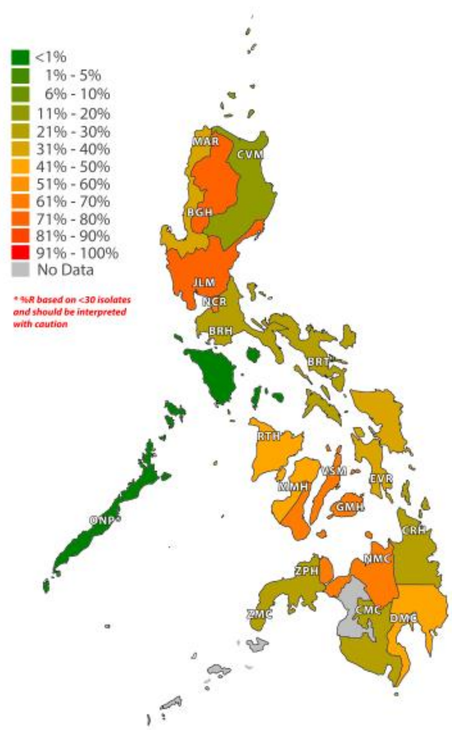


Figure 127. Resistance maps of *A. baumannii* (A) Imipenem and (B) Meropenem

Figure 127 shows the carbapenem resistance rates of *A. baumannii a*cross regions as represented by the sentinel sites. Carbapenem resistance among many sentinel sites varies but most rates are high.

Multidrug Resistant *Pseudomonas aeruginosa* and *Acinetobacter baumannii*

Among the 2023 *E. coli* isolates from all specimen types, 59.4% were MDR and 14.2% were possible XDR. Among E. coli blood isolates, 59.2% were MDR and 13.2% were possible XDR (Table 16).

Among *K. pneumoniae* isolates from all specimen types for 2023, 57.7% were MDR and 26.1% were possible XDR. Among *K. pneumoniae* blood isolates, 63.5% were MDR and 31.9% were possible XDR (Table 16).

Among *P. aeruginosa* isolates from all specimen types for 2023, 28.3% were MDR and 18.2% were possible XDR. Among *P. aeruginosa* blood isolates, 23.1% were MDR and 14.4% were possible XDR (Table 16).

Among the 2023 *A. baumannii* isolates from all specimen types, 58.1% were MDR and 49% were possible XDR. Among *A. baumannii* blood isolates, 56.2% were MDR and 47.2% were possible XDR (Table 16).

Table 15. Multidrug-resistant, extensively drug resistant and pandrug-resistant bacteria in an international expert proposal interim standard definitions for acquired resistance.

Term	Definition
MDR Multidrug-resistant	Acquired non-susceptibility to at least one agent in three or more antimicrobial categories
XDR Extensively drug-resistant	Non-susceptibility to at least one agent in all but two or fewer antimicrobial categories
PDR Pandrug-resistant	Non-susceptibility to all agents in all antimicrobial categories.

Table 16. MDR and Possible XDR *E. coli*, *P. aeruginosa* and *A. baumannii,* DOH-ARSP, 2023

	Number of isolates tested	Percentage MDR	Percentage Possible XDR
Escherichia coli			
All isolates	13,496	59.4%	14.2%
Blood isolates	1,303	59.2%	13.2%
Klebsiella pneumoniae			
All isolates	16,164	57.7%	26.1%
Blood isolates	1,577	63.5%	31.9%
Pseudomonas aeruginosa			
All isolates	9,680	28.3%	18.2%
Blood isolates	624	23.1%	14.4%
Acinetobacter baumannii			
All isolates	6,800	58.1%	49%
Blood isolates	1,065	56.2%	47.2%

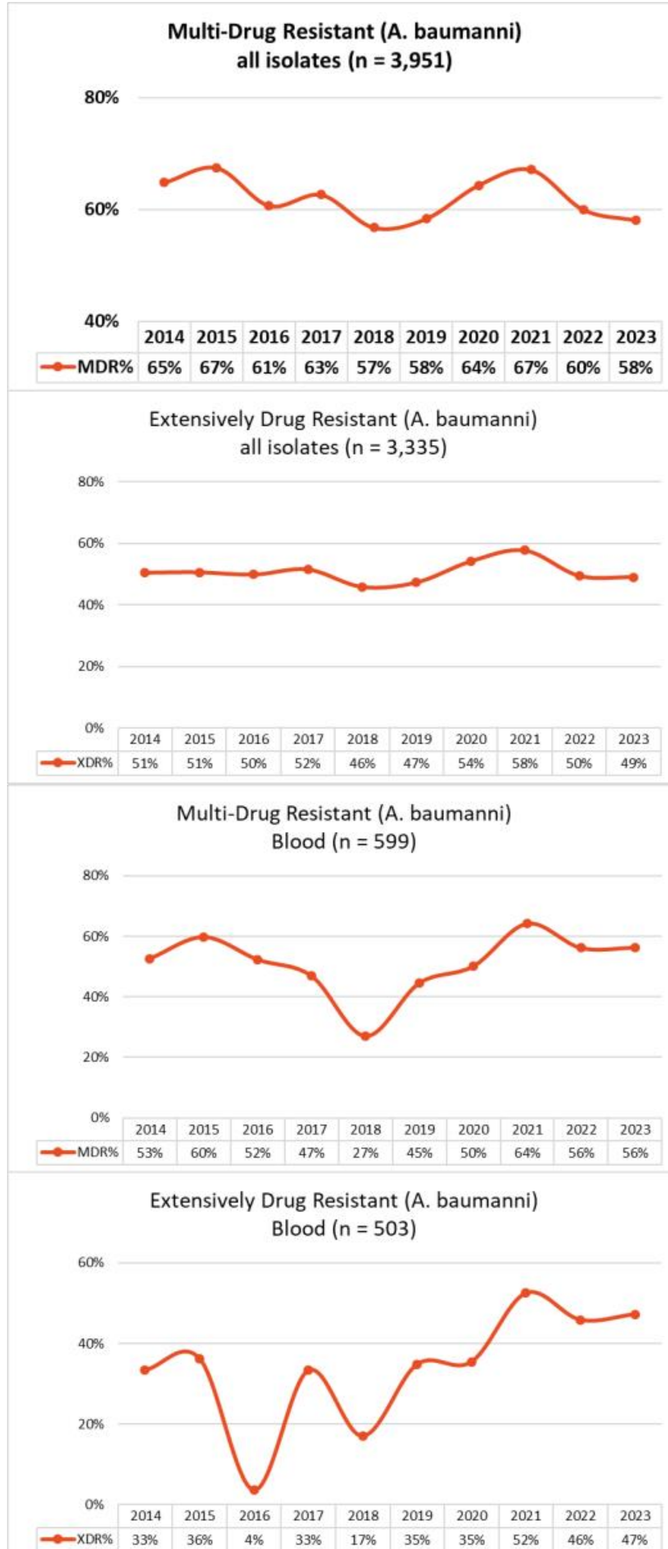


Figure 128. Yearly percentage of MDR and XDR *A. baumannii* isolates from all specimen and blood specimen, DOH -ARSP, 2014-2023

Figure 128 shows the yearly percentage of MDR and XDR *A. baumannii* isolates from all specimens and blood specimens. Multiple year analysis of MDR and XDR blood isolates of *A. baumanii* showed that the decrease in percentage of MDR and increase in XDR *A. baumannii* were statistically significant at p=0.0000

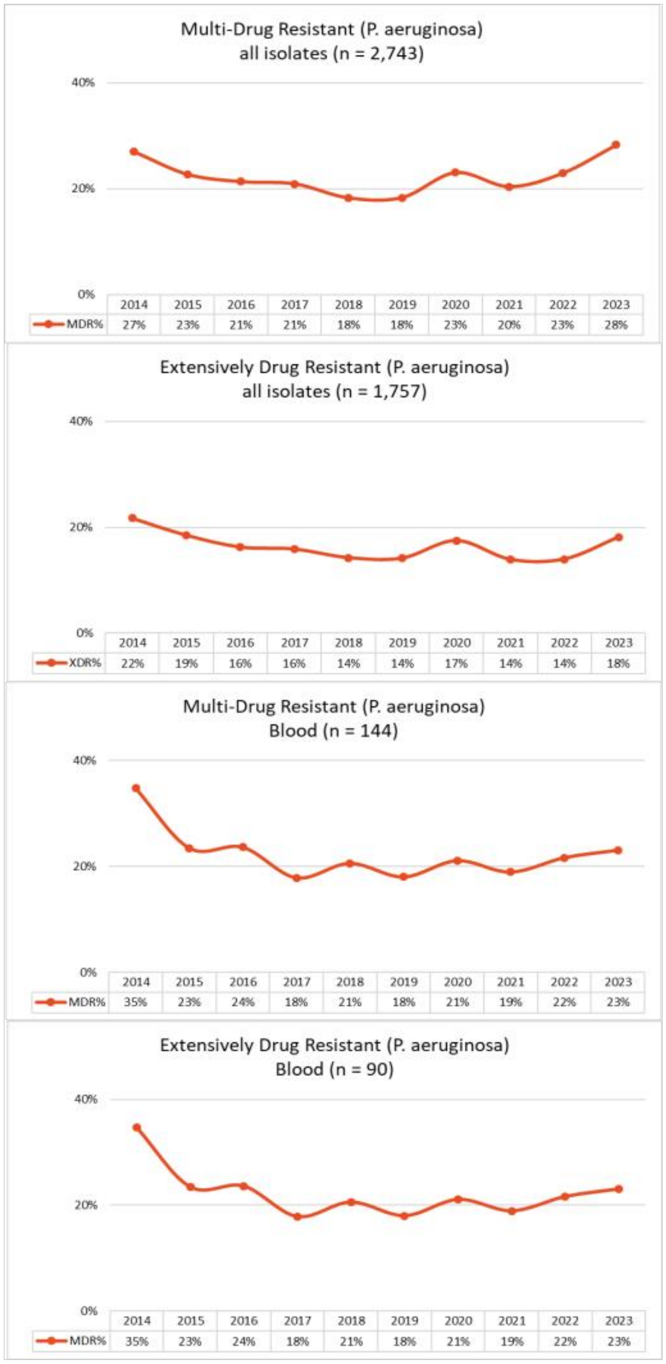


Figure 129. Yearly percentage of MDR and XDR *P. aeruginosa* isolates from all specimen and blood specimen, DOH-ARSP, 2014-2023

Figure 129 shows the yearly percentage of MDR and XDR *P. aeruginosa* isolates from all specimens and blood specimens. Multiple year analysis of MDR and XDR blood isolates of *P. aeruginosa* showed that the decrease in percentage of MDR and XDR *P. aeruginosa* blood isolates were not statistically significant.

Conclusions, Recommendations and Future Directions

Antimicrobial resistance continues to increase for most of the bacterial pathogens considered of public health importance included in this surveillance.

Recommendations based on the reported 2023 data:

Penicillin may still be used to treat non-meningitis infections secondary to *Streptococcus pneumoniae,* notwithstanding the need to monitor the shifting patterns of resistance among pneumococci. Penicillin resistance using meningitis breakpoint, however, continued to increase and may still be considered as a treatment option when guided by susceptibility test results. Better monitoring and evaluation of the government's immunization program for this disease that is vaccine preventable will be possible by expanding AMR surveillance of *Streptococcus pneumoniae* isolates to include pneumococcal serotyping.

The empiric treatment for suspected *H. influenzae* infections may include extended spectrum oral cephalosporins and beta-lactam-beta-lactamase inhibitor combinations due to high resistance rate of H. influenzae to ampicillin.

Chloramphenicol or amoxicillin/ampicillin may still be used as empiric treatment for suspected uncomplicated typhoid fever. It is recommended that microbiological data be used to support pathogen-directed therapy in light of the growing reports of ciprofloxacin and azithromycin resistance.

Limited resistance data *on Shigella* sp in the past four years show emerging resistance of *Shigella* to the quinolones and extended spectrum cephalosporins. A more vigilant surveillance of the resistance pattern of this bacteria should be pursued by encouraging clinicians to send specimens for culture.

Tetracycline, chloramphenicol and co-trimoxazole remain good treatment options for cholera cases. With the report of the first azithromycin resistant *V. cholerae* isolate for 2022, continued vigilant AMR surveillance among *V. cholerae* isolates is warranted to guide control and prevention of the spread of resistant *V. cholerae* isolates.

With the limited available data on *Neisseria gonorrhoeae*, ceftriaxone remains as empiric antibiotic of choice for gonococcal infections. More vigilant surveillance of the resistance patterns of this organism should be pursued by encouraging clinicians to send specimens for culture to their local laboratory and the sentinel sites to send isolates to the reference laboratory for confirmatory testing.

The use of oxacillin as an empiric treatment option for *S. aureus* infections remains limited by continued high rates of oxacillin resistance even as a statistically significant decrease in MRSA rates is noted beginning in 2015 until 2023. With the noted relatively lower resistance rates to clindamycin and the macrolides, these antibiotics could be considered as alternative options. Judicious use of the reserve antibiotics vancomycin and linezolid remains paramount in order to preserve the effectiveness of this antibiotic in treating *S. aureus* infections.

Multidrug resistance among the bacterial organisms *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Acinetobacter baumannii* continues to be a public health concern because of the limited treatment options and infection control challenge in containment. Real time data analysis, and genotyping to establish linkages will allow for implementation of timely patient isolation and infection control measures to prevent spread of these superbugs. Institute specific and stratified antibiograms will allow clinicians to identify the best empiric antibiotic options for suspected infections due to these superbugs.

Program Future Directions

Pursue expansion of ARSP through gradual addition of surveillance sites taking into consideration feasibility, geographical location and hospital types.

Expand susceptibility testing across all sentinel sites for new combination antibiotics such as ceftazidime-avibactam and ceftolozane-tazobactam among gram-negative rods.

Implement structured genomic surveys among the common pathogens of public health importance as part of the continuous and expanded integration of whole genome sequencing into ARSP. Pursue fostering of continued growth of technical expertise and skills in molecular diagnostics and bioinformatics within the reference laboratory through training, collaborative projects and advocacy for requisite fund and resource requirements.

Improve detection of clustering of cases in ARSP sentinel sites through the use of WHONET SaTScan analysis on ARSP data by encouraging prompt data transfer from sentinel sites. Enhance the investigation of possible outbreaks in the sentinel sites through close coordination with the Infection and Prevention Committee of sentinel sites and through the use of WGS.

Actively engage in the One Health approach to AMR surveillance together with relevant stakeholders from the food chain and environmental sectors including pursuing implementation of the Tricycle Project.

Actively contribute and participate in the implementation of the Philippine Action Plan to Combat Antimicrobial Resistance.

Advocate for and implement relevant AMR surveys, studies and researches to inform the policies towards the control and prevention of the emergence and spread of AMR in the country. Generate more relevant collaborative and investigator-initiated research.

Continue to ensure the high quality of surveillance data through active capacity building of sentinel site and reference laboratory staff, robust efforts to improve facilities, and safeguard availability of resources, equipment and services.

Incorporate the technology of geographic information system and mapping in surveillance.

Pursue ISO 15189 accreditation for the reference laboratory.

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