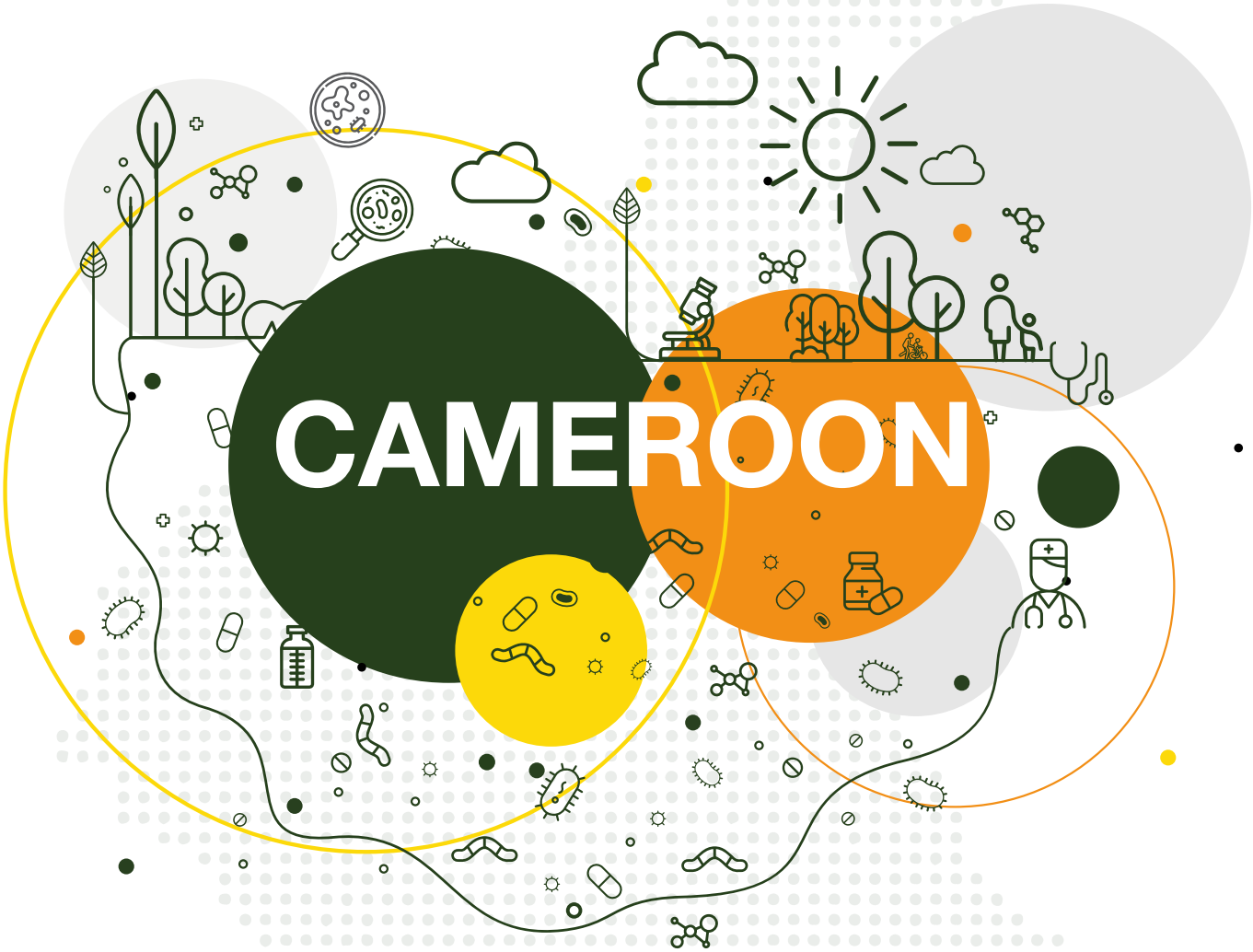
MAAP
Mapping AMR & AMU Partnership

Annual Report

National Situation of Antimicrobial Resistance and Consumption Analysis from 2017-2019



The Fleming Fund Regional Grants
UKaid from the British people
African Union
AFRICA CDC Centres for Disease Control and Prevention Safeguarding Africa's Health
ASLM African Society for Laboratory Medicine
ECOWAS
EACSA
InSTEDD Innovative Support To Emergencies Diseases and Disasters
IQVIA
ONEHEALTH TRUST

Year: 2022

Cameroon (2017-2019)

CAMEROON

Fleming Fund Regional Grant (Round 1)

Mapping Antimicrobial Resistance and Antimicrobial Use Partnership

African Society for Laboratory Medicine
Africa CDC
WAHO
ECSA-HC
Center for Disease Dynamics, Economics and Policy
IQVIA
InSTEDD

The country report summarises the analysis of retrospective data on AMR and AMC commissioned in the context for Fleming Fund Regional Grant (Round 1) programme.

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Abbreviations

AMC	Antimicrobial Consumption
AMR	Antimicrobial Resistance
AMRCC	Antimicrobial Resistance Coordinating Committee
AMU	Antimicrobial Use
ASLM	African Society for Laboratory Medicine
ASP	Antimicrobial Stewardship Programme
AST	Antibiotic Susceptibility Testing
ATC	Anatomical Therapeutic Chemical
AWaRe	Access, Watch, and Reserve
CENAME	Centre for the Procurement and Supply of Essential Medicines
CDDEP	Center for Disease Dynamics, Economics and Policy
CI	Confidence Interval
CLSI	Clinical and Laboratory Standards Institute
CMS	Central Medical Store
CSF	Cerebrospinal Fluid
DDD	Defined Daily Dose
DID	DDD per 1 000 inhabitants per day
DPLM	Department of Pharmacy Laboratory and Medicine
DRI	Drug Resistance Index
ECSA-HC	East, Central and Southern Africa Health Community
EMHSLU	Essential Medicines and Health Supplies List of Uganda (EMHSLU)
EML	Essential Medicines List
EQA	External Quality Assessment
EUCAST	European Committee on Antibiotic Susceptibility Testing
FDC	Fixed Dose Combinations
GLASS	Global Antimicrobial Resistance Surveillance System
HIS	Hospital Information System
InSTEDD	Innovative Support to Emergencies, Diseases and Disasters
JMS	Joint Medical Store
KIIs	Key Informant Interviews
LIS	Laboratory Information System
LMIC	Low- and Middle-Income Country
LQMS	Laboratory Quality Management System
MAAP	Mapping Antimicrobial resistance and Antimicrobial use Partnership
MoH	Ministry of Health
NGO	Non-Governmental Organisation
NCD	Non-Communicable Disease(s)
NDA	National Drug Authority
NMS	National Medical Store
OR	Odds Ratio
QA	Quality Assessment
QC	Quality Control
QMS	Quality Management System
RSN	ResistanceMap Surveillance Network
SLIPTA	Stepwise Laboratory Improvement Process Towards Accreditation
SLMTA	Strengthening Laboratory Management Towards Accreditation
SOP	Standard Operating Procedure
WHO	World Health Organisation

Executive Summary

Antimicrobial resistance (AMR) is a major public health concern that needs to be urgently addressed to avoid needless suffering and the reversal of medical advancement in fighting infectious diseases. A clear link has been shown between the misuse of antimicrobials and the emergence of AMR. However, owing to limited capacity of health systems and technological hurdles, the availability of comprehensive and robust AMR, antimicrobial use (AMU) and antimicrobial consumption (AMC) data in many low- and middle- income countries (LMICs), are generally lacking and there remains significant uncertainty as to the burden of drug resistance.

The Fleming Fund, a 265-million-pound United Kingdom aid, supports a range of initiatives to increase the quantity and quality of AMR data in LMICs. Regional Grant (Round 1) activities in Africa are led by The African Society for Laboratory Medicine (ASLM) and implemented by the 'Mapping Antimicrobial resistance and Antimicrobial use Partnership' (MAAP) consortium. This report summarises the activities undertaken by MAAP during the implementation of the Regional Grant, and aims to determine national AMR, AMC and AMU surveillance capacity, resistance rates and trends, and assess the antimicrobial flow in Cameroon during 2017-2019.

Cameroon had approximately 360 laboratories in the national laboratory network during the study period, of which 19 were reported to have capacity for bacteriology testing. Based on self-reported information from 19 laboratories, functioning and quality compliance were assessed to understand the laboratory preparedness for AMR surveillance.

AMR rates presented are based on the analysis of antimicrobial susceptibility results 0f 32 545 positive cultures obtained from 16 of the 19 laboratories. High levels of resistance were noted for methicillin-resistant Staphylococcus aureus (MRSA) (67-69%) and 3rd-generation cephalosporin-resistant Enterobacterales (57-61%). Rates for 3rd-generation cephalosporin-resistant Neisseria gonorrhoeae (32-46%) and fluoroquinolone-resistant N. gonorrhoeae (40-66%), were also high. Antimicrobial-resistant infections were found to be more common in males and the elderly. All results should be interpreted with caution as the participating laboratories were at different levels of service and had variable testing capacity.

AMC is measured as the quantity of antimicrobials sold or dispensed, whereas AMU reviews whether antimicrobials are used appropriately based on additional data such as clinical indicators. Only AMC data were retrievable at selected sentinel pharmacies. However, AMU data were not obtained due to lack of a unique patient identifier and tracking systems across hospital departments. The average national total AMC level in Cameroon between 2017-2019 was 5.1 Defined Daily Doses (DDD) per 1 000 inhabitants per day, ranging from 6.3 in 2017 and 4.5 in 2018 and 2019.

Antimicrobial utilisation by the World Health Organisation (WHO) Anatomical Therapeutic Chemical (ATC) classification was highest for combinations of sulfonamides and trimethoprim, including derivatives (range: 15.2% to 46.5%), followed by combinations of penicillins, including beta lactamase inhibitors (range: 13.9% to 18.1%) and tetracyclines (range: 8.4% to 14.5%). The top five most consumed antimicrobials were sulfamethoxazole/trimethoprim, amoxicillin/clavulanic acid, doxycycline, amoxicillin and fluconazole. Together, they accounted for 68% of total consumption share, suggesting a lack of variation. This consumption trend could potentially increase AMR. The total AMC came from 76.4% 'Access', 23.6% 'Watch' and 0.0% of 'Reserve' antibiotics. Between 2017-2019, use of 'Access' category antibiotics exceeded the WHO minimum recommended consumption threshold of 60%.

The drug resistance index (DRI) is a simple metric based on aggregate rates of resistance and measured on a scale of 0-100, where 0 indicates fully susceptible while 100 indicates fully resistant. The DRI estimate was found to be high at 68.0% (95% CI, 60.7–75.2%) thus implying low antibiotic effectiveness which is a threat to effective infectious disease management and calls for urgent policy intervention.

The following recommendations should be noted by policy makers and healthcare providers to further strengthen AMR and AMC surveillance for AMR mitigation in the country.

- To strengthen the delivery of services by the laboratories, we recommend that all laboratories are mapped across a range of indicators, including population coverage, infectious disease burden, testing capabilities, and quality compliance. This would inform decision makers on unmet needs and decide a way forward for expansion of the laboratory network.
- For high quality microbiology testing and reporting, staff training on laboratory standards, ability to identify common pathogens, and data management skills are essential. Capacity-building of staff may be done through in-house expertise or outsourced to external organisations or tertiary facilities.
- In order to strengthen AMR surveillance, it is essential to curate the right data and generate evidence. We recommend data collection through standardised formats at all levels (laboratories, clinics and pharmacies) as well as the use of automation for data analyses. We also recommend establishing a system of assigning permanent identification numbers for patient tracking over time.
- Due to limitations in the number of facilities assessed, MAAP, in alignment with the WHO guide on facility AMU assessment, would recommend that future AMU and AMC surveillance attempts in the country be conducted through point prevalence surveys on a larger scale to give a nationally representative portrait of antimicrobials use in country.
- MAAP recommends that a comprehensive guiding policy for routine AMC data surveillance be required in the country. The policy should aim to guide on, at the minimum, AMC data reporting variables, routine data cleaning and reporting practices to minimise the amount of time spent standardising and cleaning the data before routine surveillance exercises.
- To make future AMC surveillance more time- and cost-efficient hospitals could consider converting to electronic systems and ensure such systems have the capabilities to transfer data across systems and/or produce user-friendly reports on AMC.
- MAAP recommends that the country's Antimicrobial Resistance Coordinating Committee (AMRCC) consider the introduction of facility-level Antimicrobial Stewardship Programmes (ASPs) in order to regulate the use of these broader spectrum antibiotics and educate prescribers on the importance of reserving them to maintain efficacy.
- From the assessment, an overwhelming majority of antibiotics consumed within the 'Access' and 'Watch' categories were in the top five antibiotics in each category. Such a consumption pattern could be postulated to be sub-optimal as evolutionary pressure driving resistance would be focused only on the narrow band of antibiotics consumed. It is therefore recommended that the country's ASP explores ways to ensure a wider spread in consumption of the antibiotics within each WHO AWaRe category.
- MAAP recommends an urgent review to be conducted by the ministry of health (MoH) and AMRCC in an effort to assess the availability of the 'Reserve' category antibiotics in the country that may subsequently lead to the revision of the country's essential medicines list (EML) and treatment guidelines to include these vital antibiotics, if deemed necessary. This approach will ensure that the most vital antibiotics are available for all patients.
- National stewardship programmes led by the AMRCC could conduct educational campaigns for healthcare practitioners to ensure that they are aware of the full spectrum of antimicrobials available in the county's EML.

Overview

The Fleming Fund Grants Programme

The Fleming Fund Grants Programme is a United Kingdom-sponsored initiative aimed to address the critical gaps in surveillance of AMR in LMICs in Asia and sub-Saharan Africa.[1] The programme included Regional Grants, Country Grants and the Fleming Fellowship Scheme. Mott MacDonald was the authority for grant management.

The Fleming Fund Regional Grants Round 1 Programme

The Fleming Fund Regional Grant Round 1 covered four regions (West Africa, East and Southern Africa, South Asia and South-East Asia) and aimed to expand the volume of data available on AMR and AMU.

Problem Statement

The quantum and quality of surveillance data are suboptimal in LMICs where AMR rates are typically lacking.[2] This hinders the assessment of the current treatment efficacy and understanding of the drivers of resistance. Additionally, it impacts the adoption of appropriate policies to improve antimicrobial use, which has a downstream impact on patient care. However, in most LMICs, there are institutions (academic, research, public and private health facilities, etc.) which have, at times, been collecting data on AMR for decades.

While the 'hidden treasure' is simply inaccessible for use in large-scale analytics, collecting and, where necessary digitising data from these institutions has the potential to establish baselines of AMR across a wide range of pathogen/drug combinations and assess spatiotemporal trends. Likewise, retrieving information through prescriptions or sales in healthcare facilities, should provide a wealth of information on the potential drivers of AMR. Linking susceptibility data with patient information can further provide a valuable understanding of the current treatment efficacy, which can inform evidence-based policy and stewardship actions.

MAAP

Against this background, the Regional Grant Round 1 aimed to increase the volume of data available to improve spatiotemporal mapping of AMR and AMU across countries in each region and establish baselines. The programme was implemented by the MAAP, a multi-organisational consortium of strategic and technical partners. ASLM was the Lead Grantee for the programme.[3]

MAAP's strategic partners included ASLM, the Africa Centres for Disease Control and Prevention, West African Health Organisation, the East Central and Southern Africa Health Community (ECSA-HC). The technical partners were the Center for Disease Dynamics, Economics and Policy (CDDEP), IQVIA, and Innovative Support to Emergencies, Diseases and Disasters (InSTEDD). The ASLM oversaw consortium activities and ensured the fulfilment of ethical considerations and completion of data sharing agreements with the participating countries.

MAAP was set up to collect and analyse historical antimicrobial susceptibility and consumption or usage data in each country for the period 2017-2019 and understand the regional landscape. MAAP's primary focus was to determine the levels of resistance of the bacterial priority pathogens that were listed by the WHO and other clinically important pathogens. Through standardised data collection and analytical tools, MAAP gathered, digitised and collated the available AMR and AMC data between 2017 and 2019. Based on feasibility, MAAP set out to collect information on AMC instead of AMU.

The results of this analysis contribute to the determination of baselines and trends for AMR and AMC, AMR drivers as well as critical gaps in surveillance. The study recommendations aim at increasing the country's capacity for future collection, analysis and reporting of AMR and AMC or AMU data.

Fourteen African countries across West Africa (Burkina Faso, Ghana, Nigeria, Senegal and Sierra Leone), East Africa (Kenya, Tanzania and Uganda), Central Africa (Cameroon and Gabon), and Southern Africa (Eswatini, Malawi, Zambia and Zimbabwe) were included in MAAP activities.

Aim

To determine the spatiotemporal baselines and trends of AMR and AMC in Cameroon using the available historical data.

Specific Objectives

- To assess the sources and quality of historical AMR data generated routinely by the national laboratory network of Cameroon, including the public and private human healthcare sector
- To collect, digitise and analyse retrospective data from selected facilities using standardised electronic tools; to describe the completeness and validity of AMR data in selected facilities

- To estimate the country-level AMR prevalence and trends for WHO priority pathogens other clinically important and frequently isolated pathogens as well as comparing countries on spatiotemporal maps
- To describe the in-country antimicrobial flow and highlight the status of the in-country AMC and AMU surveillance system
- To quantify and evaluate the trends of AMC and AMU at national and pharmacy levels
- To assess the relationship between AMC and AMR through the DRI
- To assess the drivers of AMR

Outcome measures

- Number of laboratories from the national network generating AMR data and proportion of laboratories reporting compliance to standards of quality and bacteriology testing
- Level of AMR data completeness and validity among laboratories selected for AMR data collection
- AMR prevalence and trends for the WHO priority pathogens, other clinically important and frequently isolated pathogens
- A semi-quantitative analysis of the in-country status in AMC and AMU surveillance
- Total consumption of antimicrobials (defined daily dose) in addition to AMC and AMU trends over time at national and pharmacy levels
- Country-level DRI
- Association between patient factors and AMR

The results are intended to serve as a baseline for prospective AMR, AMC and AMU surveillance, highlight gaps and recommend measures for surveillance strengthening.

Key engagements and activities

The Regional Grants Round 1 engagement commenced with a kick-off meeting with representatives from Mott MacDonald (Grant Managers), MAAP consortium (for Africa Region) and CAPTURA consortium ('Capturing Data on AMR Patterns and Trends in Use in Regions of Asia') for the Asia Region. The meeting was held in Brighton, England, in February 2019. In April 2019, MAAP convened a stakeholder consultation in Addis Ababa, Ethiopia with representatives from the 14 participating countries in Africa to discuss continental efforts on AMR control and the implications of the Regional Grant. Over the next year and a half, workshops were held in each country to finalise data sharing agreements and methodologies. The workshops brought together representatives from MAAP and the countries, including representatives from the MoH, AMR coordinating committees, health facilities, laboratories, and pharmacies. This was followed by site selection and data collection in each country. Data analysis was conducted by the technical partners. The final results were then shared through dissemination meetings (Figure 1).

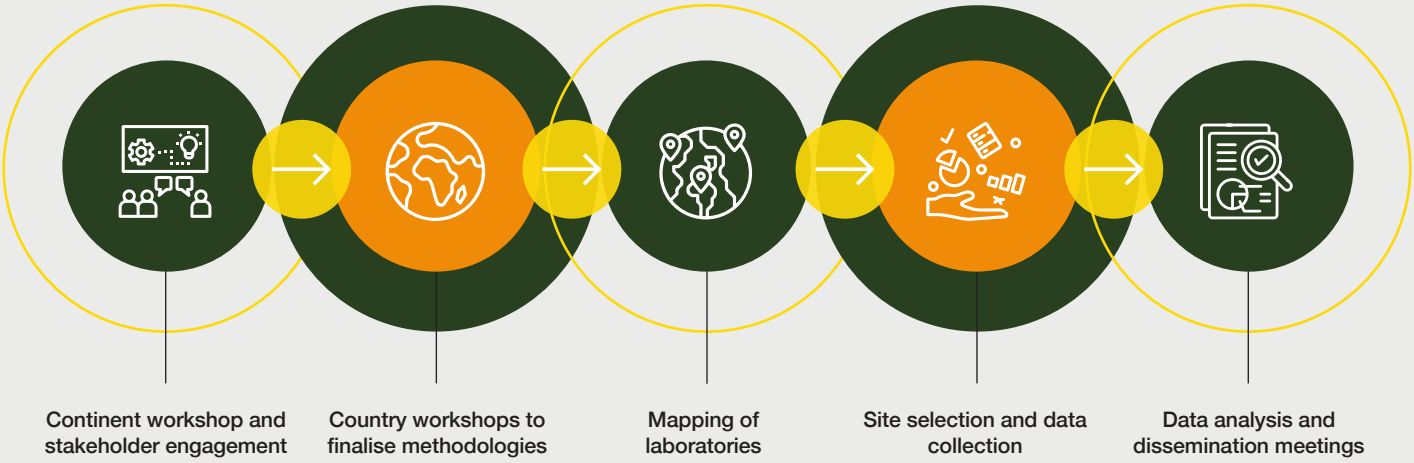


Figure 1: Key engagements and activities

Ethical issues and data sharing agreements

To ensure that ethical conduct, confidentiality, use and ownership of the data are regulated and adhered to during the project, a data-sharing agreement (DSA) was signed with the ministry of health. The DSA facilitated clear communication and established additional safeguards to the management of the collected data (see Appendix 1).

Country Profile

Health and demographic profile

As of 2020, Cameroon was estimated to have a population of 26.5 million inhabitants with a life expectancy of 59 years. The country has a high infectious disease burden with a TB incidence of 174 per 100 000 and an HIV prevalence of 3%. The country has a physician density rate of 0.1 per 1 000 inhabitants and nurse density rate of 0.53 per 1 000 inhabitants. With a universal health coverage index of 44, Cameroon appears to have a below average coverage of essential services (Table 1).

Table 1: Health and demographic profile of Cameroon

	Cameroon		Comparator values (most recent year)*		
	Year	Value	India	Argentina	United States
Population	2020	26 ,545 ,864	1 ,380 ,004 390	45 376 763	329 484 123
Life expectancy during the study period, total (years)	2019	59	70	77	79
Universal health coverage service index (0-100)	2019	44	61	67	83
GDP per capita (current US$)	2020	1 537.13	1 ,927.7	8 579.0	63 593.4
Immunisation, DPT (% of children ages 12-23 months)	2019	67	91.0	86.0	94.0
Incidence of tuberculosis (per 100 000 people)	2020	174	188.0	31.0	2.4
Prevalence of HIV, total (% of population ages 15-49)#	2020	3	0.2*	0.4 2020	0.4 2019
Primary education (%)#	2019	65.5	94.6	98.6	100
Physicians density (physicians per 1 000)#	2011	0.09	0.93	4.0	2.6
Nurses density (nurses and midwives per 1 000)#	2010	0.53	2.39	2.60	15.69

Sourced from World Bank[4,5 6] and *National AIDS Control Organisation[7]
#Data for some country parameters may not necessarily be of the same year (but sourced from the most recently available information between 2017-2020).

Policy frameworks

In May 2015, the World Health Assembly approved the Global Action Plan on Antimicrobial Resistance.[8] Later that year, the WHO launched the Global Antimicrobial Resistance Surveillance System (GLASS) to support the implementation of the Global Action Plan on Antimicrobial Resistance and strengthen AMR surveillance and research.[9,10] GLASS provides standardised methodologies for AMR data collection and analysis and encourages countries to share their data on the global surveillance platform. GLASS has various modules and tools including emerging AMR events, AMC, and promotes integration with surveillance in the animal and environment sectors.

Cameroon is enrolled in GLASS and but has not provided information on national surveillance to GLASS in any of the data calls.[9,10] In May 2018, the National Action Plan (NAP) for the control of antimicrobial resistance in Cameroon was adopted. The NAP was scheduled to be implemented within three years, beginning in 2018 and ending in 2020.[11]

Part A: Antimicrobial Resistance

Section I: Laboratory assessment

Objective

To assess the sources and quality of historical data on AMR generated routinely by the national laboratory network of Cameroon, including the public and private healthcare sectors.

Methodology

Initially, up to 16 laboratories (two reference, four private and 10 public) were expected to be included in the study for the purpose of AMR data collection. Ultimately, only those laboratories most likely to guarantee the highest level of data quality were selected. Country-specific circumstances, the actual number of selected laboratories, and their affiliations and levels necessitated some adjustments in the study protocol.

During the initial stages of in-country work, the laboratory network was mapped with support from the country's MoH. An inventory of laboratories in the tiered network was created, and laboratories capable of conducting AST were identified. A survey was administered to the identified laboratories, with the aim of obtaining site-specific details and assessing the laboratories on five aspects: status of commodities and equipment, QMS, personnel and training, specimen management, and laboratory information systems (AMR Appendix 2). Based on self-reported information on the above parameters, each laboratory was assigned a readiness score for AMR surveillance (AMR Appendix 3). The scoring scheme was standardised across all participating countries. The final selection of laboratories for data collection was made by the MoH and was not necessarily based on laboratory rankings.

Results

Mapping and selection of laboratories

During the initial stages of in-country work in Cameroon, 360 laboratories were mapped to the national laboratory network. An eligibility questionnaire was sent to 19 laboratories identified as having capacity for bacteriology testing and AST capacity. The majority of the 19 laboratories were affiliated with the government (Table 2, Supplementary Table 1). The laboratory readiness scores of the surveyed laboratories varied widely (range: 21.1-76.3%). Sixteen laboratories were selected for data collection (Figure 2). The laboratories named in the tables are listed in order of decreasing laboratory readiness scores.

Table 2: Laboratory readiness scores

Surveyed laboratories*	Laboratory readiness score (%)	Level of service	Affiliation
Selected			
HGOPED Laboratoire (HGOPED)	76.3	Reference	Government
LAMA Yaounde (Lama)	73.7	Regional/Intermediate	Private
Laboratoire de bactériologie CHU de Yaoundé (CHU Yaounde)	71.1	Reference	Government
Laboratoire Prima Sarl (Prima)	71.1	Other	Private
Regional Hospital LIMBE (Limbe)	71.1	Regional/Intermediate	Government
Laboratore de Biologie Clinique de Laquintinie (Laquintinie)	68.4	Reference	Government
Laboratoire du Centre médico-social de la CNPS Marona (Marona)	60.5	Regional/Intermediate	Other
Laboratore de Biologie Clinique de HGOPY (HGOPY)	60.5	Reference	Government
Laboratoire de l'hopital central Douala (Douala)	57.9	Reference	Government
District hospital Bonassama (Bonassama)	57.9	District/Community	Government
HMR 1 Yaoundé (HMR)	55.3	Regional/Intermediate	Government
GT Labo (Labo)	52.6	Regional/Intermediate	Private
Hopital régional d'Ebolowa (Ebolowa)	50	Regional/Intermediate	Government
Centre hospitalier Esoss Yaoundé (Esoss)	39.5	Reference	Other
Buea Regional hospital laboratory (Buea)	36.8	Regional/Intermediate	Government
Laboratoire Central de l'hopital général de Yaoundé (HG Yaoundé)	34.2	Reference	Government
Not selected			
Hopital régional de Ngaoundere	50	Regional/Intermediate	Government
Hopital régional Annexe Edea	39.5	Regional/Intermediate	Government
Hopital de référence de Sangmalima	21.1	Reference	Government

** Laboratory names are abbreviated.*

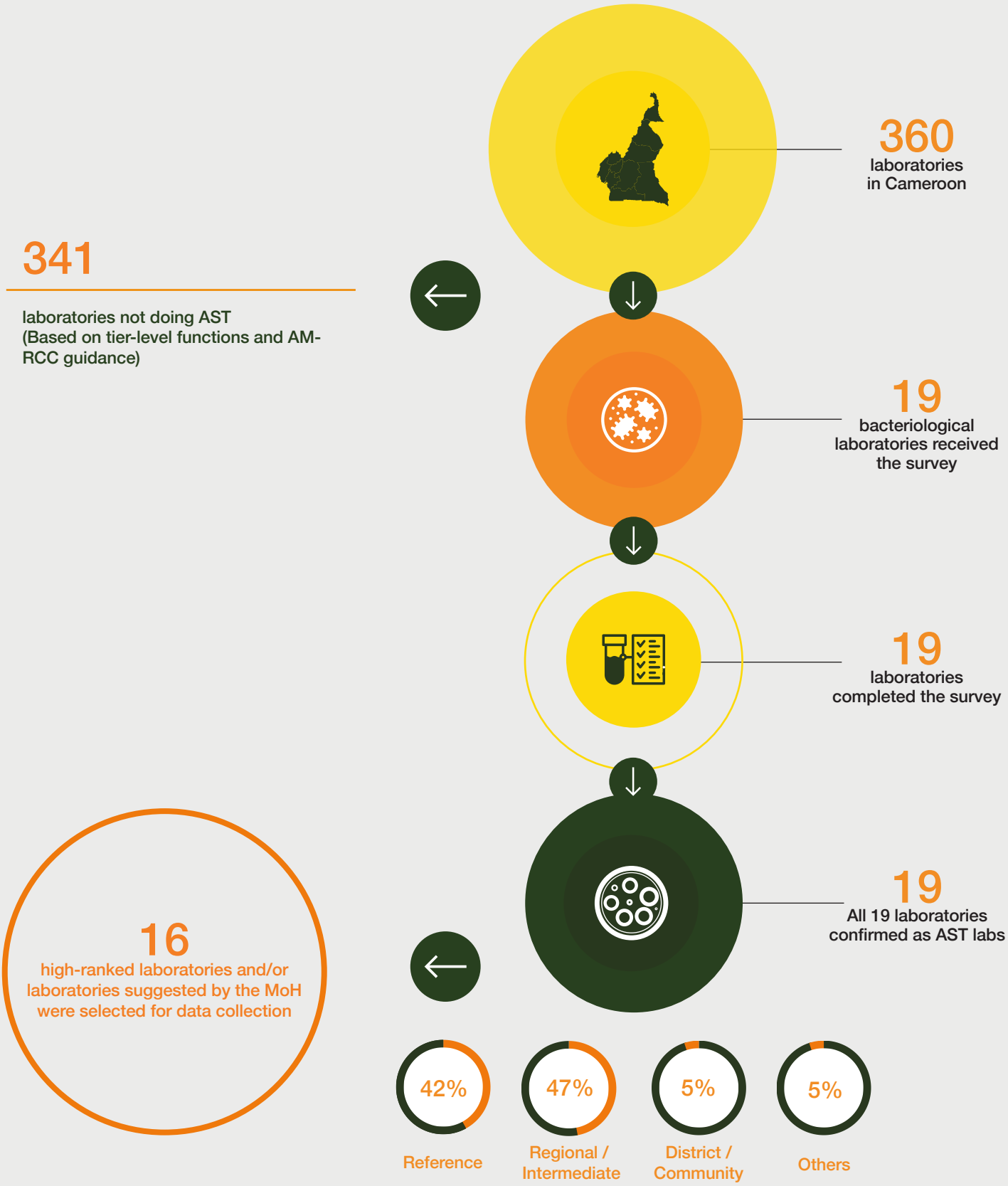


Figure 2: Selection of laboratories in Cameroon

Surveillance preparedness of surveyed laboratories

Based on self-reported information from 19 laboratories, laboratory function and quality compliance were assessed to understand the preparedness for AMR surveillance. Eleven laboratories had implemented quality management, eight used automated methods for pathogen identification while only one laboratory was accredited (Figure 3, Supplementary Table 2). Since these findings may affect the quality of laboratory data, caution is warranted in interpreting the AMR rates presented in this report.

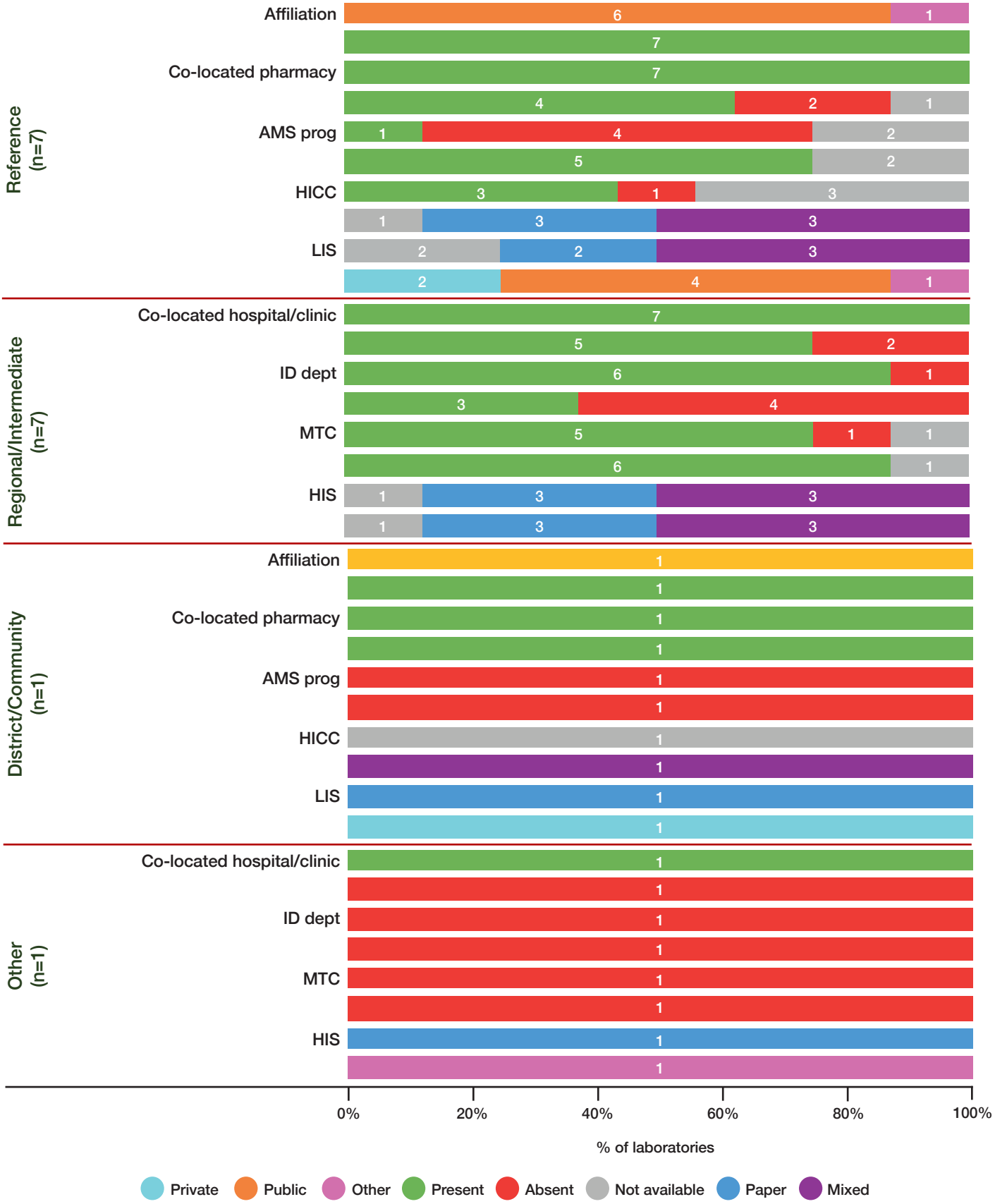
	Parameters			N (%)
Commodity and equipment status	Regular power supply and functional back up			16 (84.2)
	Continuous water supply)			17 (89.5)
	Certified and functional biosafety cabinets			7 (36.8)
	Automated methods for pathogen identification			8 (42.1)
	Automated methods for AST			7 (36.8)
	Methods for testing AMR mechanisms			7 (36.8)
QMS implementation	Reported QMS Implementation			11 (57.9)
		Types of QMS	LQMS	-
			SLIPTA	-
			SLMTA	3 (27.3)
			Mentoring	-
			Combination‡	5 (45.5)
			Others	2 (18.2)
	Quality Certification			4 (21.1)
		Types of Quality certification	SLIPTA	1 (25.0)
			Col. of Am. Path	-
			Others	1 (25.0)
	Accreditation			1 (5.3)
	Participation in proficiency testing			7 (36.8)
	Utilization of reference strains			8 (42.1)
	Reported consistent maintenance of QC records			9 (47.4)
	Designated focal quality person			11 (57.9)
	Reported compliance to standard operating procedures			17 (89.5)
	Reported compliance to AST standards			14 (73.7)
Personnel and training status	Presence of at least one qualified microbiologist			17 (89.5)
	Presence of an experienced laboratory scientist/technologist			19 (100.0)
	Up-to-date and complete records on staff training and competence			14 (73.7)
Specimen Management status	Reported compliance to SOPs on specimen collection and testing			17 (89.5)
	Reported compliance to SOPs on specimen rejection			14 (73.7)
	Average number of specimens processed for AST in 2018			18 (94.7)
LIS and Linkage to Clinical Data	Assigned specimen (laboratory) identification number			16 (84.2)
	Availability of system/database to store patient data			15 (78.9)
		Database format	Paper-based	7 (46.7)
			Electronic	-
			Mixed	8 (53.3)
	Captured patients' records on test request forms			14 (73.7)
			Retrievable	6 (42.9)

‡ Combination refers to more than one option presented in the questionnaire (laboratory quality management system, stepwise laboratory improvement process towards accreditation, strengthening laboratory management towards accreditation and mentoring).

Figure 3: Laboratory preparedness for AMR surveillance

Profile of Selected Laboratories

All 16 selected laboratories were co-located with clinical facilities. Eleven clinical facilities had an infectious diseases department and only four had an ASP. Ten facilities had medical therapeutic committees while nine had hospital infection control committees. Seven laboratories and six hospitals had paper-based information systems (Figure 4).



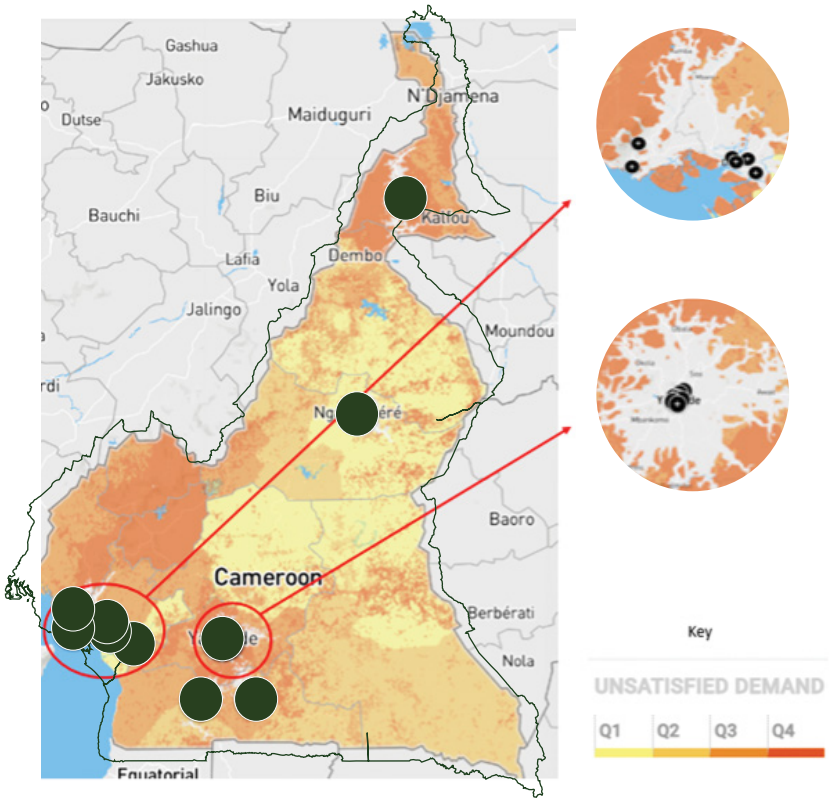
Abbreviations: AMS=antimicrobial stewardship; HICC=hospital infection control committee; HIS=hospital information system; IDD=infectious diseases department; LIS=laboratory information system; MTC=medical therapeutics committee

Figure 4: Profile of selected laboratories

Population coverage of laboratories

We analysed the data using PlanWise® solution. PlanWise incorporates data on population, road network, and other variables and applies an algorithm and geospatial optimisation techniques to show unmet needs. We evaluated the proportion of population covered by mapped laboratories within a two hours' drive (Supplementary Figure 1).

As of 2020, Cameroon had an estimated population of 26.55 million.



Supplementary Figure 1: Population coverage of AST laboratories in Cameroon

Population coverage of laboratory services is defined as the catchment population living within one-hour travel (by car or foot) from the testing laboratory. It is represented in grey on the map. The analysis uses the assumption that the laboratory has sufficient testing capacity to serve the entire population within the catchment area. The population outside the catchment area of the facilities is, by definition, representative of the overall unmet need. For ease of use, the unit of unmet need is represented on the map as a 'pixel', i.e., the lowest base unit of a raster image. To visualise the geographical areas with the most critical unmet needs, each base component is ranked from the lowest to the highest, according to the number of the population living in the 'pixel'. The ranking is then divided into quartiles made of equal population fractions (from Q1 _lowest density of population to Q4 highest density), also corresponding to different colours (from yellow to dark red, see legend). Therefore, the colour on the map relates to the level of unmet need (people not in the reach of a facility) relative to the whole population.

In Cameroon, the catchment population living within one-hour travel time from the 19 participating AMR surveillance sites covers 33% of the population. Hence, 67% of the population is not covered at all by the existing facilities. To increase the population coverage, new capacity should be introduced (either by upgrading an existing lab to start providing services or by constructing a new lab) in regions in dark red (Q3), prioritising regions with the highest absolute unmet need.

Section II: Collection, analysis and interpretation of AMR data

Objective

1. To collect, digitise and analyse retrospective data from selected facilities using standardised electronic data collection and analysis tools
2. To describe the completeness and validity of AMR data in selected facilities

Methodology

Data collection

The main variables were the patient's culture (laboratory) results, clinical information and antimicrobial usage (AMR Appendix 4). For all positive blood and cerebrospinal fluid (CSF) cultures, information on the patient's demographics, clinical profile and antimicrobial usage was also collected from clinics and hospitals. However, this was possible only where patient records could be tracked between the laboratories and hospitals (Figure 5). Additionally, data were collected on AMC at the facility and national levels.

For laboratories with paper-based records, at least 5 000 records per laboratory per year were to be collected. However, no such limit was imposed for digitised data. The goal was to obtain at least 240 000 records from 16 laboratories across three years.

As a first step, the MoH and IQVIA were jointly involved in recruiting local field data collectors. A capacity-building workshop was conducted as part of the MAAP to train the field staff on data collection, including the use of WHONET[13] and the specially developed MAAP tool for secure transfer of collected data.

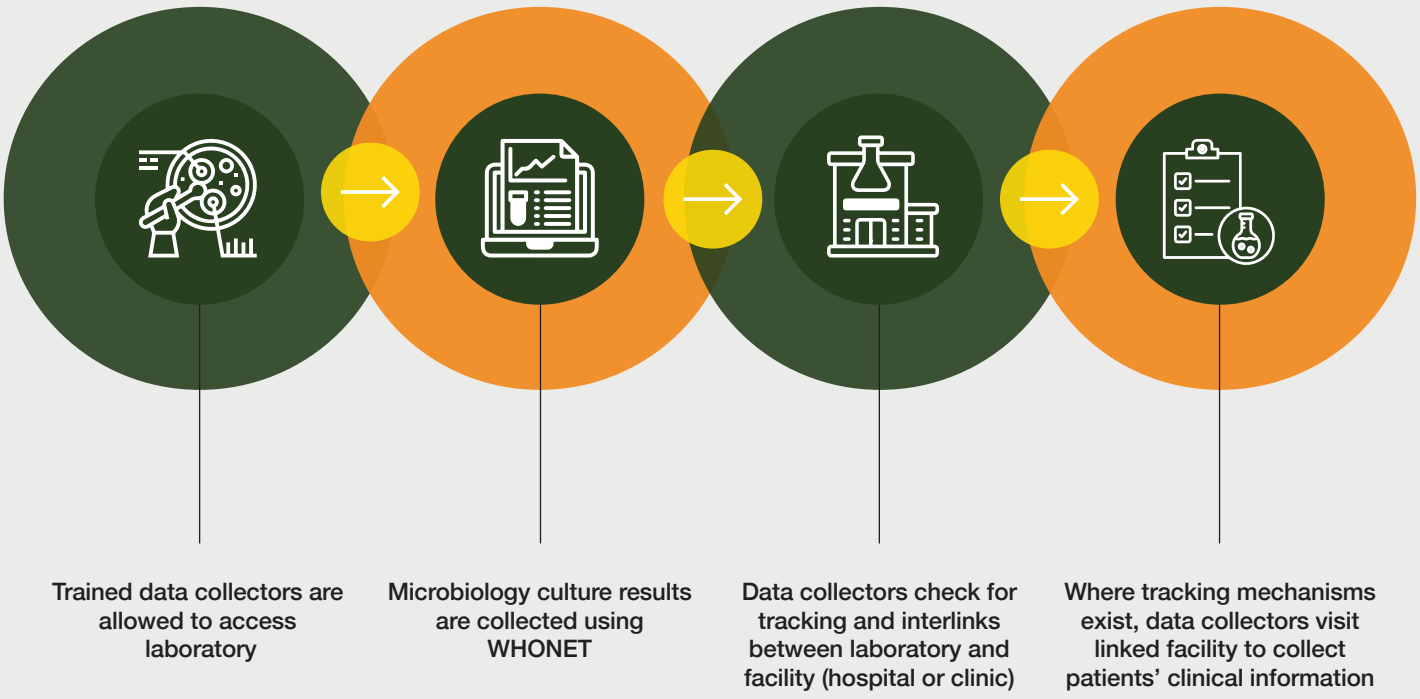


Figure 5: Steps of AMR data collection

Historical data were collected for the period January 1, 2017, through to December 31, 2019. The AMR data were initially captured through WHONET, a free Windows-based database software programme developed for the management and analysis of microbiology laboratory data. The software allowed data entry of clinical and microbiological information from routine diagnostic testing or research studies. WHONET has a simple data file structure and output formats compatible with major database, spreadsheet, statistical and word-processing software. It permits customisation to include variables of interest and has several alert features that highlight unlikely or important results. From WHONET, data were transferred onto an online application (repository) for further analysis. Each row of the database represented an individual patient's results. Where the laboratory or hospital issued unique patient identification numbers, it was also possible to track a patient along multiple visits.

Figure 6: Data collection at a Cameroon facility

Data analysis

A preliminary data review was conducted to check for data completeness, accuracy and redundancy. Data summarisation was based on the following parameters: quantum of cultures (total cultures, valid cultures, positive cultures or positive cultures with AST results); level of pathogen identification, inappropriate testing, clinical information, culture characteristics, specimen characteristics and identified pathogens. Each parameter is described below.

- **Quantum of cultures:** Total cultures were the number of patient rows in the database received from the laboratories. Valid cultures were a subset of total cultures which had complete information on the specimen type, collection date and pathogen name. Positive cultures were valid cultures for which pathogen growth was reported, irrespective of AST results. Total cultures were quantified for each laboratory and over the entire study period. Valid cultures and positive cultures were stratified for each laboratory as well as for each study year (Figure 7).
- **Level of pathogen identification:** Positive cultures with AST results were summarised based on the level of pathogen identification. Gram identification and genus-level identification were considered incomplete where reporting at a species level indicated complete pathogen identification. Data was stratified for each laboratory and assessment was done over the entire study period (Figure 7).

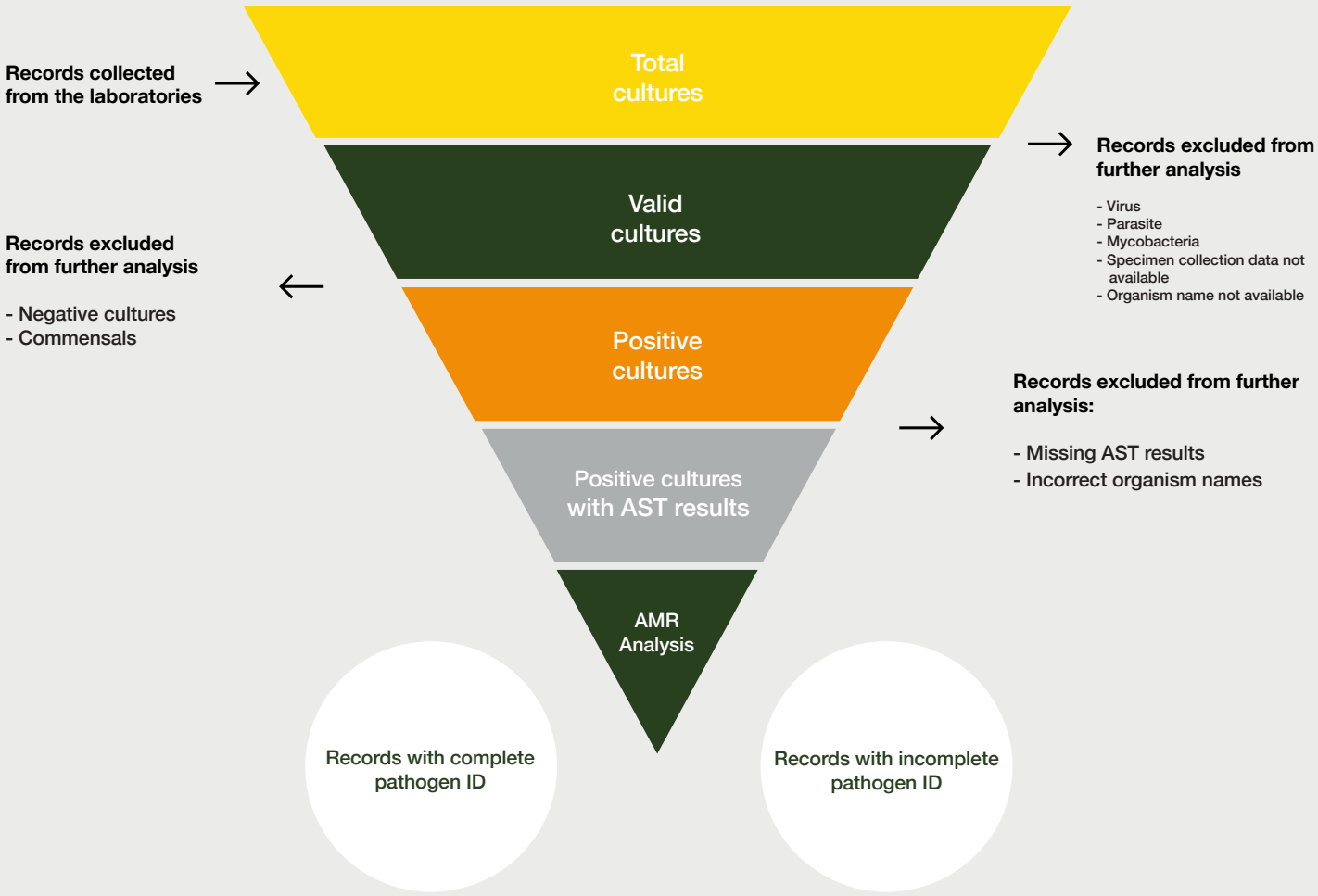


Figure 7: Conceptual framework for deriving quantum of cultures

- **Culture characteristics:** Cultures were characterised across gender, age group and pathogen type (bacteria or fungi). Data were pooled across all laboratories and assessment was conducted for each study year.
- **Inappropriate testing:** Positive cultures with AST results were assessed for compliance to AST standards. However, comprehensive assessment of validity of AST results was beyond the study scope. Data were pooled across laboratories and assessed for each study year. The conventional AST standards are Clinical and Laboratory Standards Institute (CLSI), European Committee on Antimicrobial Susceptibility Testing (EUCAST) and Comité de l'antibiogramme de la Société Française de Microbiologie, the European Committee on Antimicrobial Susceptibility Testing.
- **Clinical information:** Positive cultures with AST results were summarised based on information available for the patient's clinical profile: diagnosis, origin of infection (whether hospital acquired, or community acquired), presence of in-dwelling device, and antimicrobial use. Data were quantified for each laboratory and assessed over the entire study period.
- **Specimen characteristics:** Positive cultures with AST results were summarised based on information on specimen types. Data were pooled across all laboratories and assessed for each study year.
- **Quality of data:** We used the level of pathogen identification as a parameter to evaluate the data quality from each laboratory seeing as the complete identification of pathogens is key in AMR surveillance and implies the quality of the laboratory's testing practices. Scoring was based on quartiles of the proportion of completely identified pathogens. The laboratories with >75% of pathogens identified at the species level were awarded the highest score (4). Laboratories with <25% identification received the lowest score (1), (Table 3). Firstly, the scoring was performed per year (i.e., 2017–2019). Thereafter, the average was assigned as the laboratory data quality score for each laboratory.

Table 3: Data scoring scheme

Level of pathogen identification	Score
<25%	1
25-50%	2
51-75%	3
>75%	4

Since we pooled all the data to obtain AMR rates at a national level, we computed a single metric to estimate the overall quality of data received from a country. This metric is referred to as the country data quality score and weights the laboratory data quality score with the quantum of valid cultures contributed by each laboratory as shown in the formula below. The maximum attainable score is 4, and Table 4 below shows how the country data quality score was rated.

Table 4: Data quality rating

Score	Rating
4	Excellent
3-3.9	Good
2-2.9	Average
1-1.9	Poor

$$\text{Country data quality score} = \sum_{i=1}^{n} \frac{(\text{Laboratory data quality score}_{(i)} \times \text{Quantum of valid cultures}_{(i)}}{\sum \text{Quantum of valid cultures}_{(1\ldots n)}}$$

Where *n* is the total number of contributing labs and *i* represents individual laboratories.

Results

Retrospective data was collected for 2017–19 from 16 laboratories and corresponding facilities in Cameroon.

1. Quantum of cultures and level of pathogen identification

Data were retrieved for 116 808 total cultures of which 116 361 were valid and 43 035 were positive. Of the positive cultures, AST results were available for 32 545 cultures, the maximum (n=4 768) coming from HGOPY and the least (n=131) from Buea (Figure 8 and 9). Not all pathogens were identified completely (i.e., at species level). Complete identifications were highest for Bonassama (99.4%) and lowest for Ebolowa (63.9%) (Table 5).

Table 5: Data summary

Variable (Columns) / Laboratory (Rows)	Total Cultures (N=116 808)	Valid Cultures N=116 361	Positive cultures N=43 035	Positive cultures with AST results N=32 545	Incomplete identity* N= 3 234	Complete identity* N= 29 311
HGOPED	9 647	9 590.0 (99.4)	2 749 (28.7)	2 515 (91.5)	126 (5.0)	2 389 (95.0)
Lama	3 515	3 514.0 (100.0)	1 256 (35.7)	971 (77.3)	202 (20.8)	769 (79.2)
CHU Yaounde	3 828	3 823.0 (99.9)	1 934 (50.6)	1 629 (84.2)	234 (14.4)	1 395 (85.6)
Prima	15 187	15 174.0 (99.9)	6 000 (39.5)	4 307 (71.8)	154 (3.6)	4 153 (96.4)
Limbe	7 552	7 552.0 (100.0)	4 317 (57.2)	4 262 (98.7)	356 (8.4)	3 906 (91.6)
Laquintinie	8 934	8 918.0 (99.8)	3 392 (38.0)	2 999 (88.4)	365 (12.2)	2 634 (87.8)
Marona	2 086	2 073.0 (99.4)	531 (25.6)	473 (89.1)	89 (18.8)	384 (81.2)
HGOPY	19 805	19 750.0 (99.7)	10 270 (52.0)	4 768 (46.4)	308 (6.5)	4 460 (93.5)
Douala	11 102	10 963.0 (98.7)	2 395 (21.8)	1 629 (68.0)	115 (7.1)	1 514 (92.9)
Bonassama	1 063	10 63.0 (100.0)	314 (29.5)	314 (100.0)	2 (0.6)	312 (99.4)
HMR	5 161	5 154.0 (99.9)	1 873 (36.3)	1 739 (92.8)	348 (20.0)	1 391 (80.0)
Labo	6 901	6 901.0 (100.0)	2 561 (37.1)	2 560 (100.0)	282 (11.0)	2 278 (89.0)
Ebolowa	2 955	2 952.0 (99.9)	1 234 (41.8)	1 234 (100.0)	445 (36.1)	789 (63.9)
Esoss	15 567	15 440.0 (99.2)	2 873 (18.6)	1 867 (65.0)	142 (7.6)	1 725 (92.4)
Buea	255	255.0 (100.0)	136 (53.3)	131 (96.3)	16 (12.2)	115 (87.8)
HG Younde	3 250	3 239.0 (99.7)	1 200 (37.0)	1 147 (95.6)	50 (4.4)	1 097 (95.6)

* Subsets of the category 'Positive cultures with AST results' where 'incomplete' includes cultures with only Gram or genus-level identification; 'complete' includes cultures with species-level identification; — information not available

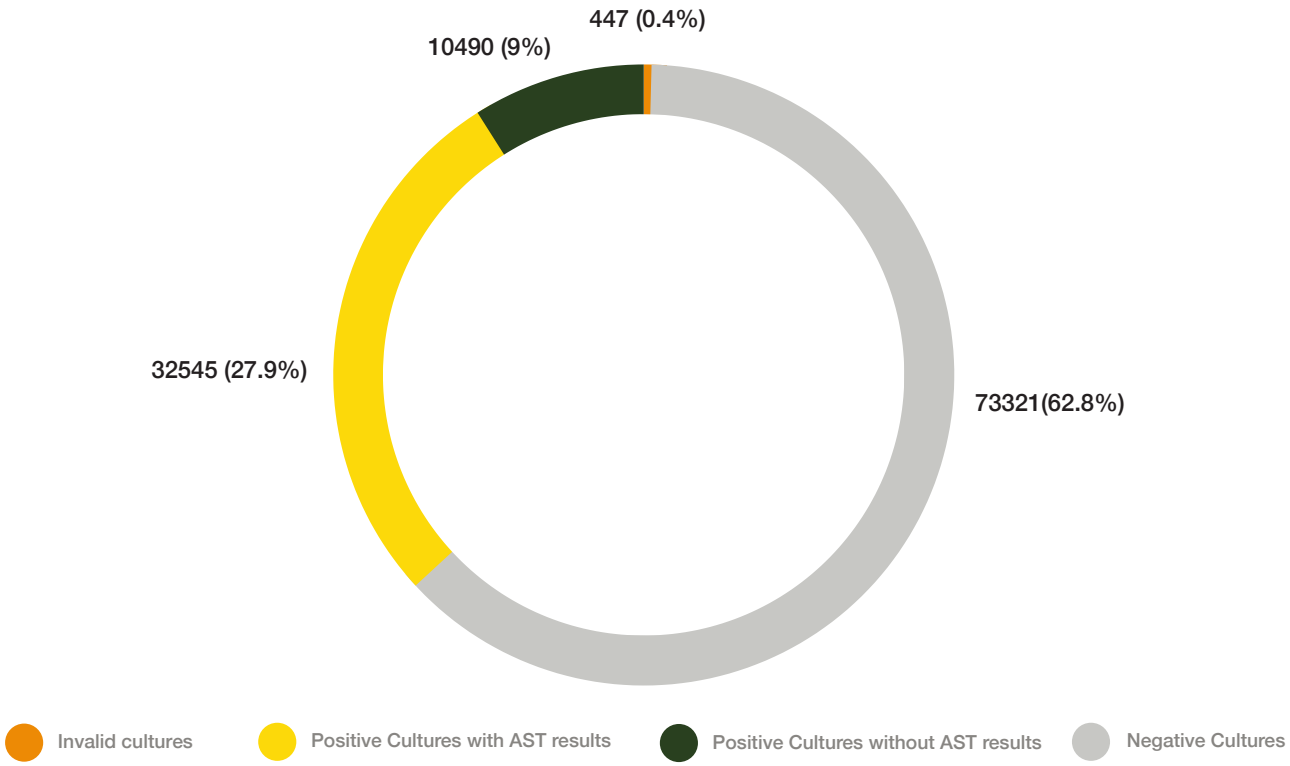


Figure 8: Quantum of cultures across all selected laboratories

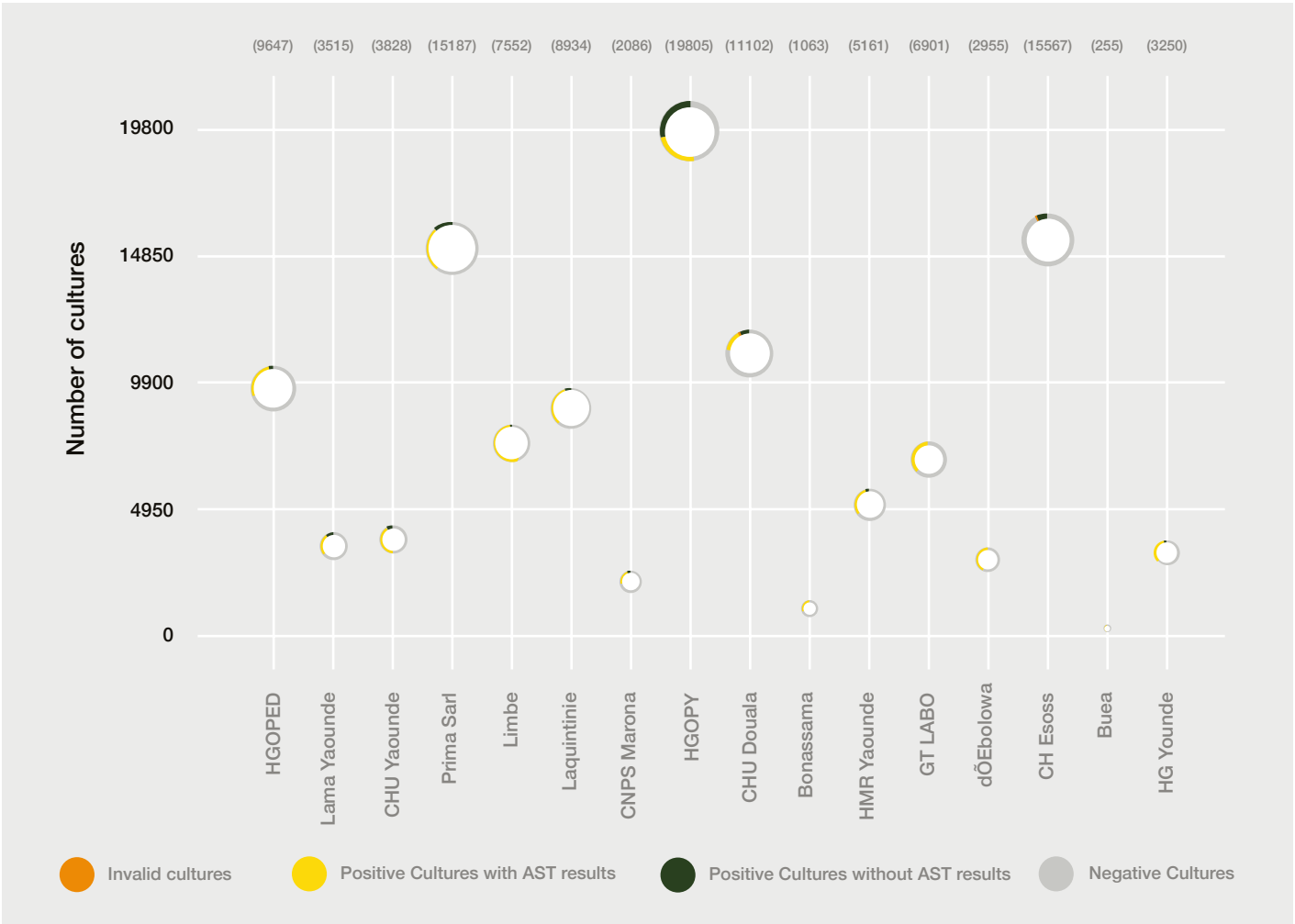


Figure 9: Quantum of cultures in each selected laboratory

2. Culture characteristics

Bacterial pathogens (27 635) were more commonly reported than fungal pathogens. Information on age was missing from 17% of cultures, but where available, data showed a median age of 33 years (range: 0–100 years) with most cultures (18 736) obtained from patients 18–49 years old. Females (24 420) contributed more to the quantum of positive cultures with AST results. More data came from 2018 (11 336) than other years (Table 6, AMR Supplementary Table 3).

Table 6: Culture characteristics

Characteristics	Positive cultures with AST results n=32 545 n (%)
Gender	
Male	8 124 (25.0)
Female	24 420 (75.0)
Unknown	1 (0.0)
Age, years	
Less than 1	1 998 (6.1)
1 to 17	2 049 (6.3)
18 to 49	18 736 (57.6)
50 to 65	2 441 (7.5)
Above 65	1 782 (5.5)
Unknown age	5 539 (17.0)
Years	
2017	9 905 (30.4)
2018	11 336 (34.8)
2019	11 304 (34.7)
Pathogen	
Bacteria	27 635 (84.9)
Fungi	4 910 (15.1)

3. Inappropriate testing

Of the 16 selected laboratories, 8 laboratories reported using EUCAST standards for AST testing; three reported compliance to the CLSI standards while others reported to a combination of CLSI/EUCAST/CASFM. However, during review of AST results, the following instances of inappropriate testing were noted:

Bacteria were tested against antifungals and fungal pathogens were tested against antibiotics (AMR Supplementary Figure 2a). Enterobacterales were tested against inappropriate agents such as vancomycin, penicillin G or oxacillin and S. aureus was tested against vancomycin using the disk diffusion method (AMR Supplementary Figure 2b).

4. Clinical information

Patient metadata, particularly clinical information, were sparse (Table 7).

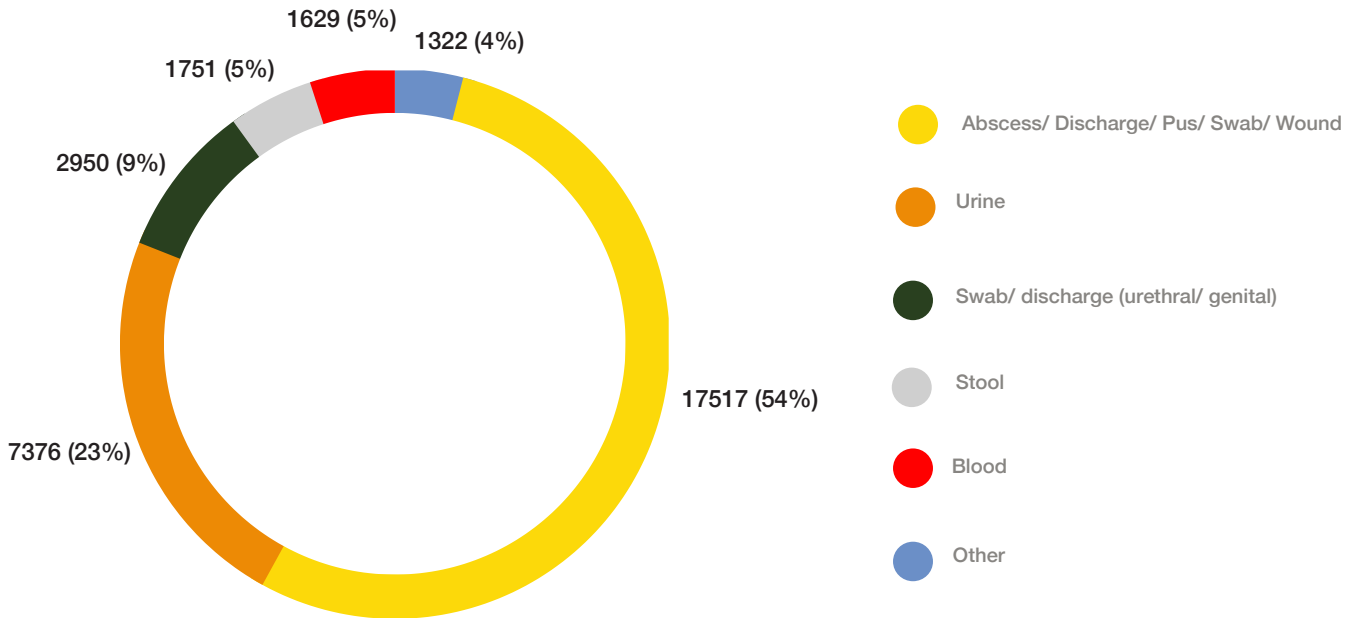
Table 7: Clinical information

Laboratory	Positive cultures with AST results N=32 545	Diagnosis data	Infection origin data*	Indwelling device data	AMU data
HGOPED	2 ,515	9	0	0	8
Lama	971	0	0	0	0
CHU Yaounde	1 ,629	237	1	241	129
Prima	4 ,307	0	0	0	0
Limbe	4 ,262	0	0	0	0
Laquintinie	2 ,999	0	0	0	0
Marona	473	2	0	2	2
HGOPY	4 ,768	156	0	0	40
Douala	1 ,629	0	0	0	0
Bonassama	314	0	0	0	0
HMR	1 ,739	0	1	0	8
Labo	2 ,560	0	0	0	0
Ebolowa	1 ,234	0	0	0	4
Esoss	1 ,867	0	0	0	1
Buea	131	0	0	0	0
HG Younde	1 ,147	0	0	0	0

- information not available; * hospital acquired, or community acquired; AMU=antimicrobial use; AST=antibiotic susceptibility testing.

5. Specimen characteristics

Purulent discharge, urine, and urethral or vaginal specimens accounted for most of the positive cultures in each study year (Figure 10, Supplementary Table 4).



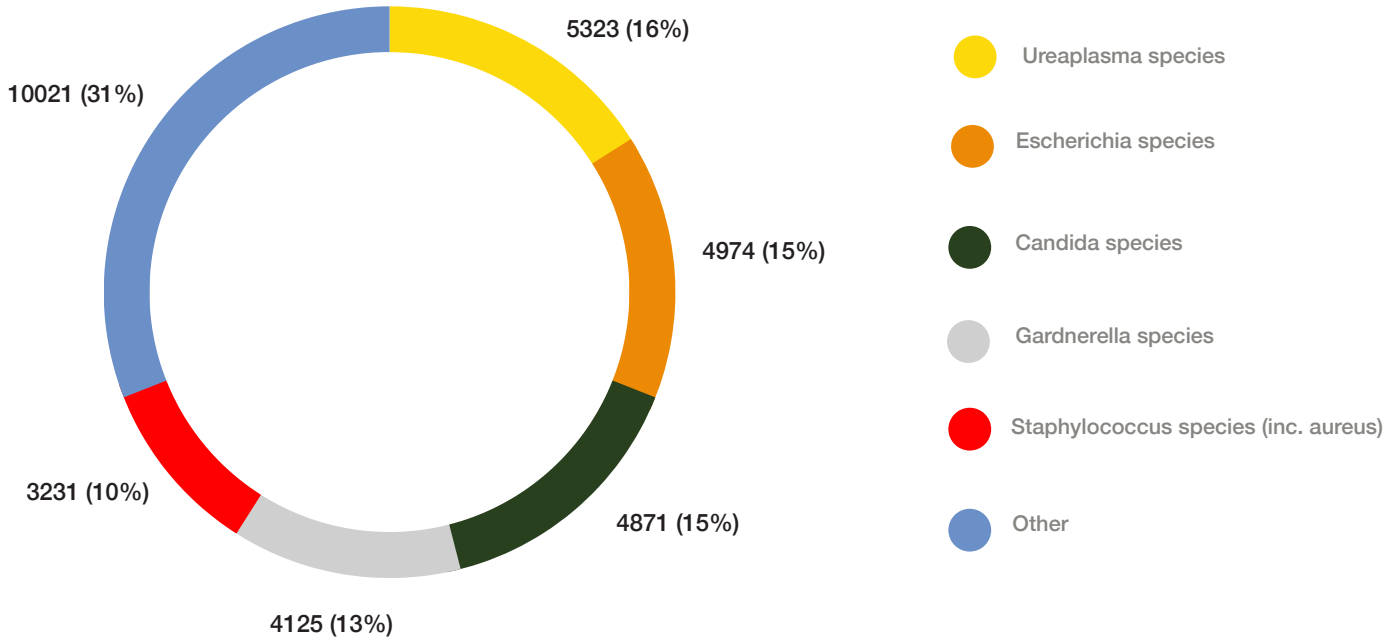
* Others include all other specimens excluding the top 5 mentioned here

Figure 10: Specimen characteristics

6. Identified pathogens

Ureaplasma species (16%), Escherichia species (15%) and Candida species (15%) largely contributed to the quantum of positive cultures (Figure 11).

In 2017, of the 9 905 positive cultures with AST results, Ureaplasma species (16%), Candida species (18%) and Escherichia species (15%) were the most reported. In 2018, of the 11 336 positive cultures with AST results, Ureaplasma species (17%), Escherichia species (15%) and Candida species (14%) were again the most reported. Similar pattern was noted in 2019, with Ureaplasma species (16%), Escherichia species (15%) and Candida species (14%) the most reported (AMR Supplementary Table 5).



* Others include all other pathogens excluding the top 5 mentioned here
Figure 11: Pathogens identified

7. Quality of data

The country data quality score of the 116 361 valid culture records obtained from the 16 laboratories in Cameroon was 3.9 and was rated as good for AMR analysis. For individual laboratory data quality scores from each contributing laboratory, see Supplementary Table 6.

Section III: AMR rates

Objective

To estimate the country-level AMR prevalence and trends for WHO priority pathogens and other clinically important and frequently isolated pathogens as well as to enable the comparison of countries on spatiotemporal maps.

Methodology

Data from positive cultures with AST results was analysed to estimate the country-level AMR prevalence of pathogens and identify the drivers of resistance.

Estimation of AMR rates

In this report, the AMR rate is the extent to which a pathogen is resistant to a particular antimicrobial agent or class as is determined by the proportion of isolates that are non-susceptible (i.e., either intermediate or resistant) over a one-year period:

$$\text{AMR rate} = \frac{\text{No. of non-susceptible isolates}}{\text{No. of tested isolates}} \times 100 \ (\text{CI } 95\%)$$

AMR rates were estimated for the WHO priority pathogens[14] where the number of tested isolates exceeded 30 regardless of the specimen type (AMR Appendix 5). AMR trends were mapped for the WHO priority pathogens depending on data availability.

In addition, AMR rates were estimated for:

1. Clinically important pathogens isolated from blood and cerebrospinal fluid (AMR Appendix 6)
2. Top three highly resistant bug-drug combinations (regardless of the specimen type)
3. Pathogens tested against the most and least consumed antimicrobial classes (regardless of the specimen type, please refer to part C)

Data were analysed as per resistance interpretation submitted by the laboratories. Where laboratories provided quantitative results (i.e., diameter measurements or minimum inhibitory concentrations), data were adjusted based on the updated breakpoints available on WHONET. Although non-susceptibility interpretations were based on results from the tested antimicrobials, they are represented at the antimicrobial class level wherever possible (AMR Appendix 7). Analysis was limited to bacterial and fungal pathogens.

Removal of duplicate records

Before AMR rates were calculated, duplicate AST results were removed such that only the results of the first pathogen isolate per patient per year, irrespective of AST profile (and body site or specimen type in the case of WHO priority pathogens), were included. This approach follows the CLSI M39A4 criteria.[15,16] Duplicate removal was based on the availability of unique patient identifiers. When no patient identifiers were available, the results of all isolates were included. The AST data from all laboratories were then aggregated and rates were calculated as the proportion of non-susceptible isolates.

AMR estimates statistics

Confidence intervals (CIs) at the 95% level of confidence were calculated to quantify the uncertainty in the estimated resistance rates. Typically, CIs for AST data have been constructed using the Wilson score method. This is a binomial calculation that assumes that all samples are independent.[17] However, there are likely correlations between data within each laboratory and between laboratories that draw from similar populations. Thus, where appropriate, the Wilson cluster robust CI method was employed to account for a lack of data independence such that each laboratory represented a cluster.[18]

Estimated AMR rates should be interpreted with caution because they were derived from aggregated data from laboratories with varying testing capabilities and not all selected laboratories contributed to the AST results. The validation of AST results was beyond the study scope and data were taken at face value for assessment of resistance rates.

Online data visualisation

AMR data was aggregated to the national level and definitions of resistance were harmonised across countries to enable comparisons. Data were uploaded to a private and secure portal for countries and laboratories to permit analysis of their data at the patient level (CDDEP's ResistanceMap Surveillance Network [RSN]). RSN provides a simple approach to analysing AMR data. Point-and-click editing tools allow the user to mine the data to answer complex questions and where the resulting analyses can be displayed as bar charts representing resistance over a time period or line graphs showing changes over time by month or year. RSN will be made available for at least one year, following completion of the study, to each participating country.

Data were also uploaded to CDDEP's ResistanceMap platform, a publicly available repository for aggregated country-level data.[19] Spatiotemporal analysis for the combined AMR and AMC-AMU datasets were built on the ResistanceMap framework. Current capabilities include maps, trend line charts and frequency bar charts.

Results

(i) AMR rates and trends for WHO priority pathogens

AMR rates for the WHO priority pathogens were calculated as the proportion of isolates that were non-susceptible over each one-year interval. Across 2017–2019, AMR rates for some organisms remained consistent; the rates for others varied. The highest AMR rates were noted for methicillin-resistant S. aureus (MRSA) (67-69%) and 3rd-generation cephalosporin-resistant Enterobacterales (57-61%). Rates for 3rd-generation cephalosporin-resistant N. gonorrhoeae (32-46%), fluoroquinolone-resistant N. gonorrhoeae (40-66%) were also high while moderate resistance was noted for carbapenem-resistant Pseudomonas aeruginosa (25-33%) and fluoroquinolone-resistant Salmonella species (12-37%) (Table 8, Figures 12 and 13). Statistics for vancomycin-resistant and intermediate Staphylococcus species and S. aureus are not included.

Table 8: AMR rate estimates for WHO priority pathogens

Pathogen	Antibiotic, class	2017				2018				2019			
		N	n (%)	95% CI	Labs* (range)	N	n (%)	95% CI	Labs* (range)	N	n (%)	95% CI	Labs* (range)
A. baumannii	Carbapenems	22	11	-	4 (3 - 10)	58	24 (41.4)	32.2-51.2	7 (1 - 29)	92	32 (34.8)	15.2-61.3	8 (1 - 30)
P. aeruginosa	Carbapenems	66	22 (33.3)	20.1-49.9	8 (1 - 26)	174	44 (25.3)	19.6-32	11 (1 - 136)	159	42 (26.4)	16.7-39.2	9 (1 - 81)
Enterobacterales	Carbapenems	946	153 (16.2)	9.2-26.9	13 (1 - 250)	1476	286 (19.4)	10-34.2	15 (1 - 420)	1 654	278 (16.8)	9.2-28.8	14 (8 - 346)
Enterobacterales	Cephalosporins (3rd generation)	2 386	1 366 (57.3)	48.7-65.3	15 (24 - 529)	3 384	2 079 (61.4)	53.6-68.7	16 (12 - 683)	3 066	1 787 (58.3)	51-65.3	16 (17 - 637)
E. faecium	Vancomycin	2	0	-	1 (2)	1	0	-	1 (1)	-	-	-	-
H. influenzae	Ampicillin	1	1	-	1 (1)	1	0	-	1 (1)	-	-	-	-
H. pylori	Clarithromycin	-	-	-	-	-	-	-	-	-	-	-	-
N. gonorrhoeae	Cephalosporins (3rd generation)	43	19 (44.2)	23.5-67.1	9 (1 - 10)	41	19 (46.3)	26.5-67.4	10 (1 - 9)	38	12 (31.6)	10.4-64.8	10 (1 - 15)
N. gonorrhoeae	Fluoroquinolones	40	16 (40)	20.5-63.3	8 (1 - 11)	32	21 (65.6)	33.2-88	9 (1 - 9)	22	10	-	9 (1 - 6)
Campylobacter species	Fluoroquinolones	1	1	-	1 (1)	-	-	-	-	-	-	-	-
Salmonella species	Fluoroquinolones	41	5 (12.2)	4.8-27.6	10 (1 - 9)	61	20 (32.8)	22.4-45.2	12 (1 - 19)	76	28 (36.8)	22.6-53.8	12 (1 - 30)
Shigella species	Fluoroquinolones	29	4	-	10 (1 - 6)	46	19 (41.3)	19.1-67.7	7 (1 - 24)	27	11	-	8 (1 - 7)
S. aureus	Methicillin	325	223 (68.6)	50-82.7	14 (2 - 73)	490	336 (68.6)	42.6-86.5	14 (1 - 107)	497	335 (67.4)	57.4-76.1	15 (3 - 166)
S. pneumoniae	Beta-lactam combinations	13	4	-	5 (1 - 6)	3	2	-	3 (1 - 1)	2	0	-	2 (1 - 1)
S. pneumoniae	Penicillins	9	7	-	4 (1 - 4)	4	2	-	3 (1 - 2)	5	1	-	4 (1 - 2)

N = number of tested isolates; n = number of non-susceptible isolates; n% and 95%CI are shown only if >30 isolates/ year; — information not available; # contributing laboratories and range of tested isolates; where the pathogen is suffixed as species, all isolates of same genus are grouped as one entity.

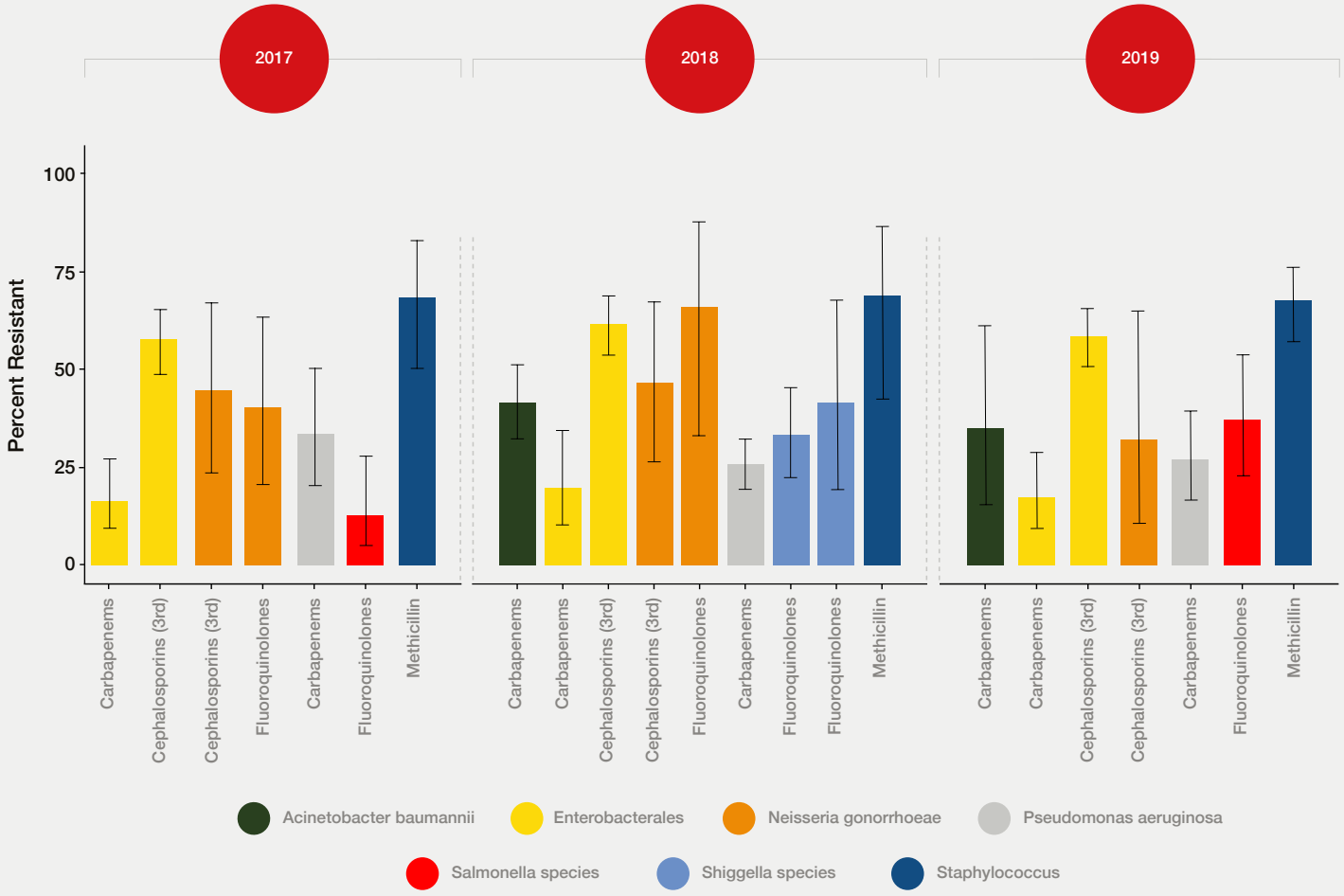


Figure 12: AMR rate estimates for WHO priority pathogens

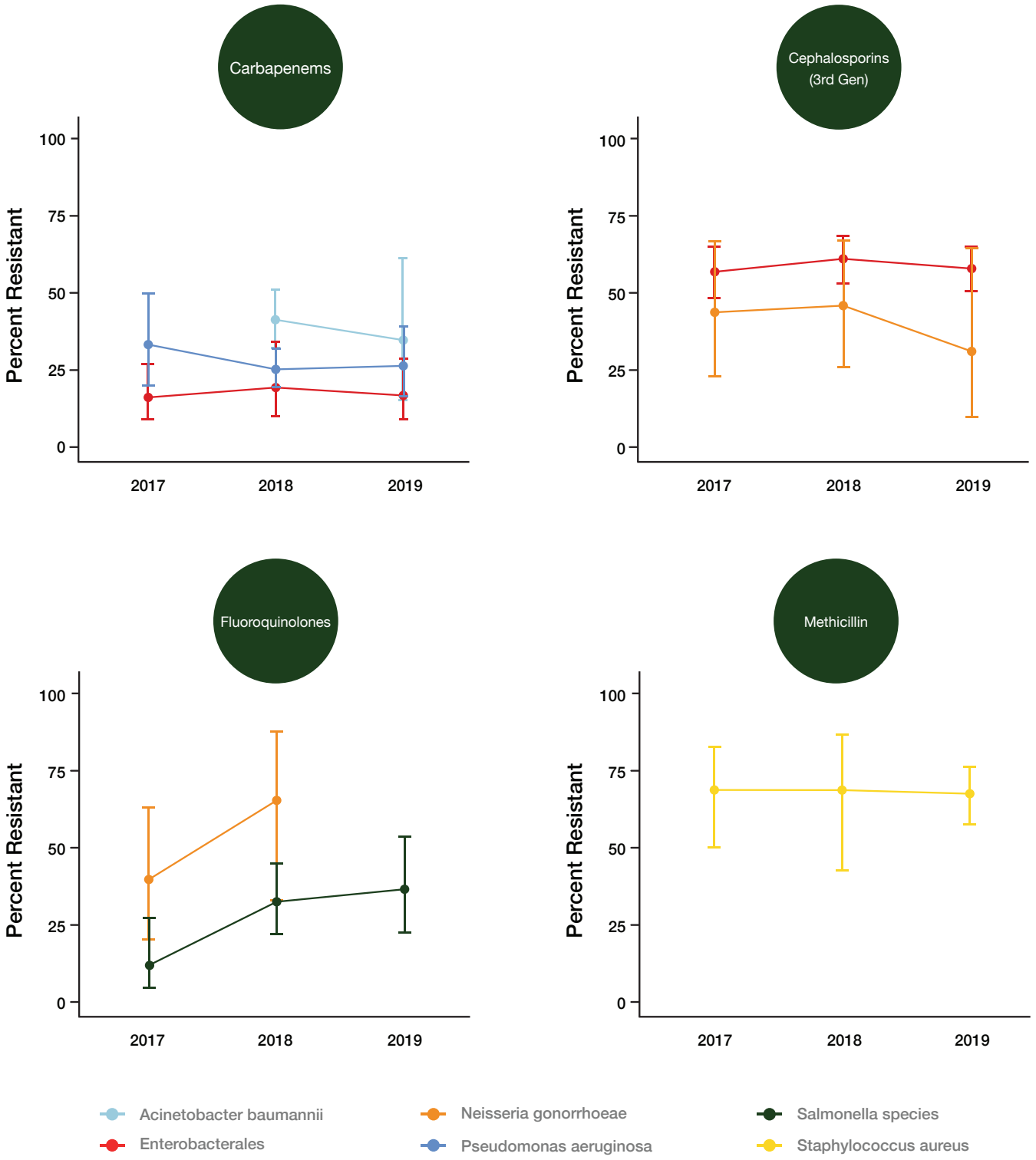


Figure 13: AMR trends for WHO priority pathogens

(ii) AMR rates for other pathogens of clinical importance

Analysis of AST data from blood and CSF isolates very high resistance rates for 3rd-generation cephalosporin-resistant Klebsiella species (76-88%) and methicillin-resistant Staphylococci species (54-72%). Resistance for carbapenem-resistant Klebsiella species was variable (8-35%) (Table 9).

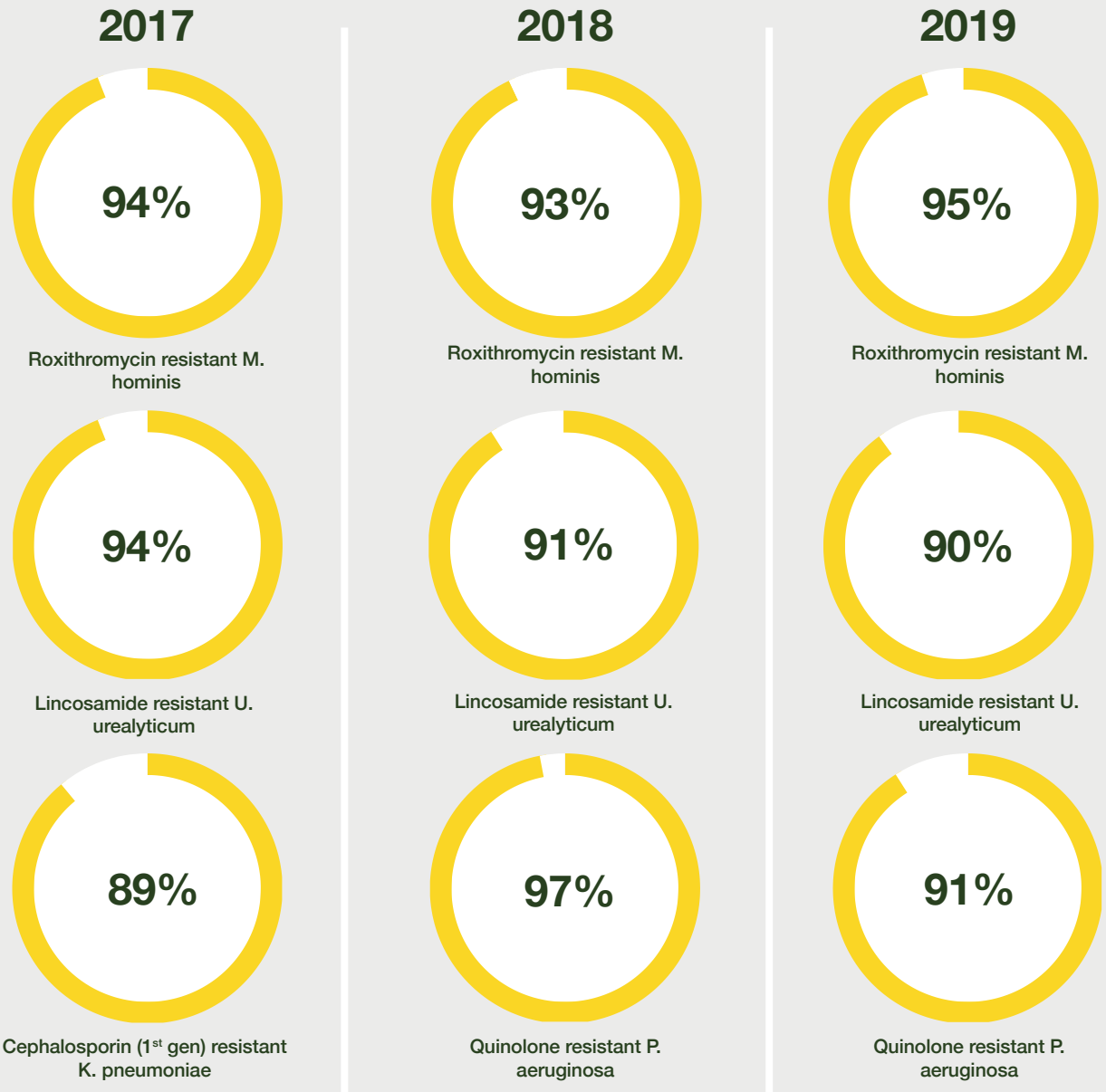
*Table 9: AMR rate estimates for other clinically important pathogens**

		2017				2018				2019			
Pathogen	Antibiotic, class	N	n (%)	95% CI	Labs# (range)	N	n (%)	95% CI	Labs# (range)	N	n (%)	95% CI	Labs# (range)
Acinetobacter species	Carbapenems	5	1	-	3 (1 - 2)	7	4	-	3 (1 - 5)	25	8	-	4 (1 - 13)
Acinetobacter species	Lipopeptides	-	-	-	-	-	-	-	-	-	-	-	-
Enterococcus species	Aminoglycosides (high level)	-	-	-	-	-	-	-	-	-	-	-	-
Enterococcus species	Vancomycin	4	0	-	2 (1 - 3)	5	0	-	1 (5)	2	0	-	2 (1 - 1)
H. influenzae	Ampicillin	-	-	-	-	1	0	-	1 (1)	-	-	-	-
H. influenzae	3rd generation cephalosporins	-	-	-	-	2	1	-	2 (1 - 1)	-	-	-	-
Klebsiella species	Carbapenems	43	15 (34.9)	14.2 - 63.5	8 (1 - 23)	69	11 (15.9)	8.8 - 27.1	9 (1 - 26)	52	4	-	2 (1 - 5)
Klebsiella species	Cephalosporins (3rd generation)	81	66 (81.5)	75 - 86.6	10 (1 - 23)	121	107 (88.4)	79 - 93.9	10 (1 - 34)	105	80 (76.2)	69.9 - 81.5	9 (1 - 44)
N. meningitidis	Ampicillin	-	-		-	-	-	-	-	-	-	-	-
N. meningitidis	Cephalosporins (3rd generation)	-	-	-	-	1	0	-	1 (1)	1	0	-	1 (1)
Pseudomonas species	Carbapenems	7	3	-	5 (1 - 2)	1	0	-	1 (1)	2	0	-	2 (1 - 1)
Pseudomonas species	Lipopeptides	-	-	-	-	-	-	-	-	-	-	-	-
Salmonella species	Fluoroquinolones	-	-	-	-	-	-	-	-	-	-	-	-
Salmonella species	Macrolides	-	-	-	-	-	-	-	-	-	-	-	-
Salmonella species	3rd generation cephalosporins	-	-	-	-	-	-	-	-	-	-	-	-
Staphylococcus aureus	Methicillin	-	-	-	-	-	-	-	-	-	-	-	-
Staphylococcus species	Methicillin	58	9 (14.8)	0.4 - 89.3	3 (1 - 50)	44	14 (31.8)	0.1- 99.5	2 (19 - 25)	29	10	-	2 (1 - 28)
S. pneumoniae	Penicillins	58	36 (62.1)		8 (1 - 45)	54	39 (72.2)	32.5 - 93.4	5 (1 - 40)	85	46 (54.1)	40.9 - 66.8	8 (1 - 71)
S. pneumoniae	Beta-lactam combinations	4	1	-	2 (1 - 3)	1	0	-	1 (1)	1	0	-	1 (1)
S. pneumoniae	Macrolides	4	2	-	2 (1 - 3)	-	-	-	-	3	1	-	2 (1 - 2)
S. pneumoniae	Vancomycin	3	2	-	2 (1 - 2)	1	0	-	1 (1)	2	1	-	2 (1 - 1)

* From blood and CSF; N = number of tested isolates; n = number of non-susceptible isolates; %n and %CI are shown only if >30 isolates/year; # contributing laboratories and range of tested isolates; — information not available; where the pathogen is suffixed as species, all isolates of same genus are grouped as one entity.

(iii) AMR rates for highly resistant pathogens

Based on available data, very high resistance (>95%) was estimated for clinically important pathogens like P. aeruginosa (vs. quinolones) and Mycoplasma hominis (vs. roxithromycin) (Figure 14).



Pathogen nomenclature is shown as reported by laboratories; antimicrobials are reported at class level
Figure 14: Top five highly resistant pathogens

(iv) AMR rates for fungal pathogens

Available AST data on fungal isolates was insufficient for further analysis.

Section IV: Drivers of antimicrobial resistance

Objective

To assess the drivers of AMR

Methodology

AMR drivers are factors that could predispose patients to AMR. To determine the association between AMR and its potential drivers, the following patient and country-level factors were considered:

- Patient-level factors: demographics (age and gender), diagnosis, comorbidities, antimicrobial usage, presence of device (catheter, central line or ventilator) and origin of infection (hospital or community)
- Country-level factors: Global Health Security index scores on AMR prevention, primary education, GDP per capita, physician and nurse density, disease prevalence and antibiotic consumption in defined daily dose (DDD) per 1 000 inhabitants (the country-level associations are presented separately at a regional or continental level)

To identify the drivers of resistance, a composite AMR rate for select groups of pathogens (Acinetobacter baumannii, Escherichia coli, Klebsiella pneumoniae, P. aeruginosa, S. aureus, Enterococcus faecium and Enterococcus faecalis) and antibiotics or antibiotic classes (aminoglycosides, broad-spectrum penicillins, carbapenems, cephalosporins, glycopeptides, narrow spectrum penicillins and quinolones) was estimated (AMR Appendix 8). The choice of pathogens and antimicrobials was guided by the DRI methodology (Part C).

Statistical analysis

An initial exploration of the data was done to identify missing information and any collinearity between the patient-level factors (drivers). Logistic regression analyses (univariate and multiple) were performed to determine the association with AMR. The analyses were adjusted for the number of contributing laboratories to account for the variation in the respective laboratory datasets. Crude odds ratios (ORs) were estimated in the univariate logistic regression analysis to describe the association between AMR and the investigated variables. Only those variables with $p<0.2$ were evaluated in a multiple logistic regression analysis (statistical significance was set at $p<0.05$). The Wilson score method with robust standard error was used to construct CIs for the AMR rates.

To explore the association between country factors (continuous variables) and AMR, correlation analysis (Pearson's) was performed with reporting at a continental level.

All results should be interpreted with caution as they were derived from data aggregated from facilities with varying capabilities in addition to the data from the laboratories being varied.

Results

Two variables namely, age and gender, were evaluated for possible association with AMR. The data availability for these variables was age: 90.3% and gender: 94.6%. The univariate logistic regression results showed that patients in the following age groups: 50 – 65 years (OR 1.30, 95% CI 1.15 – 1.45) and >65 years (OR 1.23, 95% CI 1.12 – 1.36) were more likely to have resistant infections. In addition, males were more likely to have resistant infections (OR 1.26, 95% CI 1.17 – 1.35) (Supplementary Table 7).

Gender and age were included in the multiple logistic regression model based on the defined inclusion criteria. When controlling for the effect of age, males were more likely to have resistant infections (OR 1.24, 95% CI 1.15 – 1.34). Similarly, when controlling for the effect of gender, patients aged 50 – 65 years (OR 1.26, 95% CI 1.12 – 1.41) and >65 years (OR 1.17, 95% CI 1.06 – 1.28) were more likely to have resistant infections (Table 10).

Table 10: Multiple logistic regression analysis

Variable	Options	N	NS (%)	Adjusted OR (95% CI)	P-value
Gender	Female	15 074	51.6	**Ref**	
	Male	10 031	57.3	**1.24 (1.15 - 1.34)**	0.0000
Age	<1	3 360	52.3	0.95 (0.82 - 1.11)	0.549
	1-17	3 037	51.6	0.94 (0.83 - 1.07)	0.361
	18-49	11 502	52.2	**Ref**	
	50-65	4 157	58.7	**1.26 (1.12 - 1.41)**	0.000
	>65	3 049	57.4	**1.17 (1.06 - 1.28)**	0.001

N=number of tested isolates; NS (%)=proportion of non-susceptible isolates.

Information on other patient factors was unavailable or inadequate for analysis.

Part B: Antimicrobial (antibiotic) Consumption

Section I: Background of antimicrobial consumption (AMC) and antimicrobial use (AMU)

Overuse and misuse of antimicrobials are crucial factors in the complex web of AMR causation. Widespread and unregulated antimicrobials usage exert a selective pressure by reducing the reproductive success of some of the microorganisms and consequently accelerating the development of AMR.[20,21] Therefore, close surveillance on how antimicrobials are utilised is a key step for stewardship programmes in order to stem AMR. The surveillance mechanisms recommended by WHO include the monitoring of AMC and AMU. This aligns with MAAP's aim to expand the volume of data presently available on AMR and AMC or AMU across Africa and the country's (2018-2020) National Action Plan to combat AMR.[22]

Definition of AMC and AMU

AMC is defined as the quantification of antimicrobials used within a specified setting (e.g., national-level, hospital or community healthcare level) over a specified period. AMC is calculated from aggregated data, such as import, wholesalers, insurance, or facility dispensing or procurement data sources, while AMU tracks whether antimicrobials are prescribed appropriately, for the right infections and according to treatment guidelines. AMC and AMU are terminologies that are sometimes used interchangeably and incorrectly so. It is therefore prudent to delineate these definitions further through clarification that AMC data describe quantities of antimicrobials dispensed (e.g., at national stores or pharmacies) whereas AMU data describe how and why antimicrobials are used (e.g., if required laboratory tests and clinical assessments were conducted prior to issuing a prescription, whether the right antimicrobial was prescribed at the correct strength and frequency over an appropriate duration to treat the right indication as per country guidelines and finally, whether the patient correctly and/or completely consumed the prescribed antimicrobial).[23]

Link between the antimicrobial usage and AMR

The unwarranted use of antimicrobials contributes to the emergence of AMR. This association implies that a reduction in the unnecessary consumption of antimicrobials could in turn reduce AMR levels.[20] The inappropriate use of antimicrobials refers to the use of the wrong type of antimicrobial, and/or at the wrong dose, frequencies, or duration and/or for the wrong indication. For the past few decades, there has been a global increase in the consumption of antimicrobials and a shift in consumption towards the use of both broad-spectrum and last-resort antimicrobials, particularly in LMICs. These shifts are because of improved access and increased economic strength within some of these countries. However, AMR can also develop as a result of a lack of access to antimicrobials, leading to the prolonged use of a particular antimicrobial over a long time and thus permitting selective pressure to favour microbes that evade these predominantly used antimicrobials. This is often the picture in a number of LMICs where inequities in access to antimicrobials still persist.[24] This complicated picture demonstrates the need for the research and development of new agents that counteract emerging AMR, but also strongly indicates the need to use the available antimicrobials appropriately and ensure their accessibility.

In view of obtaining an elaborate and complete picture of the link between AMC or AMU and AMR in Cameroon, the identification of prevalent gaps, as well as areas for targeted intervention to encourage rational use of antimicrobials and a surveillance system for consumption, is of paramount importance. In this regard, one of MAAP's key objectives was to evaluate the ability to conduct AMC and AMU surveillance (data collection and analysis) in Cameroon that would equip the country with valuable information to support the appropriate use of antimicrobials. The objective was to identify gaps that may exist in establishing a comprehensive surveillance system and provide the country with the needed information to support the setup of such a monitoring system.

AMC and AMU surveillance impact

To ensure the successful treatment of infectious diseases in patients, optimising the correct usage of antimicrobials is one of the strategic objectives within the WHO Global Action Plan (GAP).[8] For the successful implementation of the above objective, there is a need to understand a country's pattern of antimicrobials use and quantification of their consumption. At present, there are only a few published reports on AMC surveillance and AMU in Africa,[25-29] with no reports found on AMU from Cameroon. The process of obtaining AMC or AMU data equips the country with the local information on various problems that exist with antimicrobial use and allows for monitoring the accessibility of antimicrobials. Furthermore, obtaining of AMC or AMU data permits the continuous local assessment of correlations between antimicrobial usage to emerging local AMR, which permits for proper mitigation policies and activities to be planned for using relevant data. Data obtained from local surveillance exercises also present the opportunity to better inform stewardship programmes.

Therefore, MAAP set out to quantify consumption and analyse AMC and AMU trends at selected facilities as well as at the national level, in order to better inform the design of future stewardship programmes and policies which will optimise the use of antimicrobials in Cameroon. In addition, this will provide the country with a reference point to measure the impact and success of future implemented interventions.

The aim of this work

1. To describe the in-country antimicrobial flow in-country and highlight the status of the AMC and AMU surveillance system in Cameroon

2. To quantify and evaluate the trends of AMC and AMU at national and pharmacy level

Section II: AMC or AMU surveillance status

Objective

To describe the in-country antimicrobial flow and highlight the status of the AMC and AMU surveillance system in Cameroon

Methodology

AMC and AMU data sources

Through open-structured key informant interviews (KIIs) (AMC Appendix 1), the AMRCC contacts shared their insights about the current landscape of AMC surveillance in the country as well as from where national data can best be surveilled. From this, the Centre for the Procurement and Supply of Essential Medicines (CENAME) mechanism for public sector procurement and the IQVIA™ dataset include data from the private sector (by means of for-profit wholesalers' or distributors' supply records which were identified as potential sources for national AMC data in Cameroon). As the approval letters from the AMRCC or MoH were issued for the years (2017-2019), MAAP's data collection period was redefined to the years 2017-2019.

Under the guidance of Cameroon's AMRCC, MAAP targeted to recruit and obtain data from twice as many pharmacies as the selected AST laboratories (i.e., a total of 32 pharmacies). Pharmacy-level AMC data were targeted to be collected from the pharmacies that were co-located in the same facility with AST laboratories (n=16) (AMC Appendix 2). Additionally, community pharmacies (n=16) were also targeted for recruitment. These pharmacies were nominated by the co-located pharmacies based on their proximity to the AST laboratories. Selection was also based on these community pharmacies serving as the preferred patient medicine purchase sites or backup prescription fulfilment sources in case of stockouts in the main hospital pharmacy. Furthermore, availability of retrospective data from 2017-2019 and willingness to data sharing were key criteria considered for selection.

Besides AMC data collection AMU data were targeted for collection from hospital pharmacies (n=16) and this was to be abstracted from the facilities' prescription or patient medical records. To clarify, community pharmacies, also known as retail pharmacies, are licensed commercial pharmaceutical stores that retail medicinal products (prescription only and over-the-counter medicines) to a specific community group or region and excludes unregulated and informal medicine dispensers. Hospital pharmacies, on the other hand, are the pharmacies located within a hospital for the provision of supply of medicinal products to inpatients and outpatients who visit the hospital.

Data collection scope

MAAP purposively selected to collect data on J01 (antibiotics for systemic use) consumption trends. J01 medicines are one of the WHO core monitoring Anatomical Therapeutic Chemical (ATC) medicine categories for AMC surveillance. In addition, as per the country's request, selected P01AB (Nitroimidazole derivates) and/or selected J02 (Antimycotics for systemic use) were also included in the scope for AMC data collection (See AMC Appendix 3 for full list of selected antimicrobials in Cameroon). P01AB and J02 ATC antimicrobials are part of the WHO core and optional monitored medicine classes respectively for AMC surveillance.[30] AMC data from the above medicine categories was collected from January 2017 to December 2019.

Data collection

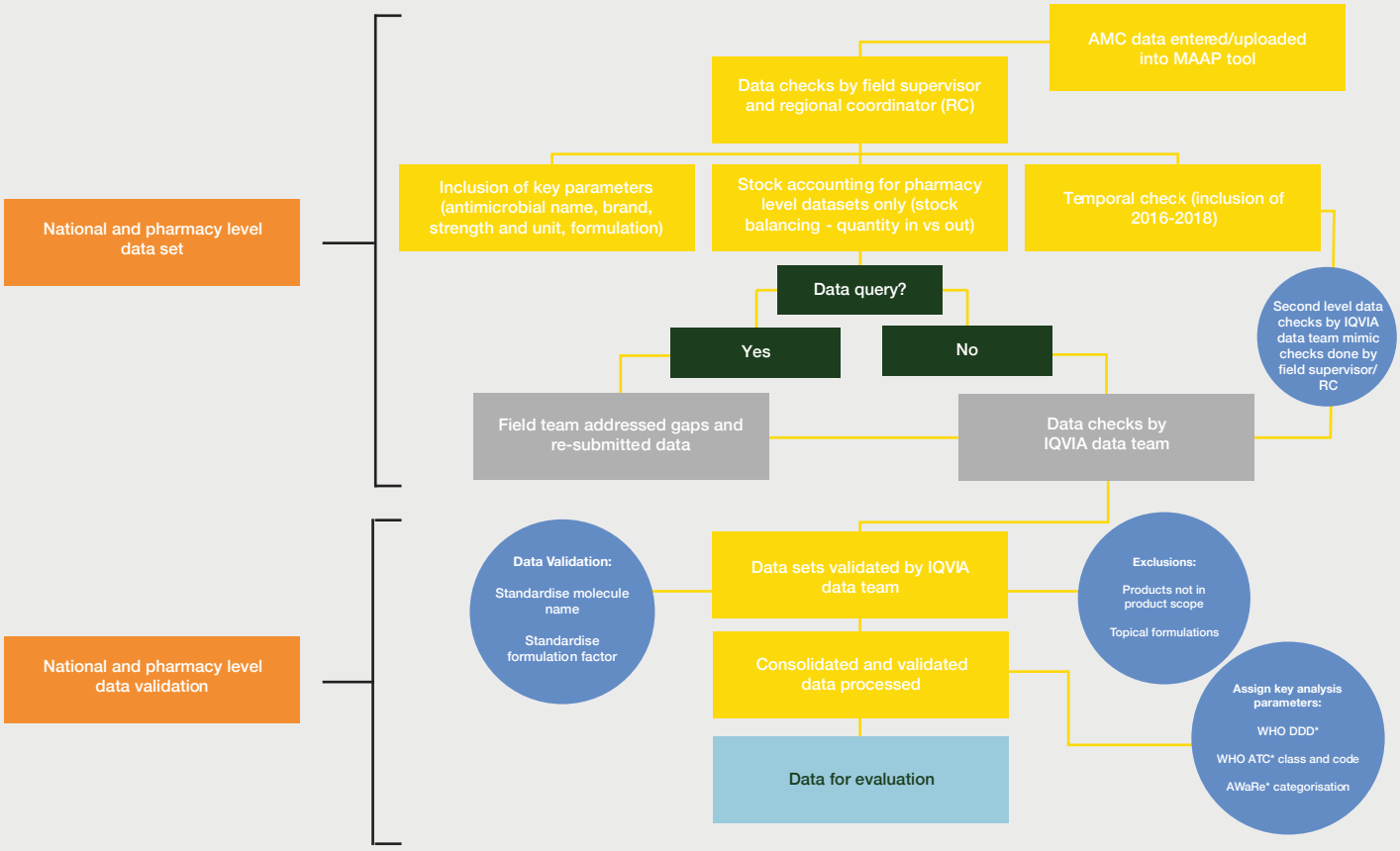
The national-level datasets from CENAME and syndicated IQVIA™ datasets were requested for the data collection period (2017-2019) from CENAME staff and the IQVIA™ regional syndicated data team, respectively. The datasets were provided to the field supervisor in the form of a Microsoft Excel™ sheet. The data collection team reviewed and cleaned the datasets in an Excel™ sheet which was then transferred securely through the MAAP tool that captured all medicines by their standard molecular name and/or product brand, pack size, strength and formulation (e.g., tablets or capsules, suspensions or syrups) (AMC Appendix 4 captures the full list of data variables collected in order to tally national- and pharmacy-level AMC).

For the pharmacy-level data, the trained MAAP data collectors extracted the consumption data from the facility's Health Information System (HIS) into an Excel™ sheet where data were available electronically. Alternatively, abstracted data from stock record cards were manually entered into the MAAP tool within facilities that held manual records. The electronic datasets were reviewed and cleaned by the data teams and then transferred securely through the MAAP tool to the central data processing and analysis team. (AMC Appendix 5 details the data collection process).

MAAP also planned to collect the AMU data in pharmacies that were co-located within the facilities also housing AST laboratories and clinical services in order to assess the appropriateness of consumed antimicrobials. Data to be captured included patient characteristics and medical condition for which the antimicrobial is being used and the appropriateness of the prescription in relation to national guidelines (including conducting of any relevant laboratory testing and clinical assessment done prior to prescribing, assessment of dose, strength, frequency and duration of prescription).

Data cleaning and validation

The national-level AMC datasets were categorised in this report as generally representing the private sector or public sector if they were sourced from IQVIA™ syndicated datasets or CENAME, respectively. Once the datasets were received by MAAP, both the national- and pharmacy-level AMC data were then subjected to a series of data validation checks to ensure accuracy and consistency (Data checks and the validation process for national AMC data are detailed in Appendix 6). Here, the pharmacy and national AMC data were subjected to secondary and tertiary checks by field supervisors, regional coordinators and the IQVIA data team, as outlined in Figure 15.



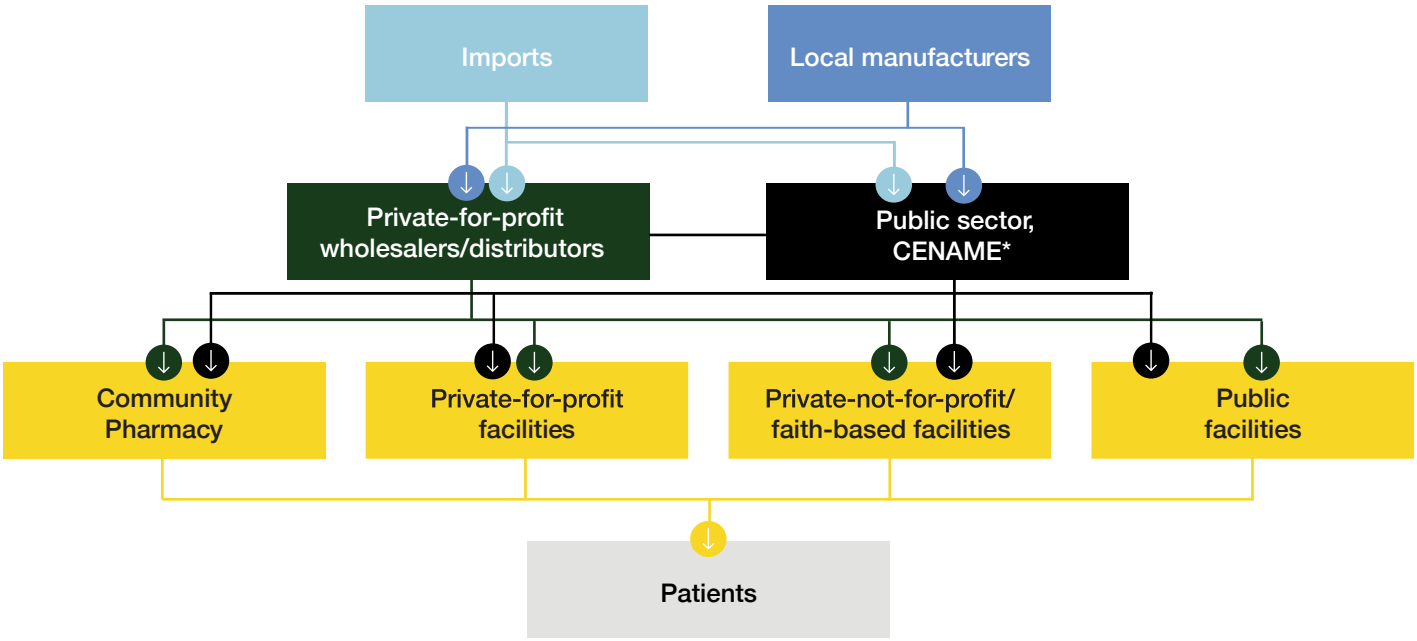
*DDD Defined Daily Dose *ATC - Anatomical Therapeutic Chemical * AWaRe Access, Watch and Reserve

Figure 15: Flow chart explains the data checks procedures and validation process for both the national and pharmacy level AMC data collected in Cameroon

Results

Flow of antimicrobials in the country

To characterise the pathway through which antimicrobials get to the patients in the country, a total of three KIIs (AMC Appendix 1) were conducted with stakeholders in the national AMRCC, Directorate of the Department of Pharmacy Laboratory and Medicine (DPLM) and the Directorate of the CENAME. DPLM regulates all importation of medicines as well as conditions for medicines manufacturing and retailing. Additionally, it acts as the pharmaceutical licensing agency of the country. There were two local medicine manufacturers in the country during the reviewed period (i.e., 2017-2019). In Cameroon, the majority of medicines including antimicrobials are purchased through imports which are managed by DPLM. The proportion of antimicrobials purchased by public health institutions accounts for 70% of the CENAME antimicrobial stocks. The private sector is mainly supplied by private central purchasing agencies and accounts for approximately 40% of the antimicrobials consumed in Cameroon. After purchase, private for-profit wholesalers or distributors, and the public sector. CENAME then passes along the antimicrobials to the community pharmacies, private (both for-profit and non-profit) facilities and public facilities who eventually issue antimicrobials to patients. The flow chart below (Figure 16) illustrates the route through which antimicrobials get to patients in Cameroon.



*JMS: Joint Mecial Store; **NMS: National Medical Store

Figure 16: Flow chart explaining the circulation of antimicrobials within the country to the patients in Cameroon. A dotted line indicates supplies are not mainstream

Regulation of antimicrobials consumption

In Cameroon, the antimicrobials for human consumption are regulated under the Cameroon National Pharmaceutical Policy, 2013.[12] This law stipulates that the antibiotics can only be dispensed upon issuance of a valid prescription and that only authorised structures have the right to dispense the antibiotics. Overuse and misuse of antimicrobials are significant contributors towards the emergence of AMR. Therefore, in an attempt to address the aforementioned and other gaps, the country developed a national action plan on antimicrobial resistance since hosting the first West Africa National Action Plan (NAP) workshop in 2017 to strengthen AMR regulations and curb the growth or emergence of AMR.

Availability of data for AMU surveillance

Attempts were made to obtain AMU data from the participating pharmacies that were co-located in the AST laboratories that also offered clinical services (n=11). Unfortunately, no AMU data was obtained during MAAP data collection. This inability to collect AMU data was due to the nature of the data sources at the participating pharmacies (i.e., stock issuance record cards) which did not allow for the retrieval of AMU variables (i.e., patient characteristics and indication for which the antimicrobial is being used, appropriateness of prescription in relation to national guidelines including conducting of any relevant laboratory testing and clinical assessment done prior to prescribing, and assessment of dose, strength, frequency and duration of prescription) as stock issuance records do not track the medicines issued to specific patients. As a result, MAAP was unable to collect AMU data in Cameroon from the selected health facilities.

National-level data

National AMC data were obtained from CENAME and syndicated IQVIA ™ Cameroon datasets for the reviewed period (2017 to 2019). The resultant national AMC data collected and analysed represented approximately 100% of the total antimicrobials market during the reviewed period (2017-2019). Both the national-level AMC data sources had all the variables required to conduct AMC analysis (including date of transaction, antibiotic name, pack size, strength and formulation (e.g., tablets or capsules, suspensions or syrups and/or injections). MAAP was able to collect CENAME and syndicated IQVIA ™ Cameroon datasets from January 2017 – December 2019 as planned within the scope of the study.

Facility-level data

Pharmacy data collection was successfully conducted in 11 pharmacies out of 32 targeted pharmacies including only hospital pharmacies (n=11). Out of the 16 targeted hospital pharmacies co-located in the same facility with AST laboratories, data collection was successfully conducted in only (n=11) targeted hospital pharmacies. Three were excluded due to being stand-alone laboratories (i.e., without a co-located hospital pharmacy) and a further (n=2) were excluded due to the unavailability of data for the study period. All of the (n=11) participating hospital pharmacies that were co-located with the AST laboratories were located within public government hospitals. Of these public hospital-based pharmacies, (n=1) was in a primary care facility while (n=3) were in secondary care facilities and the remaining (n=7) pharmacies were located in tertiary care facilities. Unfortunately, MAAP was unable to receive data from any of the targeted community pharmacies (n=16) due to their unwillingness to share data, despite obtaining and sharing a letter of introduction from the Directorate of Pharmacy and Medicine. As the total number of hospital or community pharmacies in Cameroon could not be established, data representativeness at facility level could not be assessed.

In the case of pharmacy-level data, necessary variables were available in the stock cards or electronic records of 11 pharmacies where the data were collected. However, there were instances in each of the visited facilities wherein the strength or pack size information for few line items or transactions were missing from the stock cards. These information gaps were addressed by re-visiting the facilities and gathering information from the facility staff or through secondary desk research using the available product details. Of the 11 hospital pharmacies, MAAP was able to collect data across the three years in seven pharmacies whereas three visited pharmacies shared 2018 and 2019 data, and one pharmacy shared only 2019 data due to data archival challenges.

Furthermore, due to the lack of any national AMC surveillance policy and reporting requirement during the reviewed period, it was observed that none of the recruited pharmacies actively reported AMC data regionally or centrally. Table 11 below summaries the core characteristics of the hospital pharmacies from which AMC data was collected.

Table 11: Characteristics of the recruited hospital pharmacies adjoined with the antimicrobial susceptibility testing (AST) laboratories in Cameroon.

	Pharmacy Name	Level of Service#	Affiliation	Region	Record keeping*	Pharmacy system directly linked to patient records *†	AMC reporting*
Hospital Pharmacies (co-located with AST laboratories)	Centre Hospitalier et Universitaire de Yaoundé	Tertiary	Public	Centre	*Mixed	No	No
	Hôpital de la CNPS de Yaoundé	Tertiary	Public	Centre	*Mixed	No	No
	Hôpital General de Yaoundé	Tertiary	Public	Centre	Manual	No	No
	Hôpital Gynéco-Obstétrique et Pédiatrique de Yaoundé	Tertiary	Public	Centre	Manual	No	No
	Hôpital General de Douala	Tertiary	Public	Littoral	*Mixed	No	No
	Hôpital Laquintinie de Douala	Tertiary	Public	Littoral	*Mixed	No	No
	Hôpital Gynéco-Obstétrique et Pédiatrique de Douala	Tertiary	Public	Littoral	*Mixed	No	No
	Hôpital de District de Bonassama	Primary	Public	Littoral	Manual	No	No
	Limbe Regional Hospital	Secondary	Public	South-West	Manual	No	No
	Buea Regional Hospital	Secondary	Public	South-West	Manual	No	No
	Hôpital de la CNPS de Maroua	Secondary	Public	Far-North	Manual	No	No

#Primary care describes district level hospital facilities, secondary care describes regional level hospitals located within the ten regions in Cameroon, while tertiary care describes referral hospital units providing complex care management services NB: referral units are mainly located in the capital city and economic centre.

*Mixed recording keeping refers to pharmacy dispensing and recording systems that exist partially in an electronical form and partially in a manual form. **For the review period i.e., 2017-2019. AMC: Antimicrobial consumption. † Refers to ability for pharmacy to link dispensing records with the patient's hospital records to obtain patient diagnostic and characteristic information.

Section III: AMC or AMU analysis trends over time at national and pharmacy levels

Objective

To quantify and evaluate the trends of AMC and AMU at national and pharmacy levels

Methodology

Statistical analysis

Data analysis for MAAP was conducted according to WHO's protocol for conducting AMC analysis using the DDD-ATC-AWaRe methodology.30-32 Figure 17 provides a high-level summary of the AMC analysis that was conducted. Each of these WHO methodologies are described below as well as the additional analysis conducted. In addition, and where possible, associations were drawn between AMC and AMR. Details of this analysis can be found in Part A, Section II:3c.

i. Defined Daily Dose (DDD)

DDDs or related metrics are utilised to study AMC analysis. Considering different doses (in milligram) for each antibiotic for managing infections, the DDD metric helps in standardising for easy comparison. Additionally, it is recommended to use drug utilisation figures such as DDD using a relevant denominator for the health context e.g., DDDs/1000 inhabitants/day, DDD/ inhabitant/year or as DDDs/100 bed days. Studying DDDs or associated metrics over time helps to understand the consumption pattern or determine whether any national- or facility-level interventions have led to a change (+/-) in the consumption patterns over the study period or a pre-defined base period.

Using the WHO 2020 DDD guide, the total DDDs were the quotient of the total consumed milligrams per antimicrobial divided by the standard DDD value issued by WHO to obtain total DDDs.[3] The total DDDs were then adjusted for the country population size with respect to the year of data collection 2017, 2018 and 2019,[34] and presented as DDDs/1000 inhabitants/day (DID). Pharmacy-level AMC data was to be adjusted as DDD per the number of inpatients and presented as DDD/100 patient bed days. However, the use of WHO DDD per 100 patient bed days presented limitations at the point of analysis as patient bed days were not an appropriate denominator to use across the pharmacy-level AMC datasets. In addition, for most of the hospital facilities, patient bed days and patient days information were not easily accessible. Secondly, this metric would not allow for comparison between hospital pharmacy consumption and community pharmacy consumption, as in the latter, the patient bed days metric is not applicable. Therefore, the pharmacy-level AMC data are presented as absolute DDD to aid comparison between the hospital and community pharmacies. Detailed DDD calculations can be found in AMC Appendix 7. All calculations were conducted in Excel ™.

ii. Anatomic Therapeutic Chemical (ATC) Classification

Using the standard list of antimicrobial names, data collected was coded in the Excel TM analysis database in accordance with the 2020 WHO ATC codes and then analysed to characterise the macro (above-molecule) AMC trends. The description of ATC codes is presented in AMC Appendix 7. In addition, an attempt was made to conduct statistical testing to see the year-on-year differences within each ATC class, however, this was not possible as some of the datasets were missing core components for analysis i.e., month of transaction.

iii. WHO Access, Watch and Reserve (AWaRe)

The WHO AWaRe categorisation classifies antibiotics under the 'Access', 'Watch' and 'Reserve' groups. 'Access' includes antibiotics of choice for the 25 most common infections and should be affordable and available at all times as well as the quality assured in the country or facilities. 'Watch' antibiotics are those indicated for only specific and limited infective syndromes (since they are prone to be a target of antibiotic resistance). Hence, their use is controlled via stewardship programmes and monitoring. Lastly, 'Reserve' antibiotics are considered as a "last resort" treatment option. They are indicated in case of life-threatening infections due to multi-drug resistance (closely monitored and prioritised in stewardship programmes to ensure their continued effectiveness).

Through WHO AWaRe analysis, the total AMC by DDDs per antibiotic molecule were labelled as either 'Access', 'Watch' or 'Reserve' in accordance with the 2019 WHO AWaRe list in Excel ™. Total DDDs per WHO AWaRe category were then analysed to determine the proportion of AMC per category and over time i.e., yearly and monthly (where possible). WHO recommends that at least 60% of a country's total AMC should come from the 'Access' category of antibiotics. Finally, an analysis was conducted to identify the top five antibiotics consumed in each WHO AWaRe category.

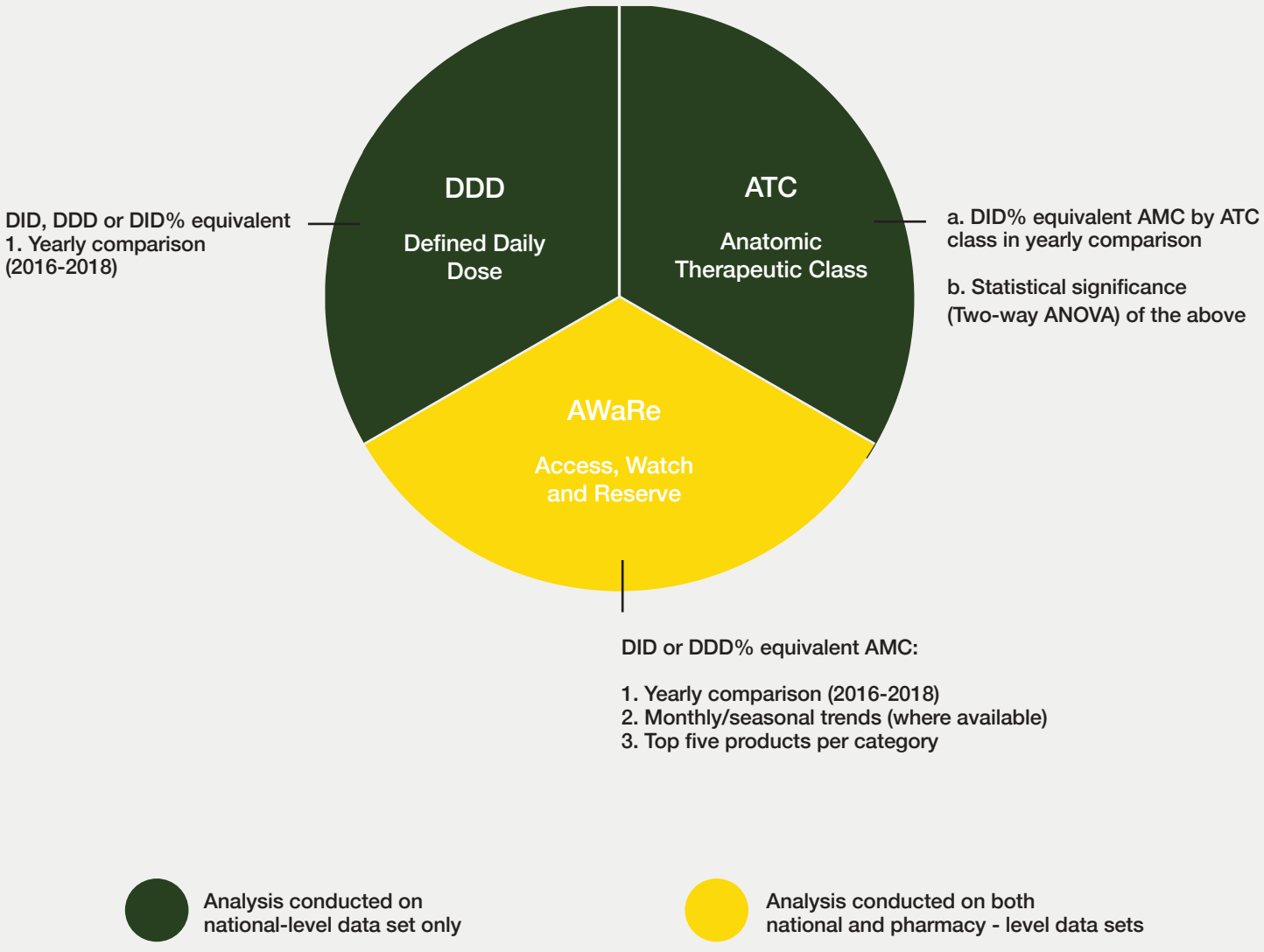


Figure 17: Methods and indicators used for the analysis of the data collected in Cameroon. Defined Daily Dose (DDD) indicators utilised for volume metric standardisation was sourced from WHOCC 2020, ATC Classification utilised to categorise the antibiotics according to the organ or system on which they act, and their therapeutic, pharmacological and chemical properties sourced from WHOCCC ATC database, and Access, Watch and Reserved categorisation was sourced from 2019 WHO AWaRe classification [32]

iv. Review of Essential Medicines List (EML)

According to the WHO, essential medicines are those that satisfy the priority healthcare needs of a population. They are selected with regard to disease prevalence and public health relevance, evidence of efficacy and safety and comparative cost-effectiveness. They are intended to always be available in functioning health systems, in appropriate dosage forms, of assured quality and at prices individuals and health systems can afford. A document analysis was conducted in which the antimicrobials listed in the WHO EML were compared with the antimicrobials listed in the Cameroon EML and against the documented antimicrobials from the national- and pharmacy-level data collection. The comparison was conducted using WHO defined AWaRe categories.

Results

National AMC datasets analysed by DDD per year

The average total in-country AMC between 2017 and 2019 was 5.1 DDD per 1 000 inhabitants per day (DID). A 28% decrease in total consumption of antimicrobials from the year 2017 to 2018 was documented and no difference in consumption from 2018 to 2019 observed (Figure 18). The decrease in overall AMC from 2017 to 2019 was driven by a notable decrease in public sector medicine consumption from 2.9 to 1.0 DID. Further disaggregation of the national AMC data across the two sectors i.e., public sector (CENAME) and private sector (IQVIA ™ syndicated datasets) found that on average, the public sector accounted for 31.1% of national AMC while the private sector accounted for the remainder (68.9%).

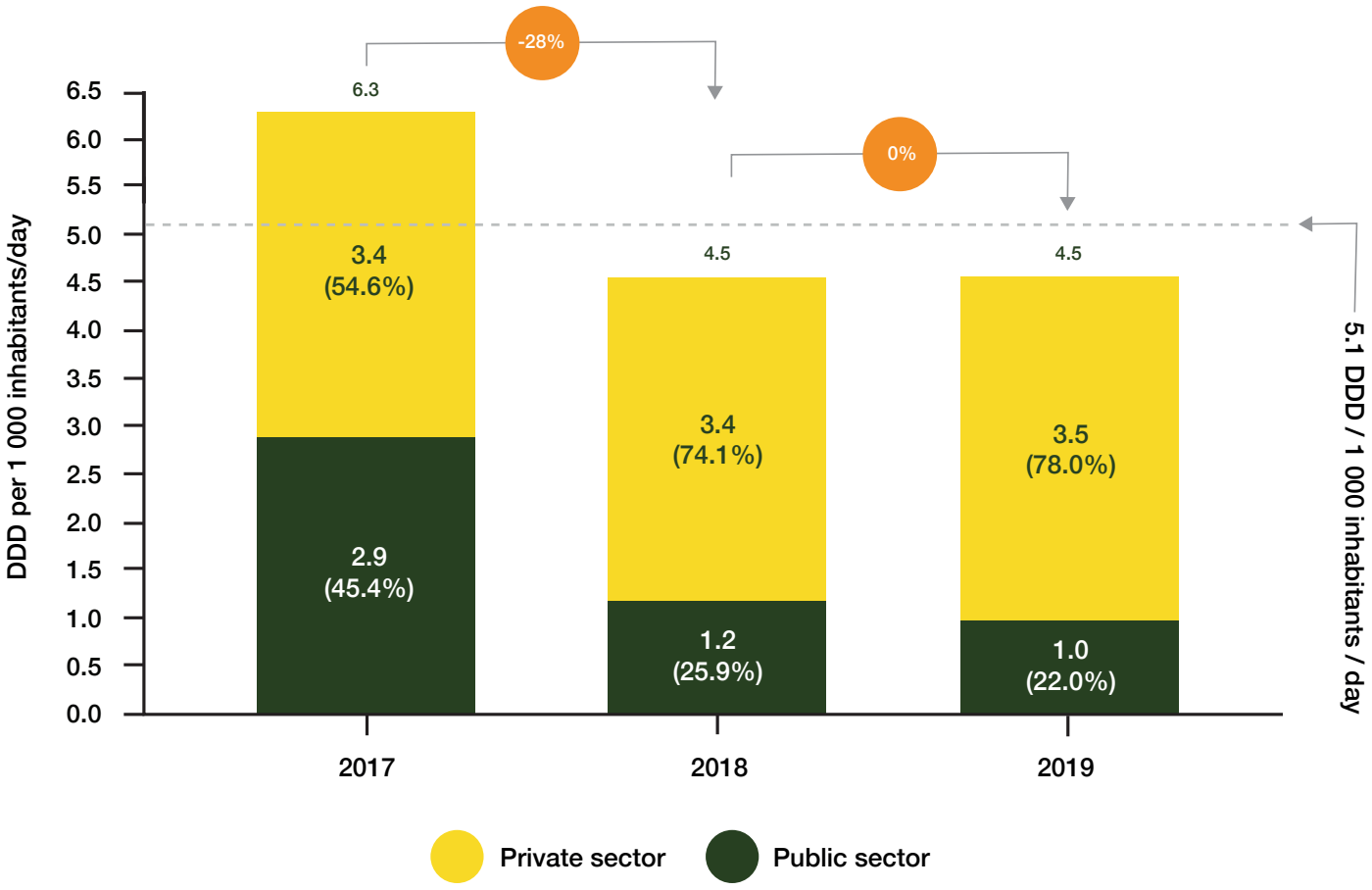


Figure 18: Bar graphs represents the total DID and percentage variation from the year 2017 to 2019 for the national level AMC data analysed in Cameroon. It further describes the disaggregation of consumption of antimicrobials across the public (represented in green) and private sectors (represented in yellow) in Cameroon, as total DID and percentage share of total consumption for each year (2017 to 2019)

National AMC analysed by ATC classification

Combinations of sulfonamides and trimethoprim, including derivatives (J01EE), were the most frequently consumed ATC class in Cameroon overall for the review period at 46.5% in 2017, 15.2% in 2018 and 16.1% in 2019 (Figure 19). However, combinations of penicillins, including beta lactamase inhibitors (J01CA) demonstrated a higher consumption when compared to combinations of sulfonamides and trimethoprim, including derivatives for the year 2019 at 18.1%. In addition, across the reviewed period, combinations of penicillins including beta lactamase inhibitors and tetracyclines (J01AA), were the second- and third-leading ATC classes overall, with the combination of amoxicillin/clavulanic acid and doxycycline leading the consumption within these ATC classes, respectively. The top five most consumed antimicrobials were sulfamethoxazole/trimethoprim, amoxicillin/clavulanic acid, doxycycline, amoxicillin and fluconazole. Together, they accounted for 68% of total consumption share. A detailed list of national AMC by antimicrobial molecule and by ATC class are mentioned in AMC Appendix 8 and AMC Appendix 9, respectively.

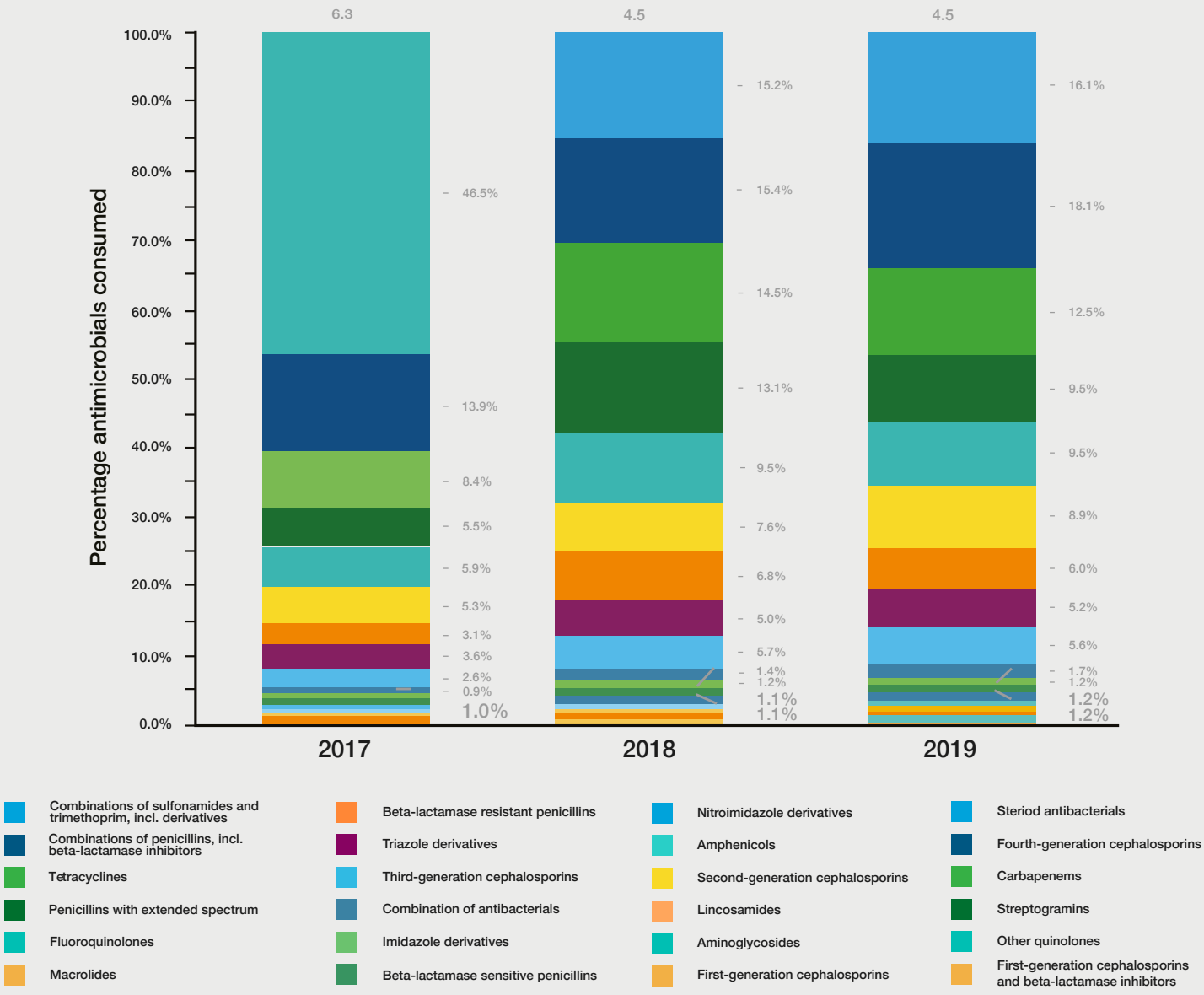


Figure 19: Results of national level AMC data analysed in Cameroon are presented by the total DID and percentage of antimicrobials consumed by ATC classes from the years 2017 to 2019. Penicillins with extended spectrum class of molecules were the highest consumed antimicrobials across all the reviewed years 2017, 2018 & 2019. Statistical testing was not carried out due to the nature of the data obtained. See Appendix 9 for a more detailed breakdown of AMC by ATC classes

National and pharmacy AMC analysed by WHO AwaRe categorization

The average national consumption of antibiotics across the three years analysed was 76.4% 'Access', 23.6% 'Watch' and 0.0% 'Reserve'. Annual AMC trends indicated a decrease of 2.0% in the consumption share of 'Access' category antibiotics between 2017 and 2018 and an increase of 12.6% between 2018 and 2019. This is against a corresponding proportional increase 2.0% in the consumption share of 'Watch' category antibiotics between 2017 and 2018, that was followed by a decrease of 12.6% between 2018 and 2019 (Figure 20). Both the overall (for three years) and within-each-year consumption of 'Access' category antibiotics in Cameroon exceeded the 60% minimum consumption threshold set by WHO. There were no stocks of 'Reserve' group antibiotics supplied in Cameroon during the reviewed period. This analysis of national AMC by WHO AWaRe categories omits 7.8% (0.4 DID) of total AMC that is not categorised within the WHO AWaRe list of 2019.

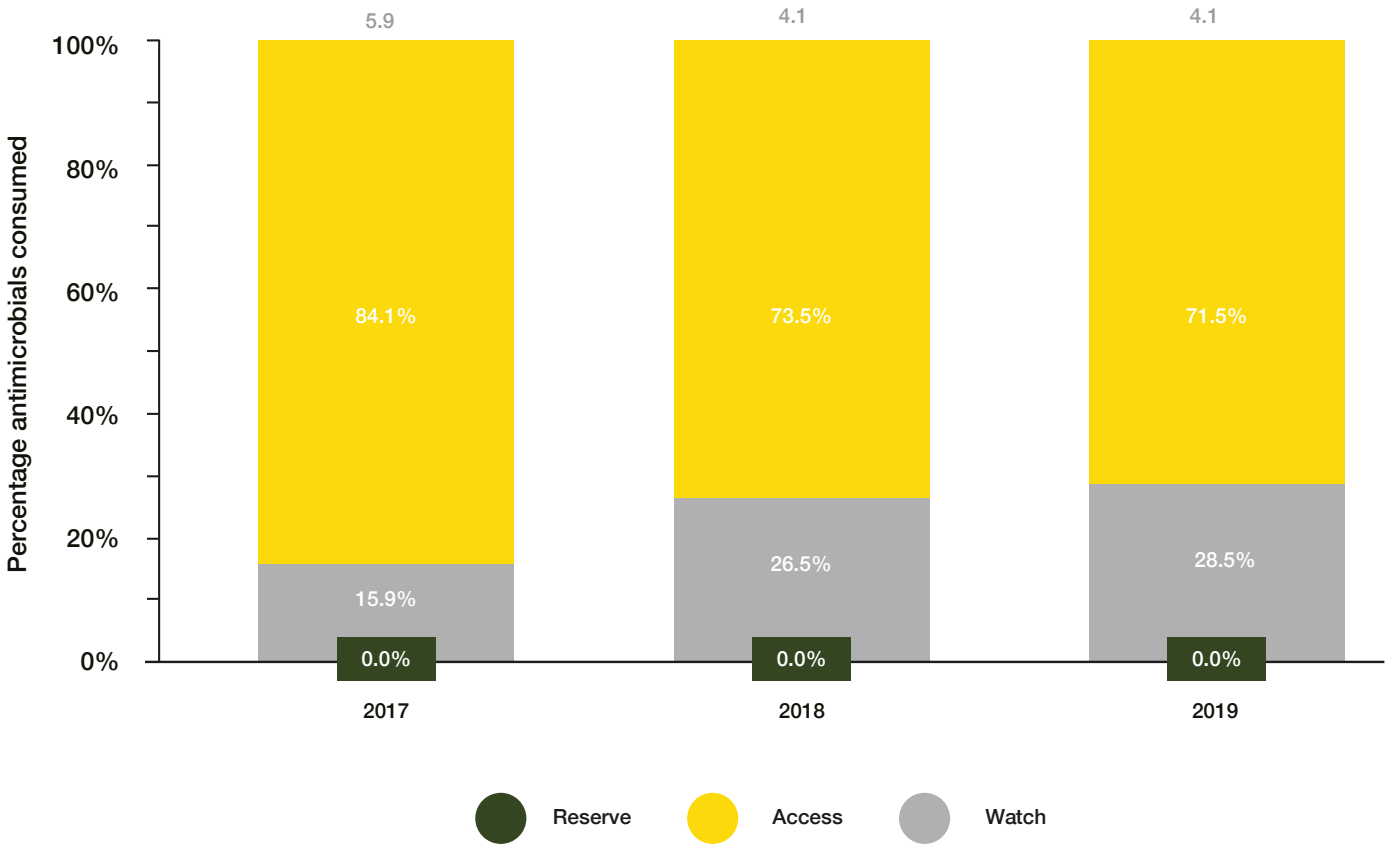


Figure 20: Results for the AMC data analysed in Cameroon are presented by the total DID and percentage of antibiotics consumed by WHO AWaRe categories across all the reviewed years 2017 to 2019. Also, it shows the percentage change in consumption of Access and Watch category antibiotics from the year 2017 to 2019

In addition, further analysis was conducted to disaggregate WHO AWaRe category antibiotics consumption across the two sectors represented in the national-level data i.e., public against private sector. The private sector consumed 28.2% more 'Watch' category antibiotics compared to the public sector (public sector at 4.6% and private sector at 32.8%) (Figure 21).

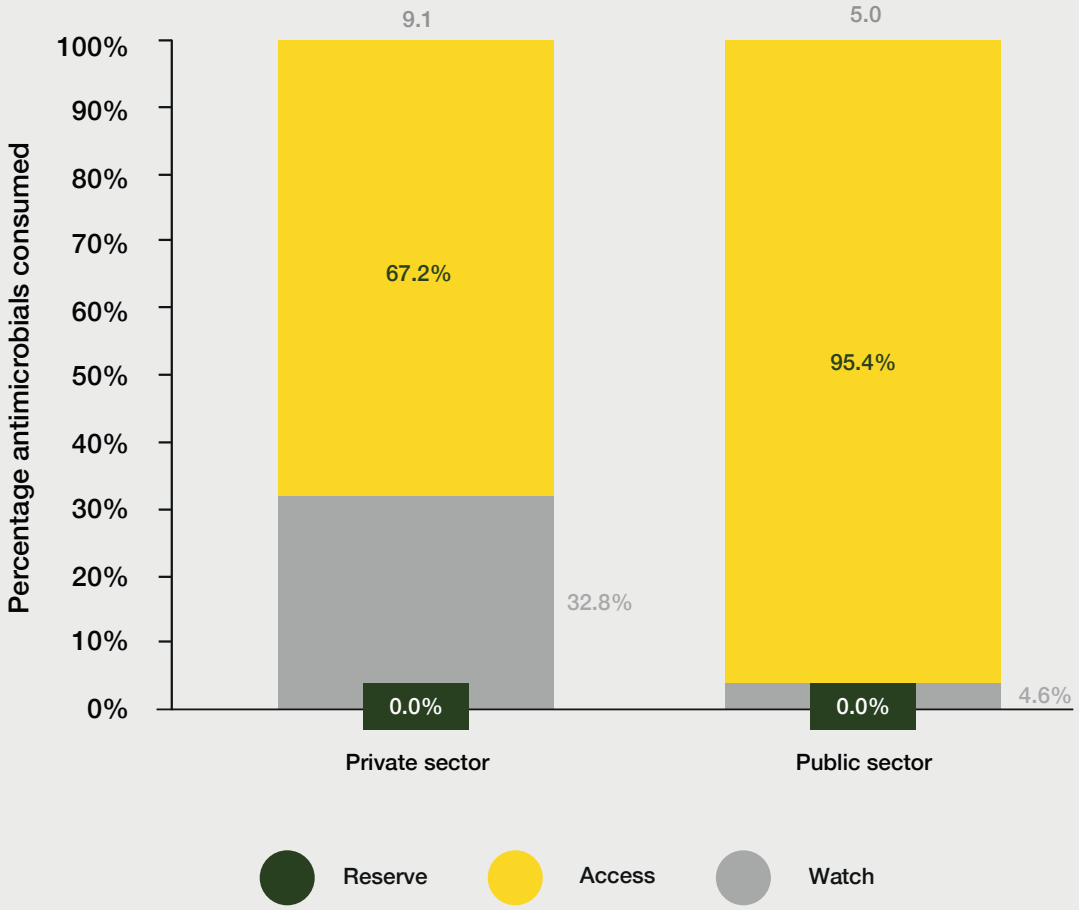
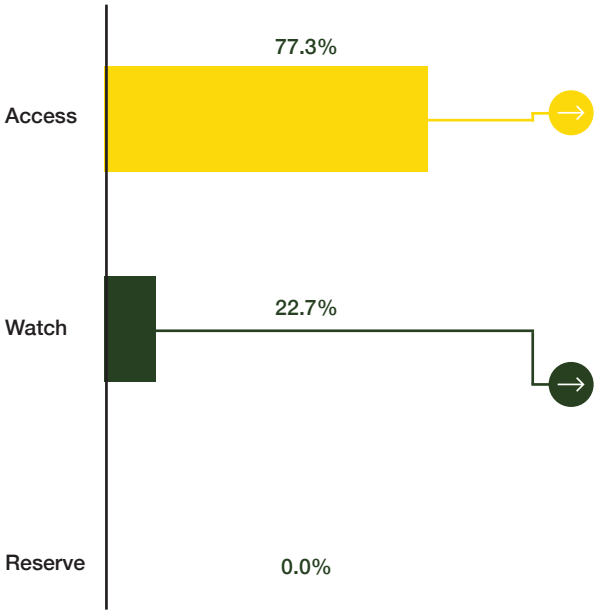


Figure 21: Disaggregation of WHO AWaRe categories antibiotics consumption by health care sector i.e., public and private sectors. Data is presented as the total DID and percentage of antibiotics consumed across all the reviewed years 2017 to 2019 in Cameroon

Further analysis was conducted to identify the most frequently consumed antibiotics nationally, within each WHO AWaRe category (Figure 22). In the 'Access' category, the top five consumed antibiotics accounted for 97.9% of all AMC within this group (as listed in Figure 22.) While in the 'Watch' category, the top five antibiotics accounted for 93.1% of all consumption within this group. Similarly, disaggregated AMC data by the sector showed that the top five consumed antibiotics in each WHO category were the same across both sectors.



Molecule Name	% Total	Mean DDD/1000 inhabitants/ day
Sulfamethoazole/Trimethoprim	39.8%	1.4
Amoxicillin/Clavulanic Acid	21.6%	0.8
Doxycycline	15.8%	0.6
Amoxicillin	12.3%	0.4
Flucloxacillin	4.1%	0.2

Molecule Name	% Total	Mean DDD/1000 inhabitants/ day
Ciprofloxacin	16.5%	0.2
Cefixime	16.3%	0.2
Azithromycin	15.0%	0.2
Ofloxacin	12.6%	0.1
CLevofloxacin	8.3%	0.1

Figure 22: Breakdown of the 'Access' and 'Watch' categories of antibiotics consumed at the national-level by percentage and total DID across all the reviewed years 2017 to 2019 in Cameroon. It also shows the top five consumed antibiotics in their respective categories

Within the WHO AWaRe database exists a list of 'antibiotics not recommended'. This group of antibiotics consists of fixed-dose combination (FDC), multiple broad-spectrum antimicrobials that are neither evidence-based nor recommended by international guidelines. In this regard, the WHO does not recommend their use in clinical practice. These antibiotics are represented as 'uncategorised' WHO AWaRe category antibiotics by MAAP and not included in the computation of category percentages. Consumption of these non-recommended FDCs (n=12) was observed, representing 1.1% consumption of the total national AMC (see list in Table 12 below). ofloxacin/ornidazole was the most frequently consumed (accounting for 33.0% of the consumption from the total consumption of the listed FDC antibiotics) (Appendix 8 details the full list of antibiotics categorised under each WHO AWaRe category).

Table 12: List and AMC rank of antimicrobials categorised as 'not recommended' for clinical utility by WHO.*

Overall AMC rank*	Not recommended combination
21	Ofloxacin/Ornidazole
24	Amoxicillin/Metronidazole
26	Ampicillin/Cloxacillin
31	Ciprofloxacin/Tinidazole
42	Ceftriaxone/Sulbactam
47	Cefuroxime/Clavulanic Acid
49	Cefixime/Clavulanic Acid
53	Cefpodoxime proxetil/Clavulanic Acid
54	Amoxicillin/Cloxacillin
55	Amoxicillin/Pivsulbactum
56	Cefadroxil/Clavulanic Acid
62	Amoxicillin/Sulbactum

**AMC rank reports the position of antibiotics consumed (in terms of the total DID and percentage share) from the reviewed list of antimicrobials in Cameroon (see Appendix 8 for consumption rate of each listed antibiotics).*

Aggregated pharmacy-level data were analysed from the (n=11) participating pharmacies and analysed by the level of service of the hospitals (primary, secondary and tertiary care) and also by their proportional consumption of WHO AWaRe category antibiotics. The hospital pharmacies well exceeded the WHO threshold of 60% consumption of antibiotics represented within the 'Access' category at 85.0%. The tertiary care facility consumed 5.9% more 'Watch' category antibiotics compared to the secondary care hospital pharmacies. The 'Watch' category consumption of the single primary care facility was comparable to that of tertiary care facilities (Table 13). Interestingly, all participating pharmacies met the minimum threshold of consuming >60% 'Access' category antibiotics. There were no stocks of 'Reserve' category antibiotics supplied to any of the recruited pharmacies during the reviewed period (2017 - 2019).

Table 13: Percentage share in the consumption of antibiotics by WHO AWaRe categories for the recruited hospital pharmacies disaggregated by service level (primary, secondary and tertiary care facilities) between the years (2017-2019) in Cameroon.

Pharmacy Type	AWaRe Categorisation	
	Access	Watch
	Percentage share (Absolute DDD)	
Hospital pharmacies (11/11)	85.0% (4 273 555)	15.0% (754 293)
Primary care facility (1/11)	84.5% (71 062)	15.5% (12 989)
Secondary care facilities (3/11)	90.1% (619 057)	9.9% (67 660)
Tertiary care facilities (7/11)	84.2% (3 583 437)	15.8%M(673 644)
Grand Total	85.0% (4 273 555)	15.0% (754 293)

Comparison of the WHO EML and the Cameroon EML with documented antibiotics by WHO AWaRe categorisation

The WHO EML includes 39 antibiotics across the AWaRe categories. A total of 90 antimicrobials were documented during national- and pharmacy-level data collection. Figure 23 shows for each AWaRe category the number of antibiotics in the WHO EML and Cameroon EML, thereby indicating if the antibiotic was documented during data collection.

It was found that three antibiotics in the 'Access' category, three in the 'Watch' category and one in the 'Reserve' category, are listed in the WHO EML and documented during data collection, although they are not part of the Cameroon EML. In addition, four 'Access' category and six 'Reserve' category antibiotics are part of the WHO EML, although they too are not listed in the Cameroon EML nor documented during data collection. For each AWaRe category, including the uncategorised, antimicrobials were documented during data collection which are neither part of the WHO EML or Cameroon EML. The detailed breakdown of antimicrobials are documented and their inclusion in both the WHO EML and Cameroon EML is provided in Appendix 10.

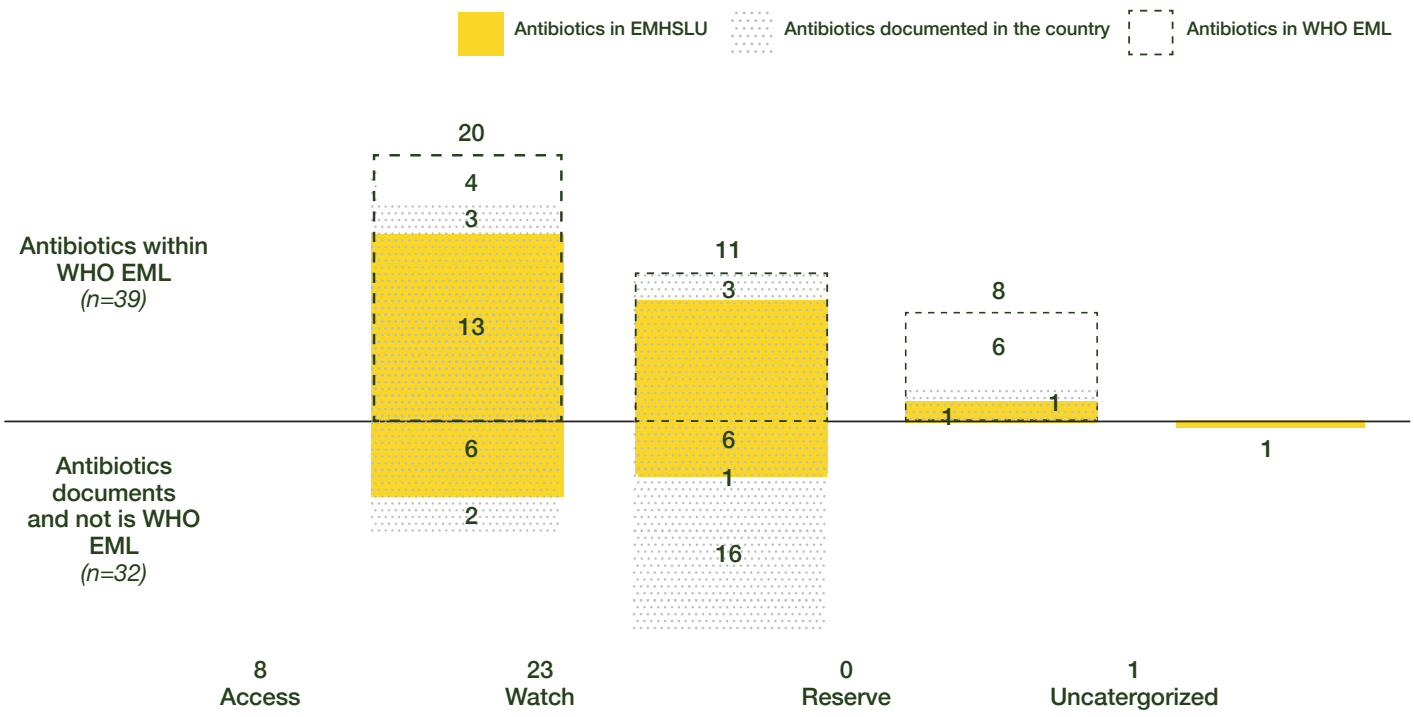


Figure 23: AWaRe analysis of documented antibiotics in national- and pharmacy-level data for the years 2017 to 2019 compared to WHO- and Cameroon- EML definitions

Part C: Resistance and Consumption Interlinkages

Objective

To assess the relationship between antimicrobial consumption and antimicrobial resistance

Methodology

The DRI was estimated to convey aggregate rates of resistance as well as measurements of AMC (at a national level since AMU data was not available) across select pathogen-antimicrobial combinations (Pathogens - A. baumannii, E. coli, K. pneumoniae, P. aeruginosa, S. aureus, E. faecium and E. faecalis; Antibiotics - aminoglycosides, broad-spectrum penicillins, carbapenems, cephalosporins, glycopeptides, narrow-spectrum penicillins and quinolones). The DRI estimates were generated using a previously published methodology35,36 (AMR Appendix 8) and help communicate the effectiveness of antibiotic therapy to decision makers. DRI values range from 0 (100% susceptibility) to 100 (100% resistance). Available AST results for at least 30 tested isolates and for at least 15 of the 25 combinations were prerequisites for estimation of the DRI. To generate CIs for the DRI as the variance of the product of variables, the variance of the proportions of non-susceptible isolates was combined with a uniform standard deviation based on the estimated DDD. [37,38]

Apart from the DRI, correlation between AMC and AMR was conducted. Data on antimicrobial consumption were obtained from facilities and based on the total DDD over the entire study period. The AMC of a particular antimicrobial class was correlated with a composite resistance rate (covering all pathogens tested against the same antimicrobial class, as reported by the laboratories). Pearson's correlation analysis was performed between the two variables (AMR rate [%] and total DDD). Antibiotic classes contributing less than 0.05% to the total antibiotics consumed were excluded from the analysis.

Based on previously described methodology, the resistance of all pathogens tested against the most and least consumed antimicrobial classes, is reported by the laboratories and based on data availability, in each study year.

Results

Drug Resistance Index

The DRI estimate was found to be high at 68.0% (95% CI, 60.7-75.2%) implying low antibiotic effectiveness, which is a threat to effective infectious disease management and calls for urgent policy intervention (Figure 24).

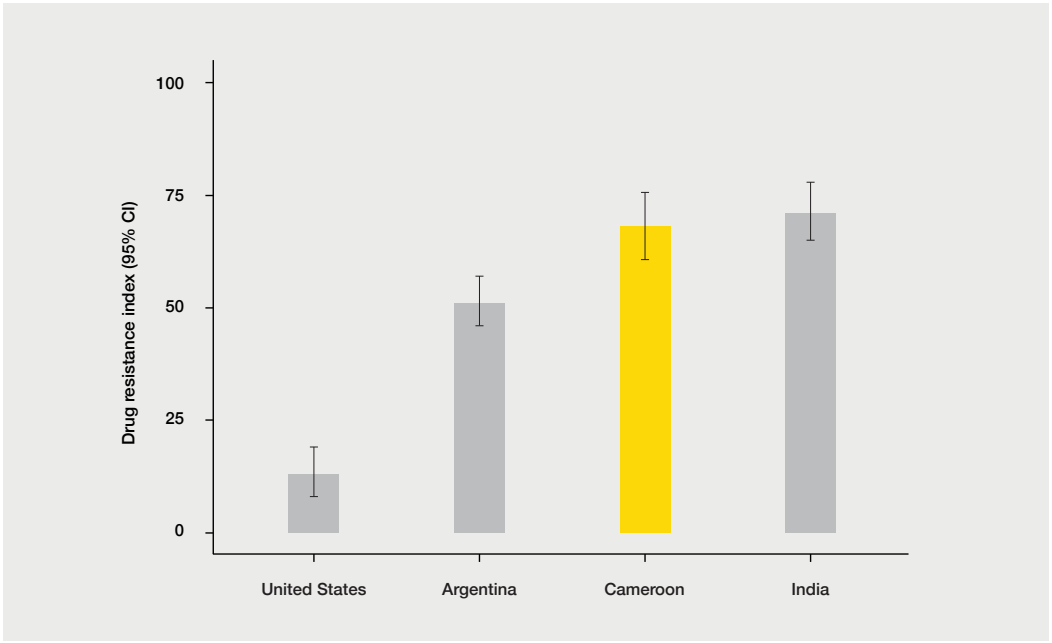


Figure 24: Drug Resistance Index

AMC and AMR correlation

The top three highly consumed antibiotic classes at facility level were aminoglycosides, folate pathway inhibitors and aminopenicillins. The AMR rates were highest for aminopenicillins (84.8%), penicillins (81.9%) and folate pathway inhibitors (80.5%). (Table 14) Pearson's correlation analysis revealed no correlation between antimicrobial resistance and antimicrobial consumption, implying that AMC is not a significant driver of AMR in Cameroon (Figure 24).

Table 14: AMC and AMR rates across antibiotic classes

Antibiotic class	Year	Total DDD in thousands	Resistance rate (%)
Aminoglycosides	2017-19	1.43	47.4
Folate pathway inhibitors	2017-19	1.07	80.5
Aminopenicillins	2017-19	0.58	84.8
Nitroimidazoles	2017-19	0.54	0.6
Macrolides	2017-19	0.37	67.9
Beta-lactam combinations	2017-19	0.25	57.9
Tetracyclines	2017-19	0.24	62.9
Fluoroquinolones	2017-19	0.19	63.8
Cephalosporins (3rd generation)	2017-19	0.16	63.5
Penicillins	2017-19	0.08	81.9
Methicillin	2017-19	0.07	50.6
Cephalosporins (2nd generation)	2017-19	0.03	63.9
Azoles (f)	2017-19	0.03	56.7

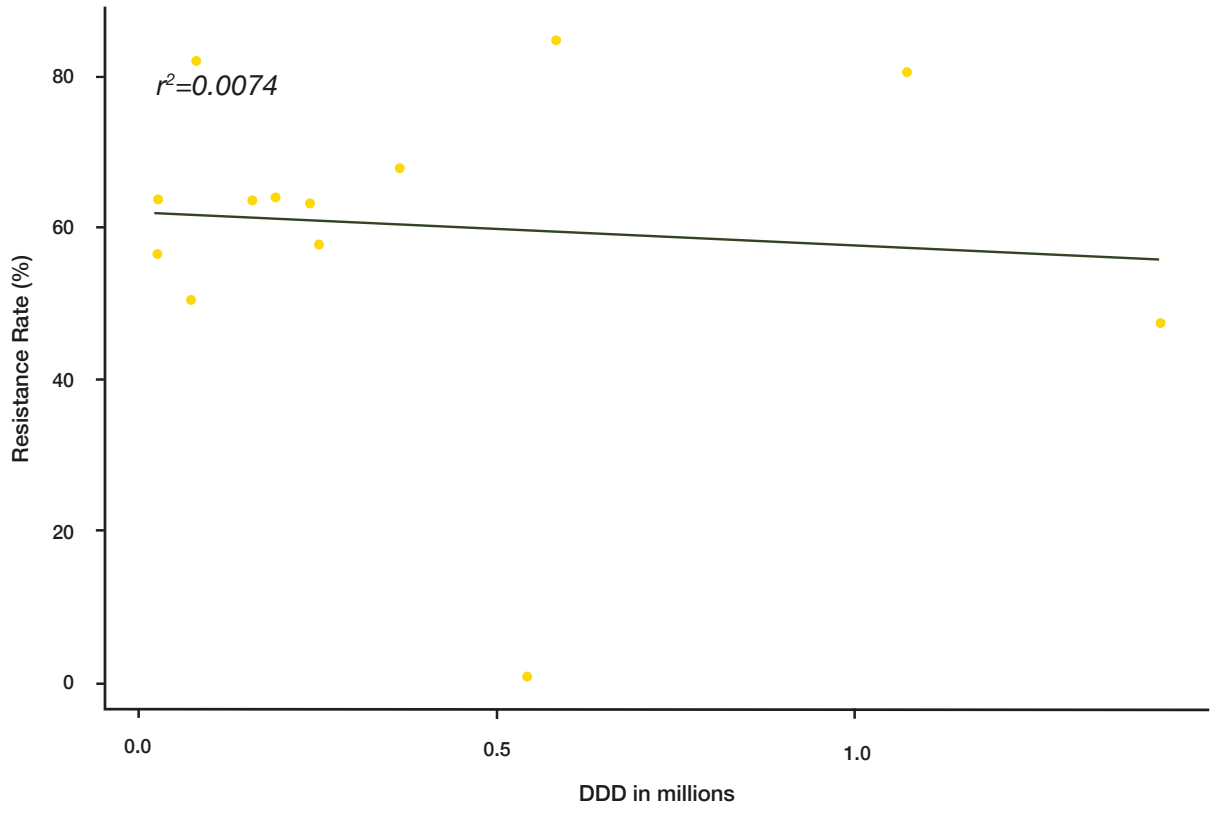


Figure 24: Correlation between AMR and AMC

Resistance profiles of most and least consumed antimicrobial classes

The most consumed antimicrobial classes across the study years were folate pathway inhibitors, beta-lactam combinations and tetracyclines. In 2017, resistance rates were more than >75% for folate inhibitor-resistant Pseudomonas species, Streptococcus species, Staphylococcus species, Klebsiella species and Escherichia species. In 2018, high resistance rates (>75%) were noted for folate inhibitor-resistant Klebsiella species and Escherichia species. In 2019, the highest resistance rates (>75%) were observed for folate inhibitor-resistant Pseudomonas species, Escherichia species, Proteus species and Klebseilla species (Figure 25,26 and 27).

The least consumed antimicrobial classes across the study years were fucidane, cephalosporins (4th-generation), streptogramins, carbapenems and beta-lactam combinations. Even though the consumption of these antimicrobial classes was low, high resistance rates were observed across many pathogen-antimicrobial class combinations. In 2017, resistance rates were more than >50% for fucidane-resistant Klebsiella species and Escherichia species, cephalosporin (4th-generation)-resistant Staphylococcus species and Pseudomonas species. In 2018, resistance rates were more than >75% for fucidane-resistant Escherichia species and cephalosporin (4th generation)-resistant Staphylococcus species, Acinetobacter species and Pseudomonas species. In 2018, resistance rates were more than >50% for cephalosporin (1st-generation)-resistant Escherichia species and Klebsiella species (Figure 25,26 and 27).

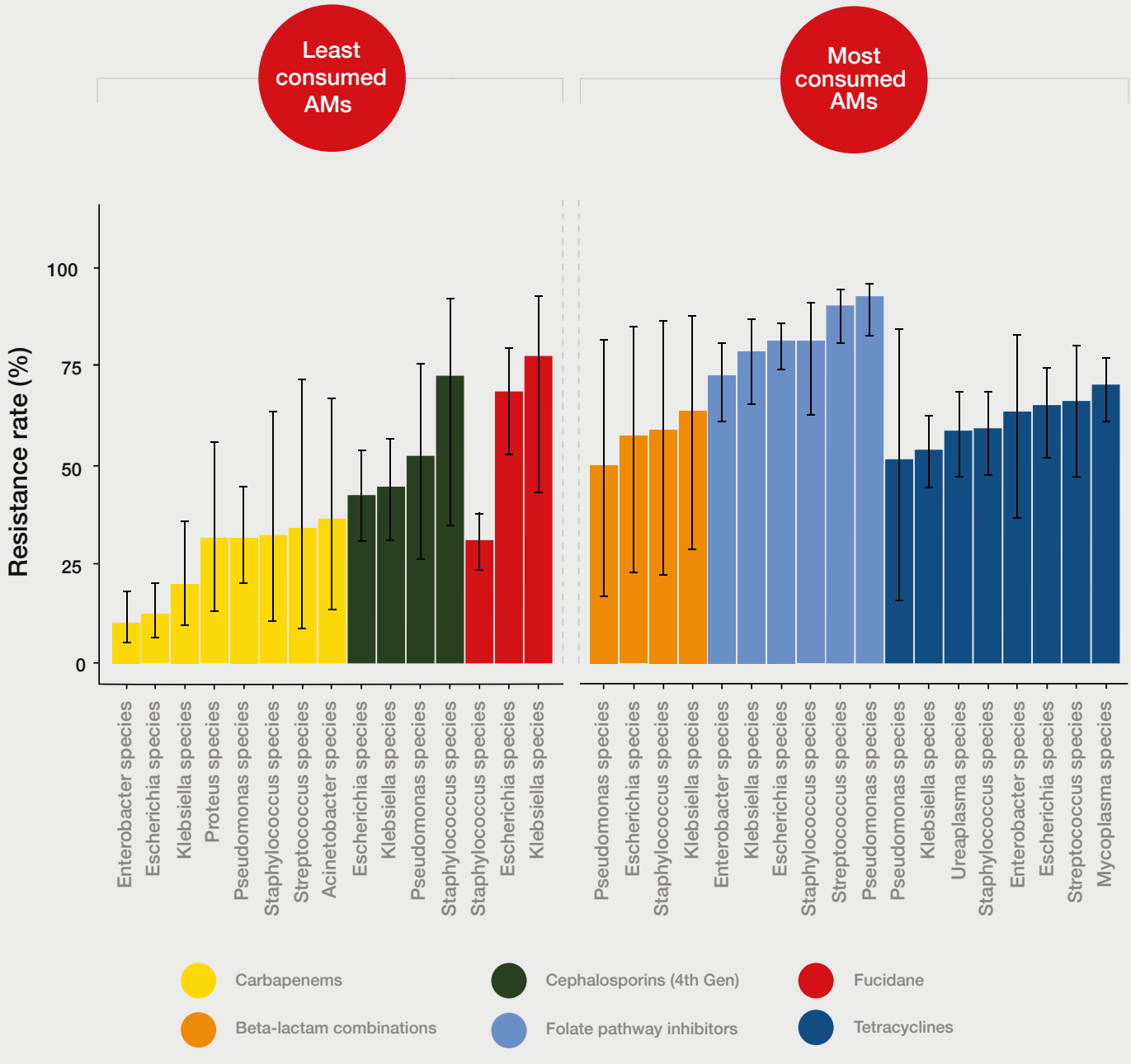


Figure 25: AMR rates for least (left) and most (right) consumed antimicrobial classes (AMs) in 2017

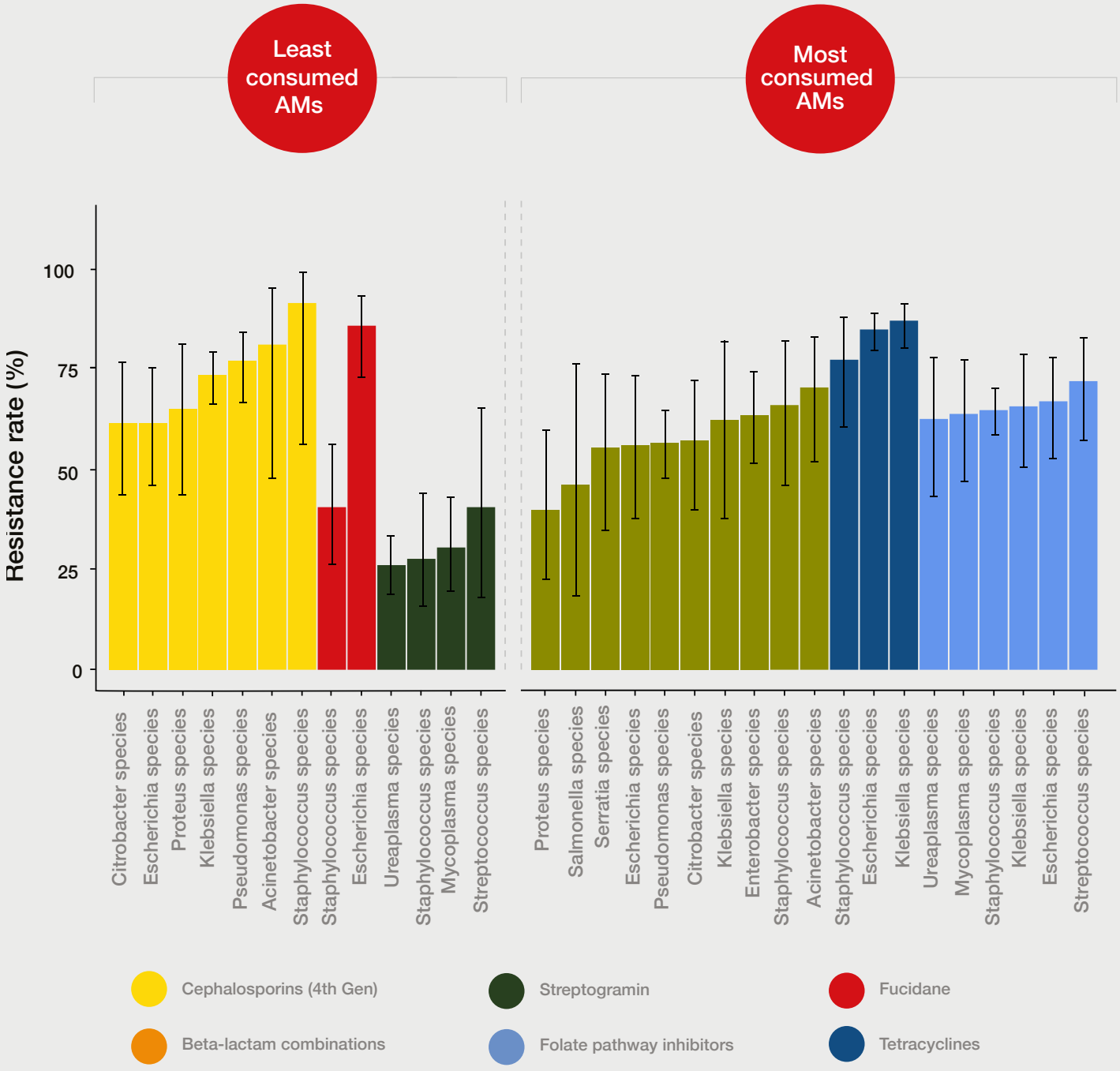


Figure 26: AMR rates for least (left) and most (right) consumed antimicrobial classes (AMs) in 2018

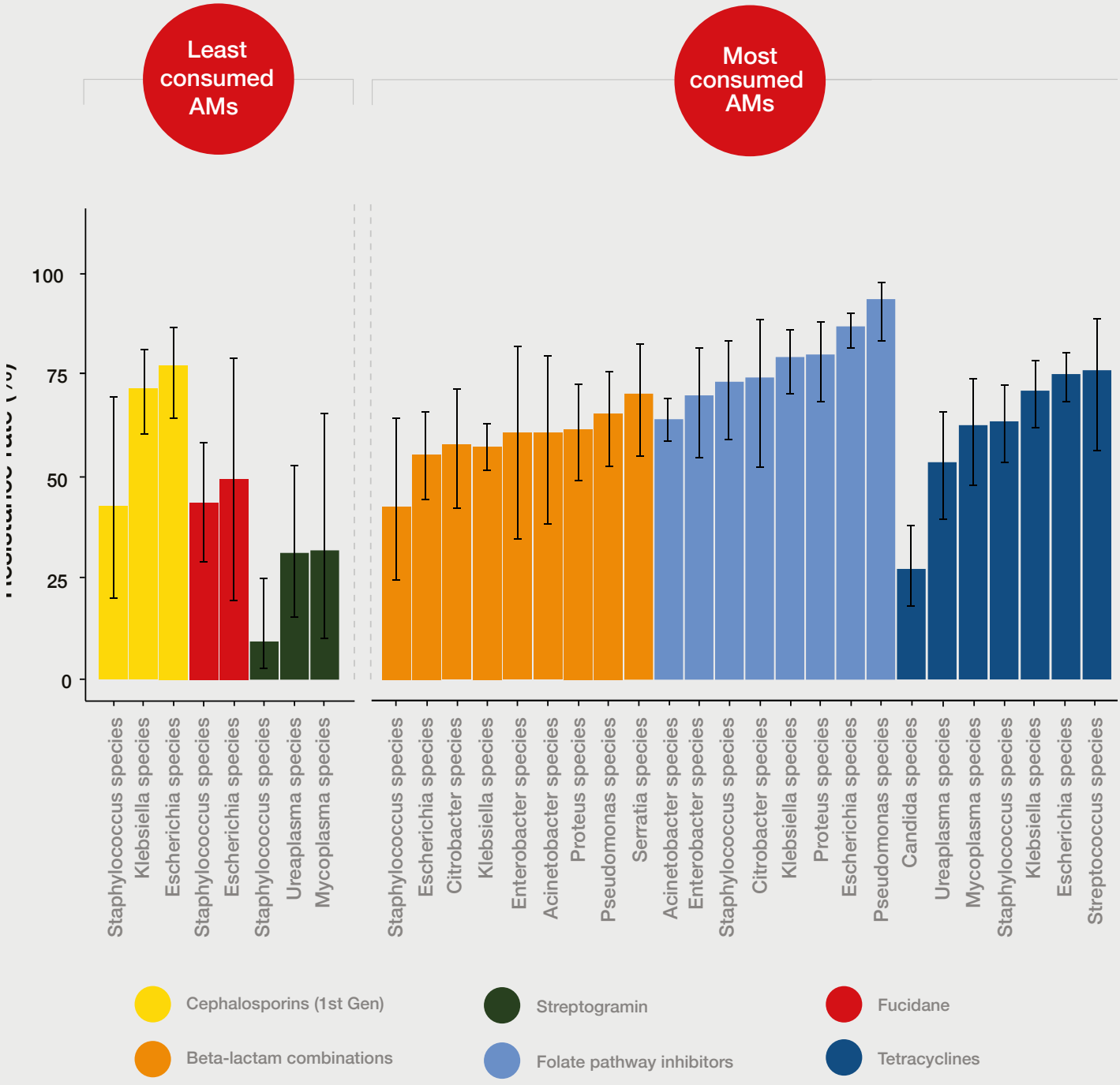


Figure 27: AMR rates for least (left) and most (right) consumed antimicrobial classes (AMs) in 2019

Part D: Recommendations

AMR is a major threat to medical advancements and has drawn global attention over the past few years and more so recently, due to the COVID-19 pandemic. Unfortunately, owing to inconsistent surveillance data, the AMR burden is not well quantified in most countries. A recent review reported non-availability of AMR data for more than 40% of African countries and expressed concerns about the quality of the microbiology data that did exist.[39] Mitigation of AMR calls for a multipronged approach including building resilient health and laboratory systems as well as improving stewardship (diagnostic, antimicrobial use, and infection prevention). Based on our study findings, we propose the following recommendations to strengthen AMR surveillance in Cameroon.

Significance of AMR and DRI data and recommendations

Analysis of available AMR data from Cameroon revealed high levels of resistance for MRSA (67-69%) and 3rd-generation cephalosporin-resistant Enterobacterales (57-61%). Enterobacterales can be asymptomatic colonisers or result in community- and healthcare-associated infections (commonly affecting the urinary tract, bloodstream, lower respiratory tract and surgical sites). Various risk factors predispose to resistance against 3rd-generation cephalosporins and carbapenems. These risk factors are prior use of cephalosporins and/or carbapenems, in-dwelling catheters, mechanical ventilation, underlying comorbidities (such as diabetes, malignancy, severe illness, etc.), injuries and transplantation. To limit the spread of resistant Enterobacterales, compliance to standard and contact precautions (including hand hygiene), minimal use of catheters and invasive devices, compliance to infection prevention bundles, and antimicrobial stewardship, is essential. Additionally, high-risk patients should be screened for rectal colonisation.

S. aureus (methicillin-resistant or sensitive) is a common cause of many skin and soft tissue infections, in both community and healthcare settings. It can also cause invasive infections like endocarditis, osteomyelitis, pneumonia, visceral abscess, brain abscess, shunt infections and bacteraemia. Risk factors for MRSA infections include past infections/colonisation, trauma, invasive device (catheters, shunts, implants, prosthesis), prior-antibiotic use, neutropenia other underlying conditions, post-surgical status, dialysis and admission to long-term care facilities.

While antimicrobial therapy and source control (drainage or catheter removal) are essential for the treatment modalities, it is as important to prevent and control the spread of MRSA infections. Use of catheters and invasive devices must be minimised, and stewardship principles practised (culture taken prior to initiating antibiotics, and prompt de-escalation from empirical to targeted therapy). High-risk and pre-operative patients must be screened for MRSA carriage and decolonised. Patients and caregivers should be educated on the importance of handwashing and contact precautions.

The estimated DRI for Cameroon was also high and indicates decreasing effectiveness of antimicrobials. Evidently, this calls for targeted interventions which should include improving ASP, infection prevention as well as regulations on the use of high-end antibiotics. We observed that males and the elderly were more prone to resistant infections, although further studies are necessary to establish an association.

Service delivery

The laboratory network in Cameroon was found to consist of 360 laboratories, of which 19 were identified as bacteriological laboratories and had AST capabilities. While most of the surveyed laboratories reported implementing QMS, few were certified or accredited. Considering a country population of over 26.5 million, the laboratories did not equitably cover the country's population. The testing load (quantum of cultures) at most participating laboratories was found to be low and suggested lack of routine microbiology testing. Hence, this risks overestimating the AMR rates as the majority of tests would have been conducted on special patient categories (such as failure of first line therapy or admission to intensive care).

To strengthen the delivery of services by the laboratories, we recommend that all laboratories are mapped across a range of indicators, including population coverage, infectious disease burden, testing capabilities, and quality compliance. This would inform decision makers on unmet needs and determine a way forward for expansion of the laboratory network. A larger network also provides a richer sampling frame for better representation and generalisation of results.

Health workforce

As reported by the surveyed laboratories, all of them had an experienced laboratory scientist or technologist, 90% had at least one qualified microbiologist, and 74% had up-to-date records on training and competence. For high quality microbiology testing and reporting, staff training on laboratory standards, ability to identify common pathogens and data management skills are essential.[40] Capacity-building of staff may be completed through in-house expertise or outsourced to external organisations or tertiary facilities.

Information systems

The Regional Grant was a step towards the collection and digitisation of data. We observed that most of the surveyed laboratories relied on a combination of electronic and paper-based records or paper-based records alone, and very few had linkages to patients' clinical records. In the current study involving 16 laboratories over a three-year period, susceptibility results could be collected for 32 545 positive cultures.

In order to strengthen AMR surveillance, it is essential to curate the right data and generate evidence. We recommend data collection through standardised formats at all levels (laboratories, clinics and pharmacies) as well as the use of automation for data analyses. For the current study, we used WHONET for data digitisation. Empirical guidelines for management of infectious diseases should be based on epidemiology specific to patient setting, and resistance data should be shared with national and supra-national platforms. We also recommend establishing a system of assigning permanent identification numbers for patient tracking over time. This would help to collect data on the patient's clinical profile, antimicrobial history as well as pathogen's molecular profile (where available), thus offering more context to the AMR epidemiology than stand-alone antimicrobial susceptibility data.

Medicines and technologies

While there are various determinants of patient care, the importance of quality diagnostics can never be undermined. Even though laboratory audit was not the scope of the current study, we observed instances of inappropriate testing and hence, data unfit for analysis. Such results can be misleading and impact patient care.

In order to strengthen AMR surveillance, it is imperative to generate reliable laboratory results through appropriate testing methods, use of authorised surrogates and ensuring the uninterrupted availability of reagents including antibiotics for susceptibility testing. Improving supply chains for essential reagents should be a country's priority and interruptions in routine testing must be minimal. Standardisation of testing methods across laboratories can aid in this process as purchases can be pooled and coordinated by the MoH. All laboratories and testing centres must conform to AST quality standards and aim for accreditation and quality certification status.

Finally, we recommend increasing the community awareness on the importance of public health interventions (vaccinations, clean water, sanitation and hand hygiene) as well as compliance to physicians' advice. The strengthening of health and laboratory systems must be prioritised at national level and complemented with the right investment.

Significance of AMC and AMU data including recommendations

This section discusses the significance of our AMC and AMU findings and puts forth suggested recommendations for Cameroon to possibly consider in order to optimise the observed trends in the consumption of antimicrobials and thus facilitate future surveillance activities.

Feasibility of obtaining AMC and AMU data in Cameroon and recommendations

MAAP successfully collected and analysed national- and pharmacy-level AMC data for Cameroon. This implies that surveillance of AMC data is possible and that Cameroon can respond to WHO's call to participate in GLASS, which now has an AMC reporting component. Interestingly, accessed CENAME annual data were complete and standardised, requiring minimal cleaning. However, the data received from the participating pharmacies required extensive cleaning and verification. Therefore, MAAP recommends that a comprehensive guiding policy for routine AMC data surveillance is required in the country. This AMC surveillance policy would fall in line with the strategic objectives set out within the Cameroon NAP which outlines the need to ensure the appropriate use of antimicrobial agents. This is conducted by first understanding the current use of antimicrobials in Cameroon through AMC or AMU studies. The policy should aim to guide, at the minimum, reporting AMC data variables, routine data cleaning and reporting practices to minimise the amount of time spent standardising and cleaning the data before routine surveillance exercises. The development of such a policy will ensure that the data used are accurate and usable for informing country policies. Additionally, availed national AMC data did not indicate which antimicrobials were distributed to the public or private sector; making it difficult to analyse consumption trends between these two sectors and obtain important insights. Therefore, MAAP recommends that efforts should be made by the suppliers of AMC datasets to also provide distribution-related information. Pharmacy-level AMC data from the hospitals were mainly collected from manual or mixed records. To make future AMC surveillance more time- and cost-efficient, hospitals could consider converting to electronic systems and ensure such systems have the capabilities to transfer data across systems and/or produce user-friendly reports on AMC.

MAAP was unable to obtain AMU data in Cameroon, which would have helped to characterise antimicrobials use and prescriptions at the facility level as per country's guidelines as well as aligned with WHO's drug use research methodology.[41] This inability to collect AMU data from participating pharmacies that were co-located in health facilities with AST laboratories, was due to the fact that AMC data sources (i.e., stock record cards at the pharmacy) did not allow back-tracing to individual patients to whom antimicrobials were dispensed as prescription chits were not archived. Hence, it was not possible to retrieve the relevant clinical and laboratory files for any patients who received antimicrobials. Unfortunately, MAAP was unable to locate any successfully collected AMU studies in Cameroon, however, AMU studies were successful in other African countries[25-29] through the use of the global point prevalence survey methodology.[31]

The success of these AMU studies implies that the retrieval of AMU data where sub-optimal data systems exist, can only be achieved through the set-up of point prevalence studies where data collection procedures are intentionally set up to assess the patient in real-time through the cascade of care. Furthermore, retrospective studies similar to those MAAP attempted to conduct in order to collect AMU data, may not be ideal. Therefore, MAAP, in alignment with the WHO guide on facility AMU assessment, would recommend that future AMU surveillance attempts in the country be conducted through point prevalence surveys on a larger scale in order to give a nationally representative portrait of antimicrobials use in country.[31] However, such an approach is time consuming unlike retrospective data collection and often requires the engagement of trained data collection teams for prolonged durations; making it expensive and thus challenging to undertake in resource-limited settings. Retrospective AMU data collection can, however, still be an option if facilities targeted for data collection are selected based on the existence of electronic patient records, the presence of cross-department unique patient identifiers and a functional and efficient patient record retention system.

Overview of AMC consumption trends and recommendations

Total AMC levels documented in this report offer a useful benchmark to be compared against future country consumption levels following implementation of stewardship programmes. Compared to studies from other countries in the region, the observed AMC levels in Cameroon exceed those described in literature for Burundi but are lower than the levels observed in Burkina Faso, Cote d'Ivoire,[20] Sierra Leone[25] and Tanzania[42]. The data for Cameroon included public and private wholesaler data, while in comparison, Burundi used data only from the public sector hospitals. For Tanzania, import data was used to calculate the DDD for the population, which is lacking local production data but is also not corrected for any exports that occur. This could be a possible reason as to why Cameroon AMC levels appear lower than those of Tanzania. The disparities in AMC within the compared countries might also be due to the different relative burden of infectious diseases within the countries and limited availability of laboratory or point-of-care diagnostics at the health facility level. This may lead to presumptive treatment and unnecessary prescriptions of antimicrobials. Widespread availability of over-the-counter antimicrobials and the unexplained use of some antimicrobials in the animal health sector, may be additional contributing factors.[20]

Despite the lower levels of AMC in Cameroon compared to the majority of the remaining African countries, AMU point prevalence surveys are recommended to better understand the country AMC levels and eventually guide any future policies to optimise the antimicrobials consumption if any overuse or misuse is detected. During the period of AMC analysis, an overall reduction in the national AMC was observed which was particularly attributed to a reduction in AMC within the public sector. This public sector AMC reduction may be attributable to the known shift in supplies made by CENAME away from some cities due to insecurity in the conflict zones within the English-speaking regions of Cameroon.

The evaluation of antibiotics consumption according to the WHO AWaRe categories showed that the proportion of narrow spectrum antibiotics in the 'Access' category well exceeded the minimum WHO recommended consumption threshold and a minimal consumption of broader spectrum 'Watch' category antibiotics was observed.[32] Therefore, this consumption trend implies that the Cameroon EML, that comprises mostly of 'Access' category antibiotics, is widely available in the country (Republique du Cameroun, 2017).[43] A similar trend of AMC was also observed when examining the consumption of 'Access' and 'Watch' category antibiotics from aggregated pharmacy-level AMC data, with all participating pharmacies exceeding the minimum 'Access' consumption threshold. This finding is quite commendable as it implies that any emerging AMR trends due to misuse or overuse will likely be restricted to a narrow spectrum of antibiotics, sparing the lesser used broader spectrum and last-resort antibiotics in the 'Watch' and 'Reserve' categories, respectively. Interestingly, while it is commendable that the pharmacy-level AMC data review found that all public hospital pharmacies met the WHO's minimum 'Access' consumption threshold, there was a notable variance in consumption amongst them. Here, we observed that the tertiary care hospital pharmacies consumed more 'Watch' category antibiotics compared to the secondary care hospital pharmacies.

Higher consumption of 'Watch' category antibiotics at the tertiary care hospital pharmacies could be attributed to the fact that these facilities deal with complex infection cases which would require treatment regimens using second- and third-line antimicrobial agents. However, the consumption of 'Watch' category antibiotics observed at the single primary care facility was comparable to that of the tertiary care facilities. This finding suggests that these 'Watch' category antibiotics are consumed at the same rate in primary care facilities as they are in tertiary care facilities. This is despite the fact that it is assumed that the primary care facility would be managing more common infection cases ideally only requiring treatment with first- and second-line antibiotic agents (i.e., narrow spectrum antibiotics). MAAP would therefore recommend that the country's AMRCC consider the introduction of facility-level ASPs in order to regulate the use of these broader spectrum antibiotics and educate prescribers on the importance of reserving them to maintain efficacy.

A closer examination of the spectrum of antibiotics used within each AWaRe category revealed that an overwhelming majority of antibiotics consumed within the 'Access' and 'Watch' categories were in the top five antibiotics in each category. Such a consumption pattern could be postulated to be sub-optimal as evolutionary pressure driving resistance focused only on the narrow band of antibiotics consumed.[44] This narrow consumption of antibiotics within the 'Access' and 'Watch' categories of antibiotics can also make the country susceptible to stockouts if manufacturing and supply chain issues are encountered for these few antibiotics. Considering these observations, it is therefore recommended that the country's ASP explores ways to ensure a wider spread in consumption of the antibiotics within each WHO AWaRe category (such as offering incentives for the importation and distribution of other antibiotics in the WHO AWaRe categories, in line with the country's EML) in order to avoid such a limited spectrum of consumed antibiotics. This should go hand-in-hand with ensuring appropriate use.

The WHO also provides guidance on antibiotics that are 'not recommended' for use in clinical practice due to their multiple broad-spectrum activity and that there exists no evidence-based clinical case that advocates for their use.[32] In Cameroon, the use of 12 such FDC antibiotics 'not recommended' by the WHO were detected. Of these combinations, the use of FDC ofloxacin/ornidazole was most prevalent. Therefore, as there is no recommendation for use of these FDC antibiotics, it would be recommended that the AMRCC identify the reasons and exact locations that commonly prescribe or dispense the identified FDC antibiotics listed in AMC Appendix 8. This will allow the country's MoH and associated medicine regulatory bodies (e.g., the FDA) to embark on sensitising prescribers on more appropriate treatments for those ailments to correct this prescribing practice. Lastly, no consumption of WHO 'Reserve' antibiotics was observed over the three years reviewed. Interestingly, the country's EML does not include any of the seven WHO 'Reserve' category antibiotics listed as vital medicines within WHO's EML.[32]

Therefore, MAAP recommends that an urgent review be conducted by the MoH, DPLM and AMRCC in an effort to assess the availability of 'Reserve' antibiotics in the country that may subsequently lead to the revision of the country's EML and treatment guidelines to include these vital antibiotics, if deemed necessary. This approach will ensure that the most vital antibiotics are available for all patients.

AMC and AMU summary and way forward

Data generated from AMC and AMU surveillance trends can provide unique insights for national stewardship programmes and for the formulation of policies to stem the emergence of AMR. Cameroon should be commended for far exceeding the minimum threshold of consumption of at least 60% of antibiotics coming from the WHO 'Access' (narrow spectrum, first-choice antibiotics) category. Yet, only five antibiotics make up for 68% of the consumption which indicates the opportunity for more diversification. Table 15 describes the next steps for AMC and AMU surveillance.

Table 15: Next steps for AMC and AMU surveillance

A. Leadership and Governance

The country will require developing an AMC surveillance policy and address by whom, how and when national AMC datasets should be reported. This effort will ensure the successful delivery of the national surveillance plan that is currently in development. This activity could be led by the AMRCC.

- Such a policy should provide guidance on the minimum required reporting variables, data quality appraisals, data analysis and reporting pathways to both the Ministry and the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) system, in order to ensure a continuous stream of localised AMC data beyond MAAP that will help inform and/or assess future policy decisions by the national antimicrobial stewardship programme.
- Lessons learned from the ongoing Fleming Fund Country Grants and MoH surveillance programmes could be taken into consideration in the development of the policy.

The MoH and national stewardship programmes, led by the AMRCC, could work to review the national treatment guidelines and the availability of the essential 'Reserve' category antibiotics within the Cameroon EML.

The regulatory authority, Cameroon's DPLM, could reconsider the registration status of unapproved fixed dose antibiotic combinations.

B. Service Delivery

Future attempts to collect AMU data in the country should seek to identify facilities that have unique patient identifiers and fully electronic medical records capabilities or as a limited number of facilities have such systems in place, the country could aim to prospectively collect this data as guided by the WHO's methodology[31] for point prevalence surveys.

National stewardship programmes led by the AMRCC could conduct educational campaigns for healthcare practitioners to ensure that they are aware of the full spectrum of antimicrobials available in the Cameroon EML.

C. Medical products and technologies

National Stewardship programmes to collaborate with pharmacists and medicine importers to increase the availability of more varieties of antibiotics as per the Cameroon EML, including the availability of 'Reserve' category antibiotics in selected facilities.

Part E: Limitations

Since the participating laboratories were at different levels of service and had variable testing capacity, all results in this report should be interpreted with caution. We encountered a few limitations during the conducting of the current study, as summarised below:

1. It was often difficult to obtain patients' hospital identifiers from laboratory records, thus impacting the collection of demographic and clinical information from medical archives. Where identifiers could be matched, it was found that hospital records were paper-based, thus requiring manual retrieval. This was often compounded by issues of illegibility and/or incomplete demographics and clinical information.

2. The laboratories had varying levels of quality and testing practices. Consequently, data contributions were uneven and it proved challenging to consolidate data to provide robust analyses of resistance and clinical impact.

3. The 16 participating laboratories may not fully represent the true resistance rates in the country as they only encompassed a small proportion of the country's population (over 26.5 million). Furthermore, as routine testing does not appear to be the norm in most hospitals and laboratories, the data may overestimate the resistance rates as infections that fail therapy may be more likely to be tested.

4. Clinical data and antimicrobial usage information were not sufficient to provide robust analysis of drivers of resistance.

5. To better understand whether the national AMC trends were mirrored in pharmacy-level AMC trends, a sample of 11 pharmacies were purposively selected for AMC data collection. However, this sample size was a relatively small proportion of total pharmacies in Cameroon and did not represent all regions and health zones in Cameroon. Therefore, a more systematic sampling strategy that factors in populations serviced and geographical locations will be required to make conclusions from pharmacy-level data more representative.

6. MAAP was unable to collect AMC data from all targeted community pharmacies due to their unwillingness to share data.

7. MAAP was unable to obtain AMU data from the participating pharmacies co-located with AST laboratories, therefore an understanding of how and why antimicrobials are prescribed as well as dispensed (i.e., appropriateness of prescriptions and antimicrobials consumed) was not achieved. This information is important as it would help better inform the country on where they would need to focus their stewardship programmes.

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Glossary

Accreditation:
According to the National Accreditation Board for Testing and Calibration Laboratories, accreditation is a procedure by which an authoritative body gives formal recognition of technical competence for specific tests or measurements, based on third-party assessment and following international standards.

Antimicrobial consumption:
According to the WHO, antimicrobial consumption is defined as quantities of antimicrobials used in a specific setting (total, community, hospital) during a specific period of time (e.g., days, months and year).

Antimicrobial resistance:
According to the WHO, antimicrobial resistance occurs when bacteria, viruses, fungi and parasites change over time and no longer respond to medicines making infections more difficult to treat and thus increasing the risk of disease spread, severe illness and death. As a result of drug resistance, antibiotics and other antimicrobial medicines become ineffective and infections become increasingly difficult or impossible to treat.

Antimicrobial resistance rate:
The extent to which a pathogen is resistant to a particular antimicrobial agent or class, determined by the proportion of isolates that are non-susceptible (i.e., either intermediate or resistant) over a one-year period: AMR rate = No. of non-susceptible isolates / No. of tested isolates [CI 95%]

Antimicrobial susceptibility testing:
Tests used to determine the specific antibiotics and extent to which a particular bacteria or fungus is sensitive.

Antimicrobial susceptibility testing standards:
A number of internationally recognised agencies that produce the standards to be followed by laboratories while performing antimicrobial susceptibility testing e.g., Clinical Laboratory Standards Institute, European Committee on Antimicrobial Susceptibility Testing, etc. It is essential that laboratories comply with at least one of these standards while performing AST.

Country data quality score:
A metric computed to estimate the overall quality of AMR data received from a country. Firstly, each laboratory was assigned a data score based on their level of pathogen identification. Scoring was based on quartiles of the proportion of completely identified pathogens where laboratories with >75% of pathogens identified at the species level were awarded the highest score (4) and those with <25% identification received the lowest score (1). Scoring was performed per year and thereafter the average of all years assigned as the laboratory data quality score for each laboratory. Secondly, the country data quality score was computed by weighting the laboratory data quality score with the quantum of valid cultures contributed by each laboratory. The maximum country data quality score was 4.

Eligibility questionnaire:
A questionnaire to be answered by laboratories in the country's laboratory network. It comprised questions on site information, commodity and equipment, quality assurance, accreditation and certification, personnel and training, specimen management and laboratory information systems. Laboratories were scored on their response.

GLASS:
According to the WHO, the Global Antimicrobial Resistance Surveillance System provides a standardised approach to the collection, analysis and sharing of AMR data by countries and seeks to support capacity development and monitor the status of existing or newly developed national AMR surveillance systems.

Laboratory readiness assessment:
It is the process of scoring the responses on the laboratory eligibility questionnaire to assess the laboratory's readiness or preparedness for AMR surveillance.

Laboratory readiness score:
The score obtained by the laboratory based on the laboratory readiness assessment. The maximum possible score was 38.

MAAP:
The Mapping Antimicrobial resistance and Antimicrobial use Partnership is a multi-organisational consortium of strategic and technical partners. It was set up to collect and analyse historical antimicrobial susceptibility and consumption or usage data collected for the period 2016-2018 in each country as well as understand the regional landscape.

Positive cultures:
Positive cultures are valid cultures for which pathogen growth was reported irrespective of AST results.

Positive cultures with AST:
Positive cultures with AST are a subset of positive cultures for which pathogen growth was reported and AST results were also available.

Proficiency testing:
According to the National Accreditation Board for Testing and Calibration Laboratories, proficiency testing is the evaluation of participant performance against pre-established criteria by means of inter-laboratory comparisons.

Quality Certification:
Certification is used for verifying that laboratory personnel have adequate credentials to practise certain disciplines as well as verifying that products meet certain requirements.

Quality Management Systems:
These are systematic and integrated sets of activities to establish and control the work processes from pre-analytical to post-analytical processes, manage resources, conduct evaluations, and make continued improvements to ensure consistent quality results.

Total cultures:
The number of patient rows in the database received from the laboratories.

Valid cultures:
Valid cultures are a subset of total cultures and include information on the specimen type, collection date and the laboratory's testing volume.

AMR Appendices and Supplementary Tables

Appendix 1: Terms of Reference and Data Sharing Agreements

REPUBLIQUE DU CAMEROUN
Paix – Travail – Patrie

MINISTERE DE LA SANTE PUBLIQUE

SECRETARIAT GENERAL

N° 881-353 /MINSANTE/SG/DROS/

REPUBLIC OF CAMEROON
Peace – Work - Fatherland

MINISTRY OF PUBLIC HEALTH

SECRETARIAT GENERAL

Yaoundé, le 24 DEC 2019

LE MINISTRE
A
Monsieur le Directeur Général,
East, Central and Southern Africa
Health Community (ECSA-HC)
Pr Yoswa Dambisya
Arusha-Tanzania
+255-27-2549362

Objet : *accord de principe*

Monsieur le Directeur Général,

Faisant suite à votre correspondance dont l'objet et les références figurent en marge,

J'ai l'honneur de vous donner mon accord de principe pour la mise en œuvre du projet de **cartographie de la résistance aux antimicrobiens (RAM) et de l'utilisation des antimicrobiens (UAM) au Cameroun.**

À cet effet, l'organisme East, Central and Southern Africa Health Community (ECSA-HC), ainsi que l'investigateur principal voudrez bien noter que cet accord ne vous dispense pas de l'obtention de la « Clairance Ethique» auprès du Comité National d'Ethique de la Recherche pour la Santé Humaine (CNERSH) et de l'Autorisation Administrative de Recherche (AAR) auprès de la Division de la Recherche Opérationnelle en Santé (DROS).

Je vous prie d'agréer **Monsieur le Directeur Général**, l'expression de mes salutations distinguées.

Copie :
- CAB/MINSANTE/SESP
- SG/MINSANTE/DPML/DLMEP/DROS
- ECSA-HC
- Archives/Chrono

LE MINISTRE
The Minister

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Appendix 2: Laboratory Eligibility Questionnaire

Question		Response			
Part 1: Site Information					
1.1	What is the name of the laboratory?				
1.2	Between 2016 and 2018, did the laboratory routinely conduct antimicrobial susceptibility testing?	Yes		No	
1.3	Is the laboratory willing to share 2016-2018 AST results with the MAAP consortium?	Yes		No	
1.4	What is the address of the laboratory?				
1.5	What is the laboratory's level of service?				
Reference- tier 3 or 4	Regional/Intermediate	District or community	Other		
1.6	What is the laboratory's affiliation?				
Government/Ministry of Health	Private	Non-government organisation	Other		
1.7	Is the laboratory co-located in a clinical facility?	Yes		No	
1.8	Is a pharmacy co-located with the laboratory?	Yes		No	
1.9	Did the laboratory serve as a national AMR surveillance site at any time between 2016 and 2018?	Yes		No	
1.10	Is your country participating in the World Health Organisation's Global Antimicrobial Resistance Surveillance System (WHO GLASS)?	Yes		No	
Part 2: Commodity and Equipment					
2.1	Did the laboratory have regular power supply with functional back up, in place at any time between 2016-18?	Yes		No	
2.2	Did the laboratory have continuous water supply, in place at any time between 2016-18?	Yes		No	
2.3	Did the laboratory have certified and functional biosafety cabinet, in place at any time between 2016-18?	Yes		No	
2.4	Did the laboratory have automated methods for bacterial identification, in place at any time between 2016-18?	Yes		No	
2.5	Did the laboratory have automated methods for antimicrobial susceptibility testing, in place at any time between 2016-18?	Yes		No	
2.6	Did the laboratory test for mechanisms of antimicrobial resistance at any time between 2016-2018?	Yes		No	
Part 3. Quality Assurance (QA), Accreditation and Certification					
3.1A	Was the laboratory implementing quality management systems at any time between 2016-2018?	Yes		No	
3.1B	If you answered 'yes' to question 1A: What quality management tools did the laboratory utilize? (e.g., LQMS, SLIPTA, SLMTA, mentoring, others)				
3.2A	Did the laboratory receive a quality certification at any time between 2016-2018?	Yes		No	
3.2B	If you answered 'yes' to question 2A: What kind of quality certification did the laboratory receive? (e.g., SLIPTA, College of American pathologists)				
3.2C	If you answered 'yes' to question 2A: What was the laboratory's level of quality certification (e.g., star rating for SLIPTA certified laboratories)?				
3.3A	Was the laboratory accredited by a national or international body at any time between 2016-2018?	Yes		No	
3.3B	If you answered 'yes' to question 3A: What was the name of the accreditation body/bodies?				

3.4	Did the laboratory participate in an inter laboratory comparison or external quality assessment (EQA) scheme for pathogen identification and AST at any time between 2016-18?	Yes		No	
3.5	Did the laboratory utilize reference strains to verify that stains, reagents, and media are working correctly at any time between 2016-18?	Yes		No	
3.6	Did the laboratory maintain records of QC results, at any time between 2016-18?	Yes		No	
3.7	Was there a quality focal person in your laboratory at any time between 2016-2018?	Yes		No	
3.8	Did the laboratory follow standard operating procedures (SOPs) on pathogen identification and AST methodology at any time between 2016-18?	Yes		No	
3.9	Did the laboratory comply with any standards (e.g., CLSI, EUCAST, others) for reporting AST results at any time between 2016-18?	Yes		No	

Part 4. Personnel and Training

4.1	Did the laboratory have at least one qualified microbiologist, in place at any time between 2016-18?	Yes		No	
4.2	Did the laboratory have a laboratory scientist/technologist /technician experienced in microbiology with skill set in bacteriology, in place at any time between 2016-18?	Yes		No	
4.3	Did the laboratory have up to date complete records on staff training and competence record for the microbiology tests they perform, in place at any time between 2016-18?	Yes		No	

Part 5. Specimen Management

5.1	Did the laboratory follow a defined standard operating procedure (SOP) for specimen collection and testing, at any time between 2016-18?	Yes		No	
5.2	Did the laboratory comply with specimen rejection criteria for rejecting inadequate specimens, at any time between 2016-18?	Yes		No	
5.3A	Does the laboratory have information on the average number of specimens processed for culture and sensitivity in 2018?	Yes		No	
5.3B	If you answered 'yes' to question 3A: What was the average number of specimens processed for bacterial culture in 2018?				
5.3C	If you answered 'yes' to question 3A: What was the average number of specimens that yielded bacterial growth and were processed for susceptibility tests, in 2018?				

<200	200-1000	1000-3000	>3000

Part 6. Laboratory Information System and Linkage to Clinical Data

6.1	Was a specimen (laboratory) identification number assigned to patient specimens received between 2016-18?	Yes		No	
6.2A	Was there a system/database to store patient data (demographic, clinical and specimen) at any time between 2016-18?	Yes		No	
6.2B	If you answered 'yes' to question 2A: What type of data was captured in the system/database?				
6.2C	If you answered 'yes' to question 2A: What was the format for storage of information?	Yes		No	
6.2D	If you answered 'yes' to question 2A: What is the location of this database, or where can this database be accessed from?				
6.3A	Were patient demographics and clinical information captured on test request forms at any time between 2016-18?	Yes		No	
6.3B	If you answered 'yes' to question 3A: Were test request forms submitted between 2016 and 2018 stored and retrievable?	Yes		No	

Note: For question 1.4, the exact address was preferred, however, the nearest landmark or street intersection was acceptable, where applicable; for questions 1.5 and 1.6, more than one response was possible and for the option 'other', the response was entered as plain text; for question 2.2 mechanisms of antimicrobial resistance can vary: common mechanisms are production of enzymes (extended spectrum beta lactamase, carbapenemase, etc.) and resistance genes (mecA gene in MRSA, etc.); for question 4.a, the qualified microbiologist should possess a postgraduate degree in microbiology (medical or non-medical); for question 6.2c, more than one response was possible and for the option 'other', responses were entered as plain text (i)

Of note, some countries received a version of the EQ which did not have the following two questions from part I: (i) Between 2016 and 2018, did the laboratory routinely conduct antimicrobial susceptibility testing? (ii) Is the laboratory willing to share 2016-2018 AST results with the MAAP consortium? However, AST capabilities were confirmed before the EQ evaluation, and the data sharing aspect of the process was already in place in agreements with the MoH.

Appendix 3: Laboratory Readiness Assessment

The EQ questions were scored for laboratory readiness as follows:

	Question	Response				Scoring
Part 1: Site Information (Maximum score=0)						
1.1	What is the name of the laboratory?					None
1.2	Between 2016 and 2018, did the laboratory routinely conduct antimicrobial susceptibility testing?	Yes		No		None
1.3	Is the laboratory willing to share 2016-2018 AST results with the MAAP consortium?	Yes		No		None
1.4	What is the address of the laboratory?					None
1.5	What is the laboratory's level of service?					None
	Reference- tier 3 or 4	Regional/Intermediate	District or community	Other		
1.6	What is the laboratory's affiliation?					None
	Government/Ministry of Health	Private	Non-government organisation	Other		
1.7	Is the laboratory co-located in a clinical facility?	Yes		No		None
1.8	Is a pharmacy co-located with the laboratory?	Yes		No		None
1.9	Did the laboratory serve as a national AMR surveillance site at any time between 2016 and 2018	Yes		No		None
1.10	Is your country participating in the World Health Organisation's Global Antimicrobial Resistance Surveillance System (WHO GLASS)?	Yes		No		None
Part 2: Commodity and Equipment (Maximum score=6)						
2.1	Did the laboratory have regular power supply with functional back up, in place at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
2.2	Did the laboratory have continuous water supply, in place at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
2.3	Did the laboratory have certified and functional biosafety cabinet, in place at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
2.4	Did the laboratory have automated methods for bacterial identification, in place at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
2.5	Did the laboratory have automated methods for antimicrobial susceptibility testing, in place at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
2.6	Did the laboratory test for mechanisms of antimicrobial resistance at any time between 2016-2018?	Yes		No		Score 1 for "Yes" and 0 for "No
Part 3. Quality Assurance (QA), Accreditation and Certification (Maximum score=10)						
3.1A	Was the laboratory implementing quality management systems at any time between 2016-2018?	Yes		No		Score 1 for "Yes" and 0 for "No
3.1B	If you answered 'yes' to question 1A: What quality management tools did the laboratory utilize? (e.g., LQMS, SLIPTA, SLMTA, mentoring, others)					Score 1 for "Yes" and 0 for "No
3.2A	Did the laboratory receive a quality certification at any time between 2016-2018?	Yes		No		Score 1 for "Yes" and 0 for "No
3.2B	If you answered 'yes' to question 2A: What kind of quality certification did the laboratory receive? (e.g., SLIPTA, College of American pathologists)					None
3.2C	If you answered 'yes' to question 2A: What was the laboratory's level of quality certification (e.g., star rating for SLIPTA certified laboratories)?					None
3.3A	Was the laboratory accredited by a national or international body at any time between 2016-2018?	Yes		No		Score 1 for "Yes" and 0 for "No
3.3B	If you answered 'yes' to question 3A: What was the name of the accreditation body/bodies?					None
3.4	Did the laboratory participate in an inter laboratory comparison or external quality assessment (EQA) scheme for pathogen identification and AST at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
3.5	Did the laboratory utilize reference strains to verify that stains, reagents, and media are working correctly at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No

3.6	Did the laboratory maintain records of QC results, at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
3.7	Was there a quality focal person in your laboratory at any time between 2016-2018?	Yes		No		Score 1 for "Yes" and 0 for "No
3.8	Did the laboratory follow standard operating procedures (SOPs) on pathogen identification and AST methodology at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
3.9	Did the laboratory comply with any standards (e.g., CLSI, EUCAST, others) for reporting AST results at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No

Part 4. Personnel and Training (Maximum Score=3)

4.1	Did the laboratory have at least one qualified microbiologist, in place at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
4.2	Did the laboratory have a laboratory scientist/technologist /technician experienced in microbiology with skill set in bacteriology, in place at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
4.3	Did the laboratory have up to date complete records on staff training and competence record for the microbiology tests they perform, in place at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No

Part 5. Specimen Management (Maximum Score=3)

5.1	Did the laboratory follow a defined standard operating procedure (SOP) for specimen collection and testing, at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
5.2	Did the laboratory comply with specimen rejection criteria for rejecting inadequate specimens, at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
5.3A	Does the laboratory have information on the average number of specimens processed for culture and sensitivity in 2018?	Yes		No		Score 1 for "Yes" and 0 for "No
5.3B	If you answered 'yes' to question 3A: What was the average number of specimens processed for bacterial culture in 2018?					None
5.3C	If you answered 'yes' to question 3A: What was the average number of specimens that yielded bacterial growth and were processed for susceptibility tests, in 2018?					None
<200	200-1000	1000-3000	>3000			

Part 6. Laboratory Information System and Linkage to Clinical Data (Maximum Score=16)

6.1	Was a specimen (laboratory) identification number assigned to patient specimens received between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
6.2A	Was there a system/database to store patient data (demographic, clinical and specimen) at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No
6.2B	If you answered 'yes' to question 2A: What type of data was captured in the system/database?	Yes		No		Score 1 for "Yes" and 0 for "No
Patient demographic data (i.e., age, date of birth, gender, location)	Patient clinical data (i.e., primary/chief diagnosis, comorbidities, current antibiotic treatment)	Patient outcome				
6.2C	If you answered 'yes' to question 2A: What was the format for storage of information?					Score 1 for paper; 2 for mixed (E/P; E/P/O; others; mixed) and 3 for electronic (max score being 3)
Paper-based	Electronic (laboratory information system, hospital information system, other databases e.g., WHONET)	Other				
6.2D	If you answered 'yes' to question 2A: What is the location of this database, or where can this database be accessed from?					Score 1 for other; 2 for clinic and 3 for lab (max score being 6)
Laboratory	Clinical facility	Other				
6.3A	Were patient demographics and clinical information captured on test request forms at any time between 2016-18?	Yes		No		Score 1 for "Yes" and 0 for "No"
6.3B	If you answered 'yes' to question 3A: Were test request forms submitted between 2016 and 2018 stored and retrievable?	Yes		No		Score 1 for "Yes" and 0 for "No"

Appendix 4: Key AMR Variables

	Variables	Mandatory/Optional
Patient laboratory variables		
1	Patient code	Mandatory
2	Specimen type (name)	Mandatory
3	Specimen site	Mandatory
4	Date of specimen collection	Mandatory
5	Culture results – (no growth/contaminated/pathogen name)	Mandatory
6	AST Results	Mandatory
7	AST Standard	Mandatory
8	Resistance mechanism - if available	Optional
Patient demographic variables		
1	Patient code	Mandatory
2	Patient gender	Mandatory
3	Patient age or date of birth	Mandatory
4	Patient location	Mandatory
5	Patient department/specialty	Mandatory
6	Patient admission date	Optional
7	Patient discharge date	Optional
8	Patient level of education	Optional
9	Patient weight and height	Optional
10	Pregnancy status	Optional
11	Premature birth	Optional
12	Whether the patient was transferred from another clinical set-up?	Optional
Patient clinical/health variables		
1	Chief complaint	Mandatory
2	Primary diagnosis at admission	Mandatory
3	ICD code	Mandatory
4	Comorbidities	Optional
5	Whether antibiotics were prescribed to patient prior to sampling; antibiotic(s) name and duration	Optional
6	Was the patient on an indwelling medical device at time of sampling; type of device	Optional
7	Origin of infection - community acquired or hospital acquired	Optional
8	Patient outcome at discharge (recovered/deteriorated/dead/others)	Optional

Laboratory-specific variables		
1	Laboratory's level of service (Reference- tier 3 or 4/ Regional/ Intermediate/ District/ Community/ Other	Mandatory
2	Laboratory's affiliation (Government/Ministry of Health/ Private/Non-government organisation/ Other)	Mandatory
3	Laboratory co-location with clinic/hospital/pharmacy	Mandatory
4	If laboratory served as a national AMR surveillance site at any time between 2016 and 2018?	Mandatory
5	Facility and Equipment related variables	Mandatory
6	Quality Assurance (QA), accreditation and certification related variables	Mandatory
7	Personnel and training related variables	Mandatory
8	Specimen management related variables	Mandatory
9	Laboratory information system and linkage to clinical data	Mandatory
Facility-specific variables (facility denotes co-located clinic/hospital or even from stand-alone laboratory as applicable; this information is obtained during phase of data collection)		
1	Ownership of facility (public/private/partnership/mission/military etc.)	Optional
2	Level of facility (primary, secondary, tertiary)	Optional
3	Facility co-location with pharmacy/lab	Optional
4	Number of inpatient beds in 2018 (and prior years as applicable)	Optional
5	Admissions in 2018 (and prior years as applicable)	Optional
6	Outpatients in 2018 (and prior years as applicable)	Optional
7	Presence of ID Department	Optional
8	No of ID physicians	Optional
9	No of ID nurses	Optional
10	Presence of AMS program	Optional
11	Frequency of AMS meetings	Optional
12	Presence of Medical therapeutic committee (MTC)	Optional
13	Frequency of MTC meet	Optional
14	Presence of HIC committee	Optional
15	Frequency of HIC meet	Optional
16	Number of bacterial cultures processed in 2018 (and prior years as applicable)	Optional
17	Number of fungal cultures processed in 2018 (and prior years as applicable)	Optional
18	Number of positive cerebrospinal fluid cultures in 2018 (and prior years as applicable)	Optional
19	Number of positive blood cultures in 2018 (and prior years as applicable)	Optional
20	Format for storing patient laboratory records	Optional
21	Format for storing patient clinical records	Optional

Appendix 5: WHO Priority Pathogens

Pathogen	Resistance	Priority
Acinetobacter baumannii	Carbapenem-resistant	Critical
Pseudomonas aeruginosa	Carbapenem-resistant	Critical
Enterobacterales*	Carbapenem-resistant, ESBL-producing	Critical
Enterococcus faecium	Vancomycin-resistant	High
Staphylococcus aureus	Methicillin-resistant, Vancomycin-intermediate and resistant	High
Helicobacter pylori	Clarithromycin-resistant	High
Campylobacter species	Fluoroquinolone-resistant	High
Neisseria gonorrhoeae	3rd generation Cephalosporin-resistant, Fluoroquinolone-resistant	High
Salmonellae	Fluoroquinolone-resistant	High
Shigella species	Fluoroquinolone-resistant	Medium
Streptococcus pneumoniae	Penicillin-non-susceptible	Medium
Hemophilus influenzae	Ampicillin-resistant	Medium

**Previously known as Enterobacteriaceae.*

Appendix 6: Other clinically important pathogens

Pathogen	Antimicrobial
Acinetobacter species*	Carbapenems Lipopeptides
Enterococcus species*	Aminoglycosides (high level) Vancomycin
E coli*	Carbapenems 3rd generation cephalosporins
H. influenzae*	Ampicillin 3rd generation cephalosporins
Klebsiella species*	Carbapenems 3rd generation cephalosporins
N. meningitidis*	Ampicillin 3rd generation cephalosporins
Pseudomonas species*	Carbapenems Lipopeptides
Salmonella species*	Fluoroquinolones Macrolides 3rd generation cephalosporins
Shigella species*	Fluoroquinolones Macrolides 3rd generation cephalosporins
Staphylococcus aureus*	Methicillin
Staphylococcus species* (other than S. aureus)	Methicillin
S. pneumoniae*	Penicillins Beta-lactam combinations Vancomycin Macrolides
Fungal pathogens**	(As per information available from countries)

*(ii) * from blood and CSF only; ** from all specimens*

Appendix 7: Pathogen Phenotype Definitions

Pathogen	Antimicrobial agent	Numerator	Denominator
Acinetobacter species	Lipopeptides (Colistin and Polymyxin B)	Any isolate that tested non-susceptible to colistin and polymyxin B	Any isolate that tested susceptible or non-susceptible to colistin and polymyxin B
Acinetobacter species	Carbapenems	Any isolate that tested non-susceptible to carbapenems	Any isolate that tested susceptible or non-susceptible to carbapenems
Campylobacter species	Fluoroquinolones	Any isolate that tested non-susceptible to fluoroquinolones	Any isolate that tested susceptible or non-susceptible to fluoroquinolones
Enterobacterales	3rd generation cephalosporins	Any isolate that tested non-susceptible to 3rd generation cephalosporins	Any isolate that tested susceptible or non-susceptible to 3rd generation cephalosporins
Enterobacterales	Carbapenems	Any isolate that tested non-susceptible to carbapenems	Any isolate that tested susceptible or non-susceptible to carbapenems
Enterobacterales	Fluoroquinolones	Any isolate that tested non-susceptible to fluoroquinolones	Any isolate that tested susceptible or non-susceptible to fluoroquinolones
Enterobacterales	Aminoglycosides	Any isolate that tested non-susceptible to aminoglycosides	Any isolate that tested susceptible or non-susceptible to aminoglycosides
Enterobacterales	Beta-lactam combinations including anti-pseudomonals	Any isolate that tested non-susceptible to beta-lactam combinations including anti-pseudomonals	Any isolate that tested susceptible or non-susceptible to beta-lactam combinations including anti-pseudomonals
Enterobacterales	Lipopeptides (Colistin and Polymyxin B)	Any isolate that tested non-susceptible to lipopeptides	Any isolate that tested susceptible or non-susceptible to lipopeptides
Enterobacterales	Ampicillin	Any isolate that tested non-susceptible to ampicillin	Any isolate that tested susceptible or non-susceptible to ampicillin
Enterobacterales	Sulfamethoxazole-Trimethoprim	Any isolate that tested non-susceptible to Sulfamethoxazole-Trimethoprim	Any isolate that tested susceptible or non-susceptible to Sulfamethoxazole-Trimethoprim
Enterobacterales	Macrolides	Any isolate that tested non-susceptible to macrolides	Any isolate that tested susceptible or non-susceptible to macrolides
Enterobacterales	Chloramphenicol	Any isolate that tested non-susceptible to chloramphenicol	Any isolate that tested susceptible or non-susceptible to chloramphenicol
Enterococcus species	Aminoglycosides (high level)	Any isolate that tested non-susceptible to aminoglycosides (high level)	Any isolate that tested susceptible or non-susceptible aminoglycosides (high level)
Enterococcus species	Quinopristin dalfopristin	Any isolate that tested non-susceptible to quinopristin dalfopristin	Any isolate that tested susceptible or non-susceptible to quinopristin dalfopristin
Enterococcus species	Vancomycin	Any isolate that tested non-susceptible to vancomycin	Any isolate that tested susceptible or non-susceptible to vancomycin
Enterococcus species	Ampicillin	Any isolate that tested non-susceptible to ampicillin	Any isolate that tested susceptible or non-susceptible to ampicillin
Haemophilus influenzae	Ampicillin	Any isolate that tested non-susceptible to ampicillin	Any isolate that tested susceptible or non-susceptible to ampicillin

Helicobacter pylori	Clarithromycin	Any isolate that tested non-susceptible to clarithromycin	Any isolate that tested susceptible or non-susceptible to clarithromycin
Neisseria gonorrhoeae	3rd generation cephalosporins	Any isolate that tested non-susceptible to 3rd generation cephalosporins	Any isolate that tested susceptible or non-susceptible to 3rd generation cephalosporins
Neisseria gonorrhoeae	Fluoroquinolones	Any isolate that tested non-susceptible to fluoroquinolones	Any isolate that tested susceptible or non-susceptible to fluoroquinolones
Pseudomonas species	Carbapenems	Any isolate that tested non-susceptible to carbapenems	Any isolate that tested susceptible or non-susceptible to carbapenems
Pseudomonas species	Aminoglycosides	Any isolate that tested non-susceptible to aminoglycosides	Any isolate that tested susceptible or non-susceptible to aminoglycosides
Pseudomonas species	Beta-lactam combinations (anti-pseudomonals)	Any isolate that tested non-susceptible to beta-lactam combinations (anti-pseudomonals)	Any isolate that tested susceptible or non-susceptible to beta-lactam combinations (anti-pseudomonals)
Pseudomonas species	Lipopeptides (Colistin and Polymyxin B)	Any isolate that tested non-susceptible to Colistin and Polymyxin B	Any isolate that tested susceptible or non-susceptible to Colistin and Polymyxin B
Pseudomonas species	Carbapenems	Any isolate that tested non-susceptible to carbapenems	Any isolate that tested susceptible or non-susceptible to carbapenems
Staphylococcus species	Methicillin	Any isolate that tested non-susceptible to penicillins (anti-staphylococcal) or cephamycins	Any isolate that tested susceptible or non-susceptible to penicillins (anti-staphylococcal) or cephamycins
Staphylococcus species (iii)	Vancomycin resistant (iv)	Any isolate that tested resistant to vancomycin (v)	Any isolate that tested susceptible or non-susceptible to vancomycin (vi)
Staphylococcus species	Vancomycin intermediate	Any isolate that tested intermediate to vancomycin	Any isolate that tested susceptible or non-susceptible to vancomycin
Staphylococcus species	Penicillins	Any isolate that tested non-susceptible to penicillins	Any isolate that tested susceptible or non-susceptible to penicillins
Staphylococcus species	Linezolid	Any isolate that tested non-susceptible to linezolids	Any isolate that tested susceptible or non-susceptible to linezolids
Streptococcus pneumoniae	Penicillins	Any isolate that tested non-susceptible to penicillins	Any isolate that tested susceptible or non-susceptible to penicillins
Gram-negatives*	3rd generation cephalosporins	Any isolate that tested non-susceptible to 3rd generation cephalosporins	Any isolate that tested susceptible or non-susceptible to 3rd generation cephalosporins
Gram-negatives*	Carbapenems	Any isolate that tested non-susceptible to carbapenems	Any isolate that tested susceptible or non-susceptible to carbapenems
Gram-negatives*	Lipopeptides (Colistin and Polymyxin B)	Any isolate that tested non-susceptible to Colistin and Polymyxin B.	Any isolate that tested susceptible or non-susceptible to Colistin and Polymyxin B.
Gram-positives*	Vancomycin	Any isolate that tested non-susceptible to vancomycin	Any isolate that tested susceptible or non-susceptible to vancomycin
Gram-positives*	Linezolid	Any isolate that tested non-susceptible to linezolids	Any isolate that tested susceptible or non-susceptible to linezolids

Note: Non-susceptible isolates include isolates which tested resistant or intermediate.

* Reflects pathogens for which only Gram stain identification was available (the number is exclusive of other pathogens identified at genus/species level).

Appendix 8: Pathogens and antimicrobials for AMR drivers and DRI

Pathogen	Antimicrobial
Acinetobacter baumannii	Aminoglycosides
Escherichia coli	Aminoglycosides
Klebsiella pneumoniae	Aminoglycosides
Pseudomonas aeruginosa	Aminoglycosides
Enterococcus faecalis	Aminoglycosides (High)
Enterococcus faecium	Aminoglycosides (High)
Enterococcus faecalis	Aminopenicillins
Enterococcus faecium	Aminopenicillins
Escherichia coli	Aminopenicillins
Acinetobacter baumannii	Carbapenems
Escherichia coli	Carbapenems
Klebsiella pneumoniae	Carbapenems
Pseudomonas aeruginosa	Carbapenems
Acinetobacter baumannii	Cephalosporins (3rd generation)
Escherichia coli	Cephalosporins (3rd generation)
Klebsiella pneumoniae	Cephalosporins (3rd generation)
Pseudomonas aeruginosa	Cephalosporins (3rd generation)
Acinetobacter baumannii	Fluoroquinolone
Escherichia coli	Fluoroquinolones
Klebsiella pneumoniae	Fluoroquinolones
Pseudomonas aeruginosa	Fluoroquinolones
Staphylococcus aureus	Methicillin
Pseudomonas aeruginosa	Beta-lactam combinations
Enterococcus faecalis	Vancomycin
Enterococcus faecium	Vancomycin

AMR Supplementary Tables

Supplementary Table 1: Level of service and affiliation of surveyed laboratories

Affiliation	Surveyed N = 19 n (%)	Reference N = 8 n (%)	Regional/ Intermediate N = 9 n (%)	District/ Community N = 1 n (%)	Unspecified N = 1 n (%)
Government	14 (73.68)	7 (87.5)	6 (66.7)	1 (100.0)	0
Private	3 (15.79)	0	2 (22.2)	0	1 (100.0)
NGO	0	0	0	0	0
Others	2 (10.53)	1 (12.5)	1 (11.1)	0	0

Supplementary Table 2: Assessment of preparedness for AMR surveillance

Parameters	Surveyed laboratories N=19 n (%)
Commodity and equipment status	
Regular power supply and functional back up	16 (84.2)
Continuous water supply	17 (89.5)
Certified and functional biosafety cabinets	7 (36.8)
Automated methods for pathogen identification	8 (42.1)
Automated methods for antimicrobial susceptibility testing	7 (36.8)
Methods for testing antimicrobial resistance mechanisms	7 (36.8)
QMS implementation	
Reported QMS Implementation	
• Reported QMS tool (n=11)	**11 (57.9)**
• LQMS	-
• SLIPTA	-
• SLMTA	**3 (27.3)**
• Mentoring	-
• Combination‡	**5 (45.5)**
• Others	**2 (18.2)**
Quality Certification	**4 (21.1)**
• Reported certification type (n=4)	
• SLIPTA	**1 (25.0)**
• College of American Pathologists	-
• Others	**1 (25.0)**
Accreditation	1 (5.3)
Participation in proficiency testing	7 (36.8)
Utilization of reference strains	8 (42.1)
Reported consistent maintenance of QC records	9 (47.4)
Designated focal quality person	11 (57.9)
Reported compliance to standard operating procedures	17 (89.5)
Reported compliance to antimicrobial susceptibility testing standards	14 (73.7)
Personnel and training status	
Presence of at least one qualified microbiologist	17 (89.5)
Presence of an experienced laboratory scientist/technologist	19 (100)
Up-to-date and complete records on staff training and competence	14 (73.7)
Specimen Management status	
Reported compliance to standard operating procedures on specimen collection and testing	17 (89.5)
Reported compliance to standard operating procedures on specimen rejection	14 (73.7)
Availability on average number of specimens processed for culture and sensitivity in year 2018	18 (94.7)
Laboratory Information System and Linkage to Clinical Data	
Assigned specimen (laboratory) identification number	16 (84.2)
Availability of system/database to store patient data	15 (78.9)
• System/database format (n=15)	
• Paper-based	7 (46.7)
• Electronic	-
• Mixed	8 (53.3)
Captured patients' demographics and clinical information on test request forms	14 (73.7)
• Retrievable test request forms (n=14)	6 (42.9)

**Data reflect laboratory functions between years 2016 - 2018; ‡ Combination refers to more than one option presented in the questionnaire (LQMS, SLIPTA, SLMTA and mentoring).*

Supplementary Table 3: Culture characteristics (yearly)

Variable		Valid			Positive			Positive with AS		
		2017	2018	2019	2017	2018	2019	2017	2018	2019
Annual Totals		**34446**	**43419**	**38496**	**13071**	**14850**	**15114**	**9905**	**11336**	**11304**
Pathogen type	bacteria				10567 (80.8)	11772 (79.3)	12231 (80.9)	8159 (82.4)	9752 (86.0)	9724 (86.0)
	fungi				2504 (19.2)	3078 (20.7)	2883 (19.1)	1746 (17.6)	1584 (14.0)	1580 (14.0)
Age, years	Less than 1	22857 (66.4)	29405 (67.7)	25400 (66.0)	9769 (74.7)	11101 (74.8)	11147 (73.8)	7628 (77.0)	8469 (74.7)	8323 (73.6)
	1 to 17	11588 (33.6)	14002 (32.2)	13090 (34.0)	3302 (25.3)	3748 (25.2)	3965 (26.2)	2277 (23.0)	2866 (25.3)	2981 (26.4)
	18 to 49	1 (0.0)	12 (0.0)	6 (0.0)		1 (0.0)	2 (0.0)		1 (0.0)	
	50 to 65	3533 (10.3)	3709 (8.5)	3919 (10.2)	1690 (12.9)	1481 (10.0)	1672 (11.1)	666 (6.7)	688 (6.1)	644 (5.7)
	Above 65	3795 (11.0)	4232 (9.7)	4988 (13.0)	1091 (8.3)	920 (6.2)	1197 (7.9)	593 (6.0)	631 (5.6)	825 (7.3)
	Unknown Age	16127 (46.8)	19736 (45.5)	18616 (48.4)	6719 (51.4)	8373 (56.4)	8280 (54.8)	5649 (57.0)	6614 (58.3)	6473 (57.3)
Gender	Male	2193 (6.4)	3004 (6.9)	3048 (7.9)	700 (5.4)	1011 (6.8)	1108 (7.3)	616 (6.2)	871 (7.7)	954 (8.4)
	Female	1265 (3.7)	1824 (4.2)	1970 (5.1)	443 (3.4)	708 (4.8)	807 (5.3)	386 (3.9)	645 (5.7)	751 (6.6)
	Unknown gender	7533 (21.9)	10914 (25.1)	5955 (15.5)	2428 (18.6)	2357 (15.9)	2050 (13.6)	1995 (20.1)	1887 (16.6)	1657 (14.7)
Laboratory	HGOPED	3139 (9.1)	3314 (7.6)	3137 (8.1)	1036 (7.9)	888 (6.0)	825 (5.5)	956 (9.7)	859 (7.6)	700 (6.2)
	Lama	1364 (4.0)	1178 (2.7)	972 (2.5)	532 (4.1)	398 (2.7)	326 (2.2)	417 (4.2)	317 (2.8)	237 (2.1)
	CHU Yaounde	1357 (3.9)	1632 (3.8)	834 (2.2)	657 (5.0)	718 (4.8)	559 (3.7)	607 (6.1)	558 (4.9)	464 (4.1)
	Prima	3283 (9.5)	7207 (16.6)	4684 (12.2)	841 (6.4)	3026 (20.4)	2133 (14.1)	577 (5.8)	2231 (19.7)	1499 (13.3)
	Limbe	3074 (8.9)	2235 (5.1)	2243 (5.8)	1701 (13.0)	1473 (9.9)	1143 (7.6)	1685 (17.0)	1451 (12.8)	1126 (10.0)
	Laquintinie	3053 (8.9)	1348 (3.1)	4517 (11.7)	1109 (8.5)	593 (4.0)	1690 (11.2)	971 (9.8)	484 (4.3)	1544 (13.7)
	Maroua	864 (2.5)	339 (0.8)	870 (2.3)	239 (1.8)	118 (0.8)	174 (1.2)	205 (2.1)	109 (1.0)	159 (1.4)
	HGOPY	6490 (18.8)	6567 (15.1)	6693 (17.4)	3471 (26.6)	3202 (21.6)	3597 (23.8)	1515 (15.3)	1670 (14.7)	1583 (14.0)
	Douala	3194 (9.3)	4994 (11.5)	2775 (7.2)	581 (4.4)	1014 (6.8)	800 (5.3)	432 (4.4)	680 (6.0)	517 (4.6)
	Bonassama	301 (0.9)	368 (0.8)	394 (1.0)	130 (1.0)	88 (0.6)	96 (0.6)	130 (1.3)	88 (0.8)	96 (0.8)
	HMR	1660 (4.8)	1913 (4.4)	1581 (4.1)	655 (5.0)	587 (4.0)	631 (4.2)	536 (5.4)	574 (5.1)	629 (5.6)
	GT Labo	2447 (7.1)	2464 (5.7)	1990 (5.2)	898 (6.9)	917 (6.2)	746 (4.9)	898 (9.1)	916 (8.1)	746 (6.6)
	Ebolowa	674 (2.0)	642 (1.5)	1636 (4.2)	288 (2.2)	252 (1.7)	694 (4.6)	288 (2.9)	252 (2.2)	694 (6.1)
	Buea	2849 (8.3)	8047 (18.5)	4544 (11.8)	776 (5.9)	1036 (7.0)	1061 (7.0)	532 (5.4)	655 (5.8)	680 (6.0)
	Esoss		86 (0.2)	169 (0.4)		45 (0.3)	91 (0.6)		44 (0.4)	87 (0.8)
	HG Yaounde	697 (2.0)	1085 (2.5)	1457 (3.8)	157 (1.2)	495 (3.3)	548 (3.6)	156 (1.6)	448 (4.0)	543 (4.8)

Supplementary Table 4: Specimen characteristics

Specimen Type	All years* N= 32545 n (%)	2017 N = 9905 n (%)	2018 N = 11336 n (%)	2019 N = 11304 n (%)
Abscess (abdominal)	2 (0)	2 (0)	-	-
Abscess/Discharge/Pus/Swab/Wound	17442 (53.6)	5451 (55)	6017 (53.1)	5974 (52.8)
Aspirate (FNAC/Fine Needle)	1 (0)	-	-	1 (0)
Aspirate/discharge	73 (0.2)	18 (0.2)	31 (0.3)	24 (0.2)
Blood	1629 (5)	431 (4.4)	563 (5)	635 (5.6)
Catheter (peripheral line)	123 (0.4)	60 (0.6)	35 (0.3)	28 (0.2)
Catheter (umbilical)	3 (0)	-	-	3 (0)
Catheter (unspecified)	78 (0.2)	15 (0.2)	15 (0.1)	48 (0.4)
Catheter (urinary)	169 (0.5)	23 (0.2)	115 (1)	31 (0.3)
CSF	115 (0.4)	58 (0.6)	28 (0.2)	29 (0.3)
Drain	15 (0)	14 (0.1)	1 (0)	-
Fluid (abdominal/peritoneal)	31 (0.1)	11 (0.1)	9 (0.1)	11 (0.1)
Fluid (bile)	1 (0)	-	-	1 (0)
Fluid (dialysis)	1 (0)	-	1 (0)	-
Fluid (Gastric)	2 (0)	2 (0)	-	-
Fluid (joint/synovial)	11 (0)	4 (0)	5 (0)	2 (0)
Fluid (pleural)	55 (0.2)	12 (0.1)	16 (0.1)	27 (0.2)
Fluid (scrotal)	51 (0.2)	19 (0.2)	21 (0.2)	11 (0.1)
Fluid (shunt)	1 (0)	-	1 (0)	-
Fluid (unspecified)	128 (0.4)	51 (0.5)	47 (0.4)	30 (0.3)
Others	30 (0.1)	17 (0.1)	4 (0)	9 (0.1)
Respiratory-Lower	23 (0.1)	5 (0.1)	6 (0.1)	12 (0.1)
Respiratory-Upper	86 (0.3)	36 (0.4)	26 (0.2)	24 (0.2)
Semen	350 (1.1)	108 (1.1)	130 (1.1)	112 (1)
Stool	1751 (5.4)	428 (4.3)	559 (4.9)	764 (6.8)
Swab (cervical)	550 (1.7)	224 (2.3)	324 (2.9)	2 (0)
Swab (urethral)	248 (0.8)	34 (0.3)	113 (1)	101 (0.9)
Swab (vaginal)	1890 (5.8)	584 (5.9)	532 (4.7)	774 (6.8)
Swab/discharge (genital)	226 (0.7)	52 (0.5)	46 (0.4)	128 (1.1)
Swab/discharge (urethral)	36 (0.1)	23 (0.2)	7 (0.1)	6 (0.1)
Tissue/biopsy	48 (0.1)	28 (0.3)	7 (0.1)	13 (0.1)
Urine	7376 (22.7)	2195 (22.2)	2677 (23.6)	2504 (22.2)

**Indicates positive cultures with AST results*

Supplementary Table 5: Pathogen identification

Pathogen	All years* N= 32,545 n (%)	2017 N = 9,905 n (%)	2018 N = 11,336 n (%)	2019 N = 11,304 n (%)
Positive cultures with specific pathogen name	29311 (90.1)	8842 (89.3)	10398 (91.7)	10071 (89.1)
Achromobacter xylosoxidans ss. denitrificans	1 (0)	-	-	1 (0)
Acidovorax facilis	1 (0)	1 (0)	-	-
Acinetobacter anitratus	1 (0)	1 (0)	-	-
Acinetobacter baumannii	314 (1)	56 (0.6)	122 (1.1)	136 (1.2)
Acinetobacter calcoaceticus	9 (0)	-	1 (0)	8 (0.1)
Acinetobacter haemolyticus	8 (0)	-	3 (0)	5 (0)
Acinetobacter lwoffii	14 (0)	-	3 (0)	11 (0.1)
Aerococcus urinae	2 (0)	2 (0)	-	-
Aerococcus viridans	13 (0)	12 (0.1)	1 (0)	-
Aeromonas hydrophila	4 (0)	1 (0)	2 (0)	1 (0)
Aeromonas sobria	17 (0.1)	11 (0.1)	4 (0)	2 (0)
Alcaligenes faecalis	3 (0)	-	-	3 (0)
Arcobacter butzleri	1 (0)	1 (0)	-	-
Aspergillus clavatus	1 (0)	-	1 (0)	-
Aspergillus flavus	1 (0)	-	-	1 (0)
Aspergillus niger	2 (0)	2 (0)	-	-
Bacteroides fragilis	1 (0)	-	-	1 (0)
Bordetella bronchiseptica	2 (0)	-	-	2 (0)
Brevundimonas diminuta	1 (0)	-	1 (0)	-
Brevundimonas vesicularis	1 (0)	-	-	1 (0)
Budvicia aquatica	1 (0)	-	1 (0)	-
Burkholderia cepacia	28 (0.1)	7 (0.1)	3 (0)	18 (0.2)
Campylobacter coli	1 (0)	1 (0)	-	-
Candida albicans	3736 (11.5)	1418 (14.3)	1225 (10.8)	1093 (9.7)
Candida ciferrii	10 (0)	-	-	10 (0.1)
Candida dubliniensis	1 (0)	-	-	1 (0)
Candida famata	7 (0)	1 (0)	1 (0)	5 (0)
Candida glabrata	20 (0.1)	2 (0)	-	18 (0.2)
Candida krusei	15 (0)	4 (0)	6 (0.1)	5 (0)
Candida lusitaniae	2 (0)	-	-	2 (0)
Candida parapsilosis	5 (0)	1 (0)	-	4 (0)
Candida rugosa	2 (0)	-	2 (0)	-
Candida tropicalis	10 (0)	2 (0)	-	8 (0.1)
Cedecea neteri	1 (0)	-	1 (0)	-
Chromobacterium violaceum	3 (0)	-	3 (0)	-
Chryseobacterium indologenes	2 (0)	-	2 (0)	-
Chryseomonas luteola	36 (0.1)	8 (0.1)	13 (0.1)	15 (0.1)
Citrobacter braakii	19 (0.1)	6 (0.1)	10 (0.1)	3 (0)

Citrobacter farmeri	7 (0)	-	5 (0)	2 (0)
Citrobacter freundii	313 (1)	84 (0.8)	97 (0.9)	132 (1.2)
Citrobacter koseri	89 (0.3)	13 (0.1)	48 (0.4)	28 (0.2)
Citrobacter sedlakii	1 (0)	-	1 (0)	-
Citrobacter werkmanii	1 (0)	-	-	1 (0)
Citrobacter youngae	15 (0)	7 (0.1)	4 (0)	4 (0)
Corynebacterium xerosis	1 (0)	1 (0)	-	-
Cronobacter sakazakii	40 (0.1)	14 (0.1)	8 (0.1)	18 (0.2)
Cryptococcus albidus	4 (0)	4 (0)	-	-
Cryptococcus laurentii	4 (0)	-	2 (0)	2 (0)
Cryptococcus neoformans	10 (0)	3 (0)	4 (0)	3 (0)
Dermatophytes	2 (0)	-	-	2 (0)
Edwardsiella tarda	3 (0)	-	1 (0)	2 (0)
Enterobacter amnigenus	4 (0)	3 (0)	-	1 (0)
Enterobacter asburiae	4 (0)	1 (0)	2 (0)	1 (0)
Enterobacter cancerogenus	1 (0)	-	1 (0)	-
Enterobacter cloacae	318 (1)	90 (0.9)	113 (1)	115 (1)
Enterobacter dissolvens	2 (0)	2 (0)	-	-
Enterobacter gergoviae	8 (0)	2 (0)	2 (0)	4 (0)
Enterobacter hormaechei	1 (0)	-	-	1 (0)
Enterococcus faecalis	35 (0.1)	15 (0.2)	8 (0.1)	12 (0.1)
Enterococcus faecium	4 (0)	2 (0)	2 (0)	-
Enterococcus gallinarum	1 (0)	-	-	1 (0)
Enterococcus raffinosus	1 (0)	-	-	1 (0)
Escherichia coli	4965 (15.3)	1478 (14.9)	1755 (15.5)	1732 (15.3)
Escherichia fergusonii	1 (0)	-	-	1 (0)
Escherichia hermannii	1 (0)	-	-	1 (0)
Escherichia vulneris	5 (0)	1 (0)	3 (0)	1 (0)
Flavimonas oryzihabitans	14 (0)	4 (0)	1 (0)	9 (0.1)
Gardnerella vaginalis	4065 (12.5)	1157 (11.7)	1455 (12.8)	1453 (12.9)
Gemella haemolysans	2 (0)	1 (0)	1 (0)	-
Gemella morbillorum	1 (0)	1 (0)	-	-
Haemophilus influenzae	3 (0)	1 (0)	2 (0)	-
Haemophilus parainfluenzae	2 (0)	-	-	2 (0)
Hafnia alvei	10 (0)	-	5 (0)	5 (0)
Klebsiella aerogenes	171 (0.5)	55 (0.6)	56 (0.5)	60 (0.5)
Klebsiella oxytoca	135 (0.4)	30 (0.3)	66 (0.6)	39 (0.3)
Klebsiella pneumoniae	2401 (7.4)	599 (6)	979 (8.6)	823 (7.3)
Kluyvera ascorbata	2 (0)	-	-	2 (0)
Kluyvera cryocrescens	3 (0)	-	-	3 (0)
Kluyvera intermedia	43 (0.1)	7 (0.1)	18 (0.2)	18 (0.2)
Kocuria kristinae	1 (0)	-	-	1 (0)

Kocuria varians	1 (0)	1 (0)	-	-
Lactococcus lactis	2 (0)	1 (0)	1 (0)	-
Leclercia adecarboxylata	2 (0)	-	2 (0)	-
Listeria monocytogenes	2 (0)	-	-	2 (0)
Microsporum canis	1 (0)	-	1 (0)	-
Morganella morganii	61 (0.2)	8 (0.1)	20 (0.2)	33 (0.3)
Mycoplasma capricolum	4 (0)	4 (0)	-	-
Mycoplasma hominis	2285 (7)	777 (7.8)	759 (6.7)	749 (6.6)
Neisseria elongata	1 (0)	-	-	1 (0)
Neisseria gonorrhoeae	152 (0.5)	64 (0.6)	47 (0.4)	41 (0.4)
Neisseria meningitidis	3 (0)	-	2 (0)	1 (0)
Neisseria subflava	2 (0)	-	2 (0)	-
Oligella ureolytica	1 (0)	-	-	1 (0)
Oligella urethralis	1 (0)	-	1 (0)	-
Ornithobacterium rhinotracheale	1 (0)	-	1 (0)	-
Pantoea (enterobacter) agglomerans	27 (0.1)	8 (0.1)	10 (0.1)	9 (0.1)
Pasteurella multocida	2 (0)	-	-	2 (0)
Pasteurella pneumotropica	4 (0)	2 (0)	2 (0)	-
Plesiomonas shigelloides	1 (0)	-	1 (0)	-
Propionibacterium acnes	2 (0)	2 (0)	-	-
Proteus hauseri	2 (0)	-	-	2 (0)
Proteus mirabilis	286 (0.9)	74 (0.7)	101 (0.9)	111 (1)
Proteus penneri	2 (0)	-	2 (0)	-
Proteus vulgaris	25 (0.1)	6 (0.1)	8 (0.1)	11 (0.1)
Providencia alcalifaciens	2 (0)	1 (0)	-	1 (0)
Providencia rettgeri	22 (0.1)	-	13 (0.1)	9 (0.1)
Providencia stuartii	14 (0)	1 (0)	7 (0.1)	6 (0.1)
Pseudomonas aeruginosa	562 (1.7)	95 (1)	222 (2)	245 (2.2)
Pseudomonas fluorescens	29 (0.1)	1 (0)	16 (0.1)	12 (0.1)
Pseudomonas mendocina	1 (0)	-	-	1 (0)
Pseudomonas putida	2 (0)	1 (0)	-	1 (0)
Pseudomonas stutzeri	4 (0)	-	1 (0)	3 (0)
Raoultella ornithinolytica	74 (0.2)	31 (0.3)	33 (0.3)	10 (0.1)
Raoultella planticola	2 (0)	2 (0)	-	-
Raoultella terrigena	10 (0)	1 (0)	2 (0)	7 (0.1)
Rickettsia conorii	2 (0)	1 (0)	-	1 (0)
Ruminococcus hansenii	1 (0)	1 (0)	-	-
Saccharomyces cerevisiae	2 (0)	-	2 (0)	-
Salmonella agona	1 (0)	-	1 (0)	-
Salmonella choleraesuis	6 (0)	3 (0)	2 (0)	1 (0)
Salmonella enterica	6 (0)	-	1 (0)	5 (0)
Salmonella enteritidis	9 (0)	1 (0)	2 (0)	6 (0.1)

Salmonella paratyphi	30 (0.1)	3 (0)	9 (0.1)	18 (0.2)
Salmonella saintpaul	1 (0)	-	-	1 (0)
Salmonella typhi	13 (0)	1 (0)	10 (0.1)	2 (0)
Serratia ficaria	13 (0)	4 (0)	4 (0)	5 (0)
Serratia fonticola	23 (0.1)	8 (0.1)	5 (0)	10 (0.1)
Serratia liquefaciens	31 (0.1)	8 (0.1)	15 (0.1)	8 (0.1)
Serratia marcescens	91 (0.3)	31 (0.3)	27 (0.2)	33 (0.3)
Serratia odorifera	48 (0.1)	17 (0.2)	21 (0.2)	10 (0.1)
Serratia plymuthica	22 (0.1)	10 (0.1)	8 (0.1)	4 (0)
Serratia rubidaea	1 (0)	-	1 (0)	-
Shewanella putrefaciens	2 (0)	1 (0)	1 (0)	-
Shigella boydii	14 (0)	5 (0.1)	6 (0.1)	3 (0)
Shigella dysenteriae	9 (0)	4 (0)	1 (0)	4 (0)
Shigella flexneri	2 (0)	-	-	2 (0)
Shigella sonnei	9 (0)	-	2 (0)	7 (0.1)
Sphingomonas paucimobilis	6 (0)	1 (0)	4 (0)	1 (0)
Staphylococcus arlettae	1 (0)	1 (0)	-	-
Staphylococcus aureus	2279 (7)	694 (7)	802 (7.1)	783 (6.9)
Staphylococcus capitis	1 (0)	1 (0)	-	-
Staphylococcus caprae	1 (0)	-	-	1 (0)
Staphylococcus chromogenes	1 (0)	-	1 (0)	-
Staphylococcus cohnii	1 (0)	-	1 (0)	-
Staphylococcus epidermidis	103 (0.3)	30 (0.3)	28 (0.2)	45 (0.4)
Staphylococcus gallinarum	1 (0)	-	-	1 (0)
Staphylococcus haemolyticus	23 (0.1)	5 (0.1)	6 (0.1)	12 (0.1)
Staphylococcus hominis	5 (0)	2 (0)	-	3 (0)
Staphylococcus pasteuri	1 (0)	1 (0)	-	-
Staphylococcus piscifermentans	3 (0)	-	1 (0)	2 (0)
Staphylococcus pseudintermedius	2 (0)	-	-	2 (0)
Staphylococcus saprophyticus	363 (1.1)	119 (1.2)	111 (1)	133 (1.2)
Staphylococcus schleiferi	132 (0.4)	33 (0.3)	28 (0.2)	71 (0.6)
Staphylococcus sciuri	7 (0)	2 (0)	1 (0)	4 (0)
Staphylococcus simulans	1 (0)	1 (0)	-	-
Staphylococcus warneri	4 (0)	-	3 (0)	1 (0)
Staphylococcus xylosus	16 (0)	3 (0)	1 (0)	12 (0.1)
Stenotrophomonas (xanthomonas) maltophilia	7 (0)	-	2 (0)	5 (0)
Streptococcus agalactiae	11 (0)	2 (0)	8 (0.1)	1 (0)
Streptococcus alactolyticus	1 (0)	1 (0)	-	-
Streptococcus anginosus	1 (0)	1 (0)	-	-
Streptococcus bovis	2 (0)	-	1 (0)	1 (0)
Streptococcus canis	2 (0)	2 (0)	-	-
Streptococcus dysgalactiae	1 (0)	1 (0)	-	-

Streptococcus ferus	1 (0)	-	1 (0)	-
Streptococcus gallolyticus	1 (0)	-	1 (0)	-
Streptococcus gordonii	1 (0)	1 (0)	-	-
Streptococcus milleri	10 (0)	3 (0)	4 (0)	3 (0)
Streptococcus mitis	5 (0)	3 (0)	2 (0)	-
Streptococcus oralis	2 (0)	1 (0)	-	1 (0)
Streptococcus parasanguinis	1 (0)	-	-	1 (0)
Streptococcus pneumoniae	37 (0.1)	18 (0.2)	11 (0.1)	8 (0.1)
Streptococcus pyogenes	11 (0)	1 (0)	6 (0.1)	4 (0)
Streptococcus salivarius	1 (0)	-	1 (0)	-
Streptococcus sanguinis	6 (0)	4 (0)	2 (0)	-
Streptococcus suis	1 (0)	-	-	1 (0)
Streptococcus thoraltensis	1 (0)	1 (0)	-	-
Streptococcus viridans	2 (0)	1 (0)	-	1 (0)
Trichophyton rubrum	1 (0)	-	1 (0)	-
Trichosporon asahii	2 (0)	-	-	2 (0)
Ureaplasma urealyticum	5321 (16.3)	1616 (16.3)	1950 (17.2)	1755 (15.5)
Vibrio metschnikovii	1 (0)	1 (0)	-	-
Yeast	2 (0)	2 (0)	-	-
Yersinia enterocolitica	6 (0)	-	3 (0)	3 (0)
Yersinia intermedia	1 (0)	-	1 (0)	-
Yersinia kristensenii	1 (0)	-	-	1 (0)
Yersinia pestis	1 (0)	-	1 (0)	-
Yersinia ruckeri	1 (0)	-	-	1 (0)
Positive cultures without specific pathogen name	3234 (9.9)	1063 (10.7)	938 (8.3)	1233 (10.9)
Achromobacter Sp.	1 (0)	-	-	1 (0)
Acidovorax Sp.	1 (0)	-	1 (0)	-
Acinetobacter Sp.	88 (0.3)	10 (0.1)	24 (0.2)	54 (0.5)
Aerococcus Sp.	1 (0)	-	1 (0)	-
Aeromonas Sp.	4 (0)	1 (0)	1 (0)	2 (0)
Aspergillus Sp.	1 (0)	-	-	1 (0)
Bacteroides Sp.	1 (0)	-	-	1 (0)
Campylobacter Sp.	1 (0)	1 (0)	-	-
Candida Sp.	1063 (3.3)	306 (3.1)	337 (3)	420 (3.7)
Chryseomonas Sp.	1 (0)	-	-	1 (0)
Citrobacter Sp.	20 (0.1)	4 (0)	9 (0.1)	7 (0.1)
Clostridium Sp.	1 (0)	1 (0)	-	-
Corynebacterium Sp.	6 (0)	1 (0)	2 (0)	3 (0)
Cryptococcus Sp.	3 (0)	-	1 (0)	2 (0)
Enterobacter Sp.	101 (0.3)	36 (0.4)	16 (0.1)	49 (0.4)
Enterococcus Sp.	87 (0.3)	25 (0.3)	44 (0.4)	18 (0.2)
Escherichia Sp.	2 (0)	1 (0)	1 (0)	-

Gardnerella Sp.	60 (0.2)	6 (0.1)	-	54 (0.5)
Geotrichum Sp.	1 (0)	1 (0)	-	-
Haemophilus Sp.	13 (0)	10 (0.1)	3 (0)	-
Klebsiella Sp.	218 (0.7)	106 (1.1)	43 (0.4)	69 (0.6)
Kluyvera Sp.	10 (0)	4 (0)	5 (0)	1 (0)
Leuconostoc Sp.	1 (0)	1 (0)	-	-
Listeria Sp.	3 (0)	-	1 (0)	2 (0)
Listonella Sp.	1 (0)	1 (0)	-	-
Micrococcus Sp.	2 (0)	2 (0)	-	-
Microsporum Sp.	1 (0)	-	1 (0)	-
Mobiluncus Sp.	1 (0)	1 (0)	-	-
Moraxella Sp.	1 (0)	-	-	1 (0)
Mycoplasma Sp.	39 (0.1)	3 (0)	-	36 (0.3)
Neisseria Sp.	6 (0)	1 (0)	1 (0)	4 (0)
Ochrobactrum Sp.	1 (0)	-	-	1 (0)
Other	6 (0)	6 (0.1)	-	-
Pantoea Sp.	99 (0.3)	28 (0.3)	42 (0.4)	29 (0.3)
Pasteurella Sp.	4 (0)	-	3 (0)	1 (0)
Photobacterium Sp.	1 (0)	-	-	1 (0)
Proteus Sp.	81 (0.2)	20 (0.2)	17 (0.1)	44 (0.4)
Providencia Sp.	11 (0)	2 (0)	3 (0)	6 (0.1)
Pseudomonas Sp.	93 (0.3)	34 (0.3)	28 (0.2)	31 (0.3)
Raoultella Sp.	2 (0)	1 (0)	1 (0)	-
Salmonella Sp.	216 (0.7)	46 (0.5)	81 (0.7)	89 (0.8)
Serratia Sp.	16 (0)	3 (0)	7 (0.1)	6 (0.1)
Shewanella Sp.	1 (0)	-	-	1 (0)
Shigella Sp.	106 (0.3)	23 (0.2)	53 (0.5)	30 (0.3)
Sphingobacterium Sp.	1 (0)	1 (0)	-	-
Staphylococcus Sp.	286 (0.9)	109 (1.1)	89 (0.8)	88 (0.8)
Stenotrophomonas Sp.	2 (0)	-	1 (0)	1 (0)
Streptobacillus Sp.	4 (0)	2 (0)	2 (0)	-
Streptococcus Sp.	351 (1.1)	106 (1.1)	104 (0.9)	141 (1.2)
Streptomyces Sp.	1 (0)	-	1 (0)	-
Trichosporon Sp.	1 (0)	-	-	1 (0)
Unspecified (Gram negative bacilli)	81 (0.2)	72 (0.7)	2 (0)	7 (0.1)
Unspecified (Gram negative bacteria)	91 (0.3)	77 (0.8)	-	14 (0.1)
Unspecified (Gram positive bacilli)	1 (0)	-	-	1 (0)
Unspecified (Gram positive bacteria)	5 (0)	4 (0)	-	1 (0)
Unspecified (Gram positive cocci)	30 (0.1)	4 (0)	13 (0.1)	13 (0.1)
Unspecified (Gram variable coccobacilli)	1 (0)	1 (0)	-	-
Ureaplasma Sp.	2 (0)	2 (0)	-	-
Yersinia Sp.	1 (0)	-	-	1 (0)

*Note: * indicates positive cultures with AST results; '-' means information was not available.*

Supplementary Table 6: Laboratory data scoring

Laboratory name	Laboratory data score (out of 4)			
	2017	2018	2019	Average
HGOPED	4	4	4	4
Lama Yaounde	4	4	3	3.7
CHU Yaounde	4	4	4	4
Prima Sarl	4	4	4	4
Limbe	4	4	4	4
Laquintinie	3	4	4	3.7
CNPS Marona	4	4	4	4
HGOPY	4	4	4	4
CHU Douala	4	4	4	4
Bonassama	4	4	4	4
HMR 1 Yaounde	4	3	3	3.3
GT LABO	4	4	4	4
d'Ebolowa	3	3	3	3
CH Esoss	4	4	4	4
Buea		4	4	4
HG Younde	4	4	4	4

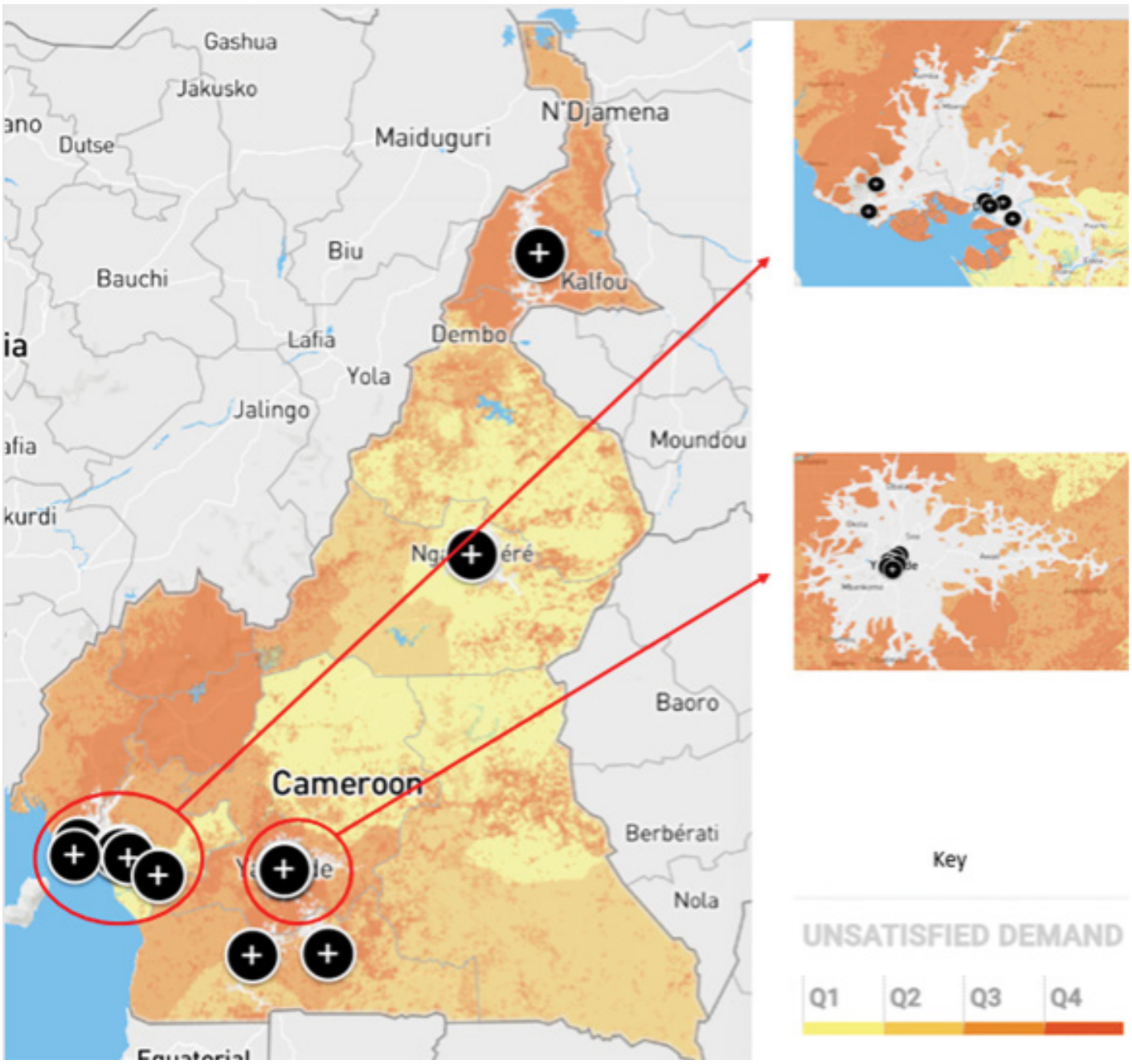
Supplementary Table 7: Univariate logistic regression analysis

Variable	Options	N	NS (%)	Crude OR (95% CI)	P-value
Gender	Female	15935	51.6	Ref	0.000
	Male	10834	57.2	1.26 (1.17 - 1.35)	
Age, years	<1	3551	52.4	1.00 (0.86 - 1.18)	0.000
	1-17	3112	51.5	0.97 (0.84 - 1.12)	
	18-49	11604	52.3	Ref	
	50-65	4199	58.7	1.30 (1.15 - 1.45)	
	>65	3069	57.5	1.23 (1.12 - 1.36)	

N-number of tested isolates; NS (%)-Proportion of non-susceptible isolates; Ref: Reference category

AMR Supplementary Figures

Supplementary Figure 1: Population coverage of laboratories



Supplementary Figure 2a: Inappropriate testing A

Organism Name	Antimicrobial Agent	Agent Code	Interpreted Results	Antimicrobial Susceptibility Method	Year
Pseudomonas aeruginosa	Clotrimazole	CTR_ND10	R	Disk	2017
Serratia marcescens	Clotrimazole	CTR_ND10	R	Disk	2017
Escherichia coli	Clotrimazole	CTR_ND10	R	Disk	2017
Serratia ficaria	Clotrimazole	CTR_ND10	R	Disk	2017
Gardnerella vaginalis	Fluconazole	FLU_NM	R	Disk	2017
Gardnerella vaginalis	Miconazole	MCZ_NM	R	Disk	2017
Escherichia coli	Amphotericin B	AMB_ND10	R	Disk	2017
Escherichia coli	Miconazole	MCZ_ND10	R	Disk	2017
Escherichia coli	Ketoconazole	KET_ND15	R	Disk	2018
Salmonella paratyphi B	Fluconazole	FLU_ND25	R	Disk	2018
Salmonella sp.	Fluconazole	FLU_ND25	R	Disk	2018
Escherichia coli	Fluconazole	FLU_ND25	R	Disk	2018
Escherichia coli	Ketoconazole	KET_ND15	I	Disk	2018
Salmonella paratyphi B	Miconazole	MCZ_ND10	R	Disk	2018
Klebsiella aerogenes	Pimaricin	PMR_ND	R	Disk	2019
Escherichia coli	Pimaricin	PMR_ND	R	Disk	2019
Shigella Sp.	Amphotericin B	AMB_ND10	R	Disk	2019
Salmonella paratyphi B	Nystatin	NYS_ND50	I	Disk	2019
Candida albicans	Ciprofloxacin	CIP_ND5	R	Disk	2017
Candida albicans	Erythromycin	ERY_ND15	R	Disk	2017
Candida albicans	Tetracycline	TCY_ND30	I	Disk	2017
Candida albicans	Ciprofloxacin	CIP_ND5	I	Disk	2017
Candida albicans	Ciprofloxacin	CIP_ND5	R	Disk	2018
Candida albicans	Clindamyclin	CLI_ND2	R	Disk	2018
Candida albicans	Ofloxacin	OFX_ND5	I	Disk	2018
Candida albicans	Tetracycline	TCY_ND30	I	Disk	2018
Candida albicans	Chloramphenicol	CHL_NM	R	Disk	2018
Candida albicans	Flucloxacillin	FLC_NM	R	Disk	2018
Candida krusei	Chloramphenicol	CHL_NM	R	Disk	2018
Candida albicans	Flucloxacillin	FLC_NM	R	Disk	2018
Candida albicans	Chloramphenicol	CHL_NM	R	Disk	2019
Candida albicans	Chloramphenicol	CHL_NM	R	Disk	2019
Candida albicans	Trimethoprim	TMP_ND5	R	Disk	2019

Supplementary Figure 2b: Inappropriate testing B

Organism Name	Antimicrobial Agent	Agent Code	Interpreted Results	Antimicrobial Susceptibility Method	Year
Escherichia coli	Penicillin G	PEN_NM	I	Disk	2017
Escherichia coli	Oxacillin	OXA_ND1	R	Disk	2017
Enterobacter sp.	Oxacillin	OXA_ND1	I	Disk	2017
Escherichia coli	Penicillin G	PEN_ND10	R	Disk	2017
Escherichia coli	Oxacillin	OXA_ND1	R	Disk	2017
Escherichia coli	Vancomycin	VAN_NM	S	Disk	2018
Salmonella sp.	Penicillin G	PEN_ND10	I	Disk	2018
Klebsiella pneumoniae ss. pneumoniae	Oxacillin	OXA_ND1	R	Disk	2018
Klebsiella pneumoniae ss. pneumoniae	Penicillin G	PEN_ND10	R	Disk	2018
Enterobacter cloacae	Oxacillin	OXA_NM	R	Disk	2018
Escherichia coli	Penicillin G	PEN_ND10	R	Disk	2018
Shigella sp.	Penicillin G	PEN_ND10	R	Disk	2018
Klebsiella pneumoniae ss. pneumoniae	Penicillin G	PEN_ND10	R	Disk	2019
Klebsiella pneumoniae ss. pneumoniae	Penicillin G	PEN_ND10	R	Disk	2019
Klebsiella pneumoniae ss. pneumoniae	Oxacillin	OXA_ND1	R	Disk	2019
Proteus mirabilis	Penicillin G	PEN_ND10	R	Disk	2019
Staphylococcus aureus ss aureus	Vancomycin	VAN_ND30	R	Disk	2017
Staphylococcus aureus ss aureus	Vancomycin	VAN_ND30	R	Disk	2017
Staphylococcus aureus ss aureus	Vancomycin	VAN_ND30	R	Disk	2017
Staphylococcus schleiferi	Vancomycin	VAN_ND30	S	Disk	2018
Staphylococcus schleiferi	Vancomycin	VAN_ND30	S	Disk	2018
Staphylococcus schleiferi	Vancomycin	VAN_ND30	S	Disk	2018
Staphylococcus aureus ss aureus	Vancomycin	VAN_ND30	R	Disk	2019
Staphylococcus aureus ss aureus	Vancomycin	VAN_ND30	I	Disk	2019
Staphylococcus aureus ss aureus	Vancomycin	VAN_ND30	R	Disk	2019
Staphylococcus aureus ss aureus	Vancomycin	VAN_ND30	R	Disk	2019
Staphylococcus aureus ss aureus	Vancomycin	VAN_ND30	R	Disk	2019

AMC Appendices

Appendix 1: Key Informant Interview (KII) tool

(Contains ALL questions: However, during implementation, only specific questions were asked to suitable stakeholders)

Domestic Producers and Importers

1.1	What quantity/proportion of antibiotics are produced/manufactured (if any) within the country?	N/A
1.2	If domestically produced what manufactured quantity is later exported?	
1.3	What quantity/proportion of antibiotics are imported?	
1.4	What proportion (if any) are then re-exported?	

Procurement, Storage and Distribution

1.5	Are there any specific regulations regarding Procurement and/or storage of antibiotics?	Yes		No	

Public Sector

1.6	Who supplies to the public sector (names of the companies/organisations)?
1.7	What role (if any) does the Central Medical Stores play in the procurement, storage and distribution of antibiotics in the country?
1.8	What quantity/proportion of antibiotics is purchased by public healthcare facilities from central medical stores and what quantity/ proportion from wholesalers/other suppliers? (specify who these other suppliers are)
1.9	How do public facilities procure and receive their antibiotic supplies?

Private Sector

1.10	Who supplies to the private sector (names of the companies/organisations)?
1.11	What quantity/proportion of antibiotics is purchased by Private healthcare facilities from central medical stores and what quantity/ proportion from wholesalers/other suppliers? (specify who these other suppliers are)
1.12	How do private facilities procure and receive their antibiotic supplies?

Donor Funded Supply

1.13	Is there any donor support for procurement of antibiotics in the country?	Yes		No	
1.14	If yes to above, who are the donors and what are the procedures regarding import and distribution of donated antibiotics?				
1.15	Which sector(s) is supported with supplies procured through donor agencies?				
	Public Sector		Private		
1.16	If there is donor support, are antibiotics sourced locally or imported?				
1.17	Does the available donor data indicate specific country antibiotic consumption? Do these procurement mechanisms fit in with the countries regulatory systems and WHOs recommended surveillance practices? or are there challenges?				
1.18	What proportion/quantity of antibiotics are procured/supplied from donor programs; and using which mechanisms are such products procured e.g., WAMBO for The Global Fund, pooled procurement mechanisms etc.				
1.19	What are the requirements and procedures for suppliers to import/export antibiotics in the country?				

2. Data and Information Systems

2.1	What information systems are currently in use at **national level** for managing data on antibiotics?						
2.2	Are the systems manual or electronic?						
Manual				Electronic			
2.3	What type of information is captured using these systems? (e.g. generic names, dose strengths, formulations, pack size, brand names and volumes)						
Generic names		Dose strengths		Formulations		Pack size/ Volumes	
Brand names		Other:					
2.4	Does the country have a centralised data source for all antibiotics that are imported/exported?						
No		Yes, manual data system		Yes, electronic data system			
2.5	What are the available data sources to quantify antibiotic consumption at **facility level** (records from pharmacies, data from health insurance programs, prescribing records of physicians, dispensing records of pharmacists etc.)?						
2.6	What are the available data sources to quantify antibiotic consumption at **sub – national level** (records from pharmacies, data from health insurance programs, prescribing records of physicians, dispensing records of pharmacists etc.)?						
2.7	What are the available data sources to quantify antibiotic consumption at **the national level** (records from pharmacies, data from health insurance programs, prescribing records of physicians, dispensing records of pharmacists etc.)?						
2.8	What challenges (if any) are faced in terms of data availability on antibiotics?						
2.9	Do public sector healthcare providers have LMIS to monitor and retrieve data of logistics of antibiotics? How is it managed and what data does it gather and for what use?				Yes		No

3. Informal Supply Chains

3.1	Is there an estimate of the antibiotic black-market size in the country?
3.2	Are there any mechanisms utilized by relevant authorities to track and trace illegally imported antibiotics in the country?

Appendix 2: Eligibility questionnaire for pharmacies

Purpose:
To determine eligibility of community pharmacies for data collection Antimicrobial Consumption (AMC)

Instructions

Pre-requisite for administering the Questionnaire:
List of public hospitals/ private facilities where the laboratories are situated/ where eligibility of laboratories is being tested
Contact details of pharmacy situated within/ connected to the above public/ private hospital
Mode of administering the Questionnaire:
Administered over email and/ or over the phone

Eligibility questionnaire for Community Pharmacies:

A. General information				
1. What is the name and complete address of your pharmacy?				
2. Does the pharmacy house a laboratory?	Yes		No	
3. Does the pharmacy have relevant certification/ accreditation (in example by the pharmacy and poison board etc.)	Yes		No	
4. Did the pharmacy have the following in place at any time between 2016-18?				
4.1 At least one Pharmacist	Yes		No	
4.2 At least one pharmacy technician	Yes		No	
4.3 Are there SOPs in place for entering issues / sales of antibiotics?	Yes		No	
B. Antibiotic Consumption Data				
1. Are the following data at the pharmacy stored electronically? (State Y/N for each)				
2. Sales of antibiotics to patients/customers	Yes		No	
3. Purchases (from wholesalers/distributors/open markets etc.)	Yes		No	
4. Current stock in hand of antibiotics (at end of month)	Yes		No	
5. No electronic records are maintained	Yes		No	
6. If answer is YES to Q5, how far back in time do the electronic records exist (indicate start month and year – for 2018, 2017 and 2016 for each of the below)?				
7. Sales to patients/customers	Month:			
	Year:			
8. Purchases (from wholesalers/distributors/open markets etc.)	Month:			
	Year:			
9. Current stock in hand of medicines (at end of each month)	Month:			
	Year:			
10. As a follow up to Q6, is it possible to extract historical data (for 2018, 2017, 2016 or part thereof) in excel, CSV or any other format from electronic pharmacy system? (State Y/N for each)				
11. Sales to patients, customers and/ or Prescriptions	Yes		No	
12. Purchases (from wholesalers/distributors/open markets etc.)	Yes		No	
13. Current stock of medicines (at end of each month)	Yes		No	
14. If answer is NO to Q5, does the pharmacy manually hold paper-based data for medicines? (State Y/N for each)				
15. Sales to patients/customers	Yes		No	

16. Purchases from wholesalers/distributors etc.	Yes		No	
17. Current stock in hand of medicines	Yes		No	
18. How far back in time do the manual/ paper-based records exist for the following (indicate start month and year – for 2018, 2017 and 2016 for each of the below)?				
19. Sales to patients/customers	Month:			
	Year:			
20. Purchases (from wholesalers/distributors/open markets etc.)	Month:			
	Year:			
21. Current stock in hand of medicines	Month:			
	Year:			
22. What records can be used for historical data extraction for antibiotic sales? (State Y/N for each option)				
23. Sales invoices / prescriptions to customers/patients (sell-out)	Yes		No	
24. Supplier invoices received by pharmacy (sell-in)	Yes		No	
25. Any other (please state)	Yes		No	
26. What kind of stock control system does the pharmacy store maintain? (State Y/N for each option)				
27. Issues/ sales book	Yes		No	
28. Stock card/Bin Card	Yes		No	
29. Electronic	Yes		No	
30. Any other (please state)	Yes		No	
31. In case of dispensing antibiotics to patients, can the pharmacy trace if there was a prescription?	Yes		No	

Based on historical data, will it be possible to obtain month-wise disaggregated data for the following fields for 2018, 2017 and 2016?	In the table below just indicate Y/N to understand availability of the kind of data – DO NOT fill actual data for now

Antibiotic Name	Form* (Tablets, Vials, Capsules, Syrup etc.)	Strength* (in MG)	Pack* size	Manufacturer	Data available for- No. of units DISPENSED in a month	Data available for- No. of units PURCHASED in a month	Data available for- Stock in Hand end of each month
AMOXICILLIN	Y/N	Y/N	Y/N	Y/N	Y/N	Y/N	Y/N
		Y/N	Y/N	Y/N	Y/N	Y/N	Y/N
		Y/N	Y/N	Y/N	Y/N	Y/N	Y/N
	Y/N	Y/N	Y/N	Y/N	Y/N	Y/N	Y/N
	Y/N	Y/N	Y/N	Y/N	Y/N	Y/N	Y/N
	Y/N	Y/N	Y/N	Y/N	Y/N	Y/N	Y/N

* A single antibiotic may come in different forms, with different strength and in different pack sizes. Idea here is to understand whether consumption / purchase data can be made available at the pharmacy for each of the different form-strength-pack size combinations. For instance, Amoxicillin 'Capsules' (form) '250 mg' (strength) '100' (pack size) will be one row, and so on.

Stock out status of antibiotics (State Y/N to each of the below statements)				
a. Is there often a stock-out of antibiotics at the pharmacy?	Yes		No	
b. If yes to a, is a record of the stocked-out antibiotics maintained?	Yes		No	
c. In case some antibiotic is out of stock or not available, how do patients purchase that medicine generally?	Yes		No	
d. Purchase from the public hospital pharmacy	Yes		No	
e. Purchase from nearby other private pharmacy	Yes		No	
f. Purchase from private pharmacy near their residence	Yes		No	
g. Purchase from the market	Yes		No	

Appendix 3: Harmonised list of antimicrobials to be included in data collection

Antimicrobial name	WHO ATC Index	A/W/R/U category
Acetyl Kitasamycin	J01	U
Acetylspiramycin	J01	W
Alatrofloxacin	J01	U
Amoxicillin/Ampicillin	J01	U
Amoxicillin/Cloxacillin	J01	U
Amoxicillin/Dicloxacillin	J01	U
Amoxicillin/Flucloxacillin	J01	U
Amoxicillin/Metronidazole	J01	U
Amoxicillin/Sulbactam	J01	A
Ampicillin/Cloxacillin	J01	U
Ampicillin/Dicloxacillin	J01	U
Ampicillin/Flucloxacillin	J01	U
Ampicillin/Oxacillin	J01	U
Ampicillin/Sulbactam	J01	A
Ampicillin/Sultamicillin	J01	A
Antofloxacin	J01	W
Astromicin	J01	W
Balofloxacin	J01	W
Benzylpenicillin/Phenoxymethylpenicillin	J01	A
Benzylpenicillin/Phenoxymethylpenicillin/Streptomycin	J01	U
Benzylpenicillin/Streptomycin	J01	U
Bleomycin A5	J01	U
Cefadroxil/Clavulanic Acid	J01	A
Cefathiamidine	J01	A
Cefepime/Sulbactam	J01	U
Cefepime/Tazobactam	J01	U
Cefixime/Azithromycin	J01	U
Cefixime/Cefpodoxime	J01	U
Cefixime/Clavulanic Acid	J01	W
Cefixime/Cloxacillin	J01	U
Cefixime/Dicloxacillin	J01	U
Cefixime/Levofloxacin	J01	U
Cefixime/Linezolid	J01	U
Cefixime/Moxifloxacin	J01	U
Cefixime/Ofloxacin	J01	U

Cefixime/Sulbactam	J01	U
Cefoperazone/Sulbactam	J01	U
Cefoperazone/Tazobactam	J01	U
Cefoselis	J01	R
Cefotaxime/Sulbactam	J01	U
Cefpodoxime/Azithromycin	J01	U
Cefpodoxime/Cloxacillin	J01	U
Cefpodoxime/Dicloxacillin	J01	U
Cefpodoxime/Levofloxacin	J01	W
Cefpodoxime/Ofloxacin	J01	W
Ceftazidime/Avibactam	J01	R
Ceftazidime/Sulbactam	J01	U
Ceftazidime/Tazobactam	J01	U
Ceftazidime/Tobramycin	J01	U
Ceftizoxime/Tazobactam	J01	U
Ceftolozane	J01	R
Ceftriaxone/Sulbactam	J01	U
Ceftriaxone/Tazobactam	J01	U
Ceftriaxone/Vancomycin	J01	U
Cefuroxime/Clavulanic Acid	J01	W
Cefuroxime/Linezolid	J01	U
Cefuroxime/Sulbactam	J01	U
Cephalosporin C	J01	U
Ciclacillin	J01	U
Erythromycin Stearate	J01	U
Erythromycin Stinoprate	J01	U
Etimicin	J01	W
Furbenicillin	J01	W
Guamecycline	J01	U
Imipenem	J01	U
Kitasamycin	J01	U
Lenampicillin	J01	U
Levofloxacin/Azithromycin	J01	W
Levofloxacin/Metronidazole	J01	U
Meleumycin	J01	U
Meropenem/Sulbactam	J01	U
Norvancomycin	J01	W
Novobiocin	J01	U

Ofloxacin/Azithromycin	J01	U
Panipenem	J01	W
Piperacillin/Sulbactam	J01	U
Piperacillin/Tazobactam	J01	W
Pivampicillin/Pivmecillinam	J01	U
Polymyxin M	J01	R
Sulfadoxine/Trimethoprim	J01	U
Sulfalene/Trimethoprim	J01	U
Sulfamethizole/Trimethoprim	J01	A
Sulfamethoxypyridazine/Trimethoprim	J01	U
Demeclocycline	J01AA01	U
Doxycycline	J01AA02	A
Chlortetracycline	J01AA03	W
Lymecycline	J01AA04	W
Metacycline	J01AA05	W
Oxytetracycline	J01AA06	W
Tetracycline	J01AA07	A
Minocycline	J01AA08	W, R (IV)
Rolitetracycline	J01AA09	U
Penimepicycline	J01AA10	U
Clomocycline	J01AA11	U
Tigecycline	J01AA12	R
Eravacycline	J01AA13	R
Chloramphenicol	J01BA01	A
Thiamphenicol	J01BA02	A
Ampicillin	J01CA01	A
Pivampicillin	J01CA02	A
Carbenicillin	J01CA03	W
Amoxicillin	J01CA04	A
Carindacillin	J01CA05	U
Bacampicillin	J01CA06	A
Epicillin	J01CA07	U
Pivmecillinam	J01CA08	A
Azlocillin	J01CA09	W
Mezlocillin	J01CA10	W
Mecillinam	J01CA11	A
Piperacillin	J01CA12	W
Ticarcillin	J01CA13	W
Metampicillin	J01CA14	U

Talampicillin	J01CA15	U
Sulbenicillin	J01CA16	W
Temocillin	J01CA17	W
Hetacillin	J01CA18	U
Aspoxicillin	J01CA19	U
Benzylpenicillin	J01CE01	A
Phenoxymethylpenicillin	J01CE02	A
Propicillin	J01CE03	U
Azidocillin	J01CE04	U
Pheneticillin	J01CE05	W
Penamecillin	J01CE06	A
Clometocillin	J01CE07	A
Benzathine phenoxymethylpenicillin	J01CE10	U
Dicloxacillin	J01CF01	A
Cloxacillin	J01CF02	A
Meticillin	J01CF03	U
Oxacillin	J01CF04	A
Flucloxacillin	J01CF05	A
Nafcillin	J01CF06	A
Sulbactam	J01CG01	U
Tazobactam	J01CG02	U
Ampicillin/Clavulanic Acid	J01CR01	A
Amoxicillin/Clavulanic Acid	J01CR02	A
Ticarcillin/Clavulanic Acid	J01CR03	W
Sultamicillin	J01CR04	A
Cefalexin	J01DB01	A
Cefaloridine	J01DB02	U
Cefalotin	J01DB03	A
Cefazolin	J01DB04	A
Cefadroxil	J01DB05	A
Cefazedone	J01DB06	A
Cefatrizine	J01DB07	A
Cefapirin	J01DB08	A
Cefradine	J01DB09	A
Cefacetrile	J01DB10	A
Cefroxadine	J01DB11	A
Ceftezole	J01DB12	A
Cefoxitin	J01DC01	W
Cefuroxime	J01DC02	W

Cefamandole	J01DC03	W
Cefaclor	J01DC04	W
Cefotetan	J01DC05	W
Cefonicid	J01DC06	W
Cefotiam	J01DC07	W
Loracarbef	J01DC08	U
Cefmetazole	J01DC09	W
Cefprozil	J01DC10	W
Ceforanide	J01DC11	W
Cefminox	J01DC12	W
Cefbuperazone	J01DC13	W
Flomoxef	J01DC14	W
Cefotaxime	J01DD01	W
Ceftazidime	J01DD02	W
Cefsulodin	J01DD03	U
Ceftriaxone	J01DD04	W
Cefmenoxime	J01DD05	W
Latamoxef	J01DD06	W
Ceftizoxime	J01DD07	W
Cefixime	J01DD08	W
Cefodizime	J01DD09	W
Cefetamet	J01DD10	W
Cefpiramide	J01DD11	W
Cefoperazone	J01DD12	W
Cefpodoxime	J01DD13	W
Ceftibuten	J01DD14	W
Cefdinir	J01DD15	W
Cefditoren	J01DD16	W
Cefcapene	J01DD17	W
Cefteram	J01DD18	W
Cefotaxime/Clavulanic Acid	J01DD51	W
Ceftazidime/Clavulanic Acid	J01DD52	W
Ceftazidime/Clavulanic Acid	J01DD52	W
Cefoperazone/Clavulanic Acid	J01DD62	W
Ceftriaxone/Clavulanic Acid	J01DD63	W
Cefpodoxime/Clavulanic Acid	J01DD64	W
Cefepime	J01DE01	W
Cefpirome	J01DE02	R

Cefozopran	J01DE03	R
Aztreonam	J01DF01	R
Carumonam	J01DF02	U
Meropenem	J01DH02	W
Ertapenem	J01DH03	W
Doripenem	J01DH04	W
Biapenem	J01DH05	W
Tebipenem Pivoxil	J01DH06	W
Imipenem/Cilastatin	J01DH51	W
Meropenem/Vaborbactam	J01DH52	R
Panipenem/Betamipron	J01DH55	U
Ceftobiprole Medocaril	J01DI01	R
Ceftaroline Fosamil	J01DI02	R
Faropenem	J01DI03	W
Ceftolozane/Tazobactam	J01DI54	U
Ceftolozane/Clavulanic Acid	J01DI54	R
Trimethoprim	J01EA01	A
Brodimoprim	J01EA02	U
Iclaprim	J01EA03	U
Sulfaisodimidine	J01EB01	U
Sulfamethizole	J01EB02	U
Sulfadimidine	J01EB03	U
Sulfapyridine	J01EB04	U
Sulfafurazole	J01EB05	U
Sulfanilamide	J01EB06	U
Sulfathiazole	J01EB07	U
Sulfathiourea	J01EB08	U
Sulfamethoxazole	J01EC01	U
Sulfadiazine	J01EC02	U
Sulfamoxole	J01EC03	U
Sulfadimethoxine	J01ED01	U
Sulfalene	J01ED02	U
Sulfametomidine	J01ED03	U
Sulfametoxydiazine	J01ED04	U
Sulfamethoxypyridazine	J01ED05	U
Sulfaperin	J01ED06	U
Sulfamerazine	J01ED07	U
Sulfaphenazole	J01ED08	U

Sulfamazone	J01ED09	U
Trimethoprim/Sulfamethoxazole	J01EE01	A
Sulfadiazine/Trimethoprim	J01EE02	A
Sulfametrole/Trimethoprim	J01EE03	A
Sulfamoxole/Trimethoprim	J01EE04	A
Sulfadimidine/Trimethoprim	J01EE05	U
Sulfadiazine/Tetroxoprim	J01EE06	U
Sulfamerazine/Trimethoprim	J01EE07	U
Erythromycin	J01FA01	W
Spiramycin	J01FA02	W
Midecamycin	J01FA03	W
Oleandomycin	J01FA05	W
Roxithromycin	J01FA06	W
Josamycin	J01FA07	W
Troleandomycin	J01FA08	U
Clarithromycin	J01FA09	W
Azithromycin	J01FA10	W
Miocamycin	J01FA11	U
Rokitamycin	J01FA12	U
Dirithromycin	J01FA13	W
Flurithromycin	J01FA14	U
Telithromycin	J01FA15	W
Solithromycin	J01FA16	U
Clindamycin	J01FF01	A
Lincomycin	J01FF02	W
Pristinamycin	J01FG01	W
Quinupristin/Dalfopristin	J01FG02	R
Streptomycin	J01GA01	A
Streptoduocin	J01GA02	U
Tobramycin	J01GB01	W
Gentamicin	J01GB03	A
Kanamycin	J01GB04	A
Neomycin	J01GB05	W
Amikacin	J01GB06	A
Netilmicin	J01GB07	W
Sisomicin	J01GB08	W
Dibekacin	J01GB09	W
Ribostamycin	J01GB10	W
Isepamicin	J01GB11	W

Arbekacin	J01GB12	W
Bekanamycin	J01GB13	U
Ofloxacin	J01MA01	W
Ciprofloxacin	J01MA02	W
Pefloxacin	J01MA03	W
Enoxacin	J01MA04	W
Temafloxacin	J01MA05	U
Norfloxacin	J01MA06	W
Lomefloxacin	J01MA07	W
Fleroxacin	J01MA08	W
Sparfloxacin	J01MA09	W
Rufloxacin	J01MA10	W
Grepafloxacin	J01MA11	U
Levofloxacin	J01MA12	W
Trovafloxacin	J01MA13	U
Moxifloxacin	J01MA14	W
Gemifloxacin	J01MA15	W
Gatifloxacin	J01MA16	W
Prulifloxacin	J01MA17	W
Pazufloxacin	J01MA18	W
Garenoxacin	J01MA19	W
Sitafloxacin	J01MA21	W
Tosufloxacin	J01MA22	W
Delafloxacin	J01MA23	W
Rosoxacin	J01MB01	U
Nalidixic acid	J01MB02	U
Piromidic Acid	J01MB03	U
Pipemidic Acid	J01MB04	U
Oxolinic Acid	J01MB05	U
Cinoxacin	J01MB06	U
Flumequine	J01MB07	W
Nemonoxacin	J01MB08	U
Cefuroxime/Metronidazole	J01RA03	U
Spiramycin/Metronidazole	J01RA04	W
Levofloxacin/Ornidazole	J01RA05	U
Cefepime/Amikacin	J01RA06	U
Azithromycin/Fluconazole/Secnidazole	J01RA07	U
Tetracycline/Oleandomycin	J01RA08	U
Ofloxacin/Ornidazole	J01RA09	U

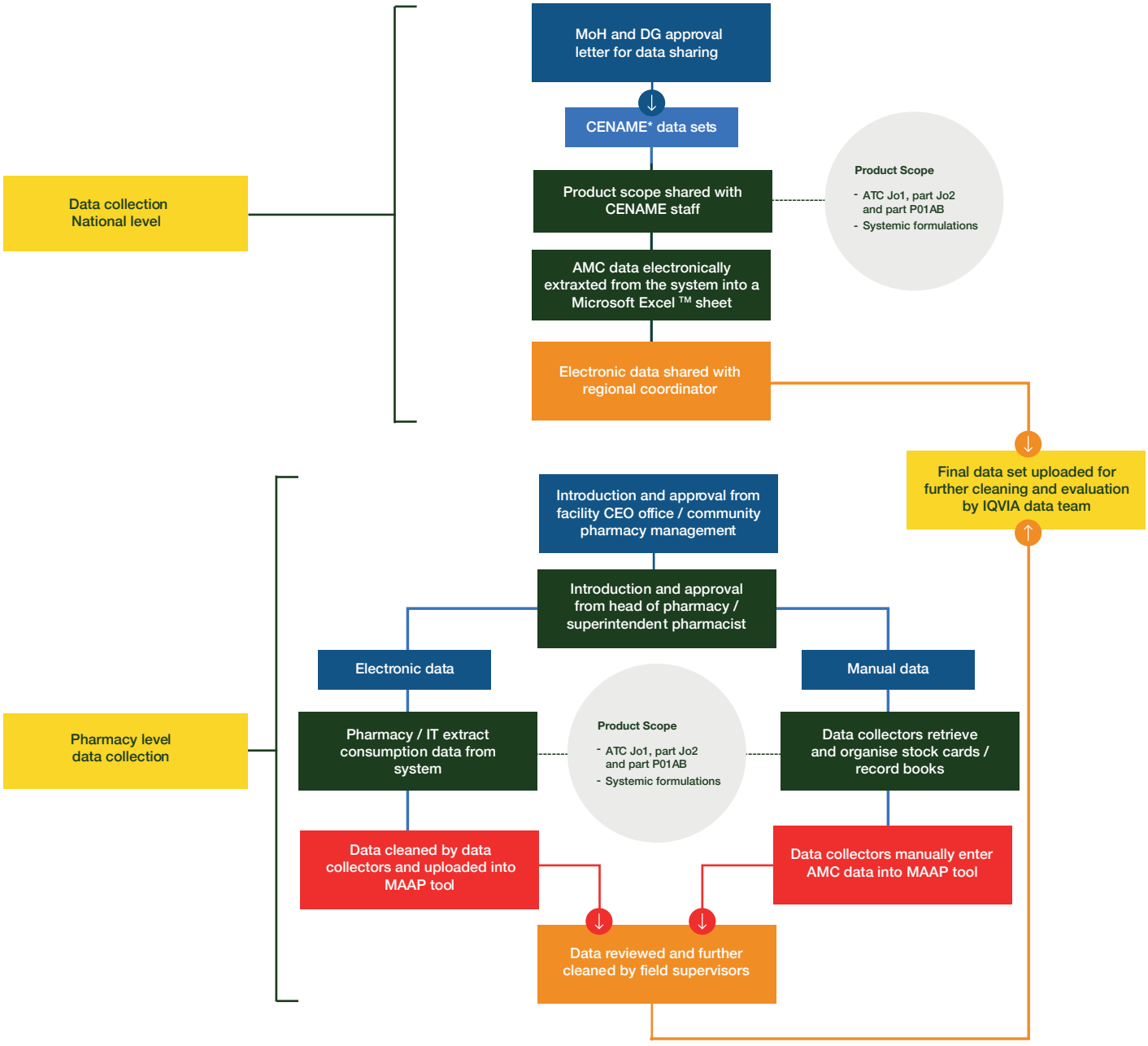
Ciprofloxacin/Metronidazole	J01RA10	U
Ciprofloxacin/Tinidazole	J01RA11	U
Ciprofloxacin/Ornidazole	J01RA12	U
Norfloxacin/Tinidazole	J01RA13	U
Vancomycin	J01XA01	W
Teicoplanin	J01XA02	W
Telavancin	J01XA03	R
Dalbavancin	J01XA04	R
Oritavancin	J01XA05	R
Colistin	J01XB01	R
Polymyxin B	J01XB02	R
Fusidic Acid	J01XC01	W
Metronidazole	J01XD01	A
Tinidazole	J01XD02	U
Ornidazole	J01XD03	U
Nitrofurantoin	J01XE01	U
Nifurtoinol	J01XE02	U
Furazidin	J01XE03	U
Fosfomycin	J01XX01	R
Xibornol	J01XX02	U
Clofoctol	J01XX03	W
Spectinomycin	J01XX04	A
Linezolid	J01XX08	R
Daptomycin	J01XX09	R
Bacitracin	J01XX10	U
Tedizolid	J01XX11	R
Amphotericin B	J02AA01	N/A
Fluconazole	J02AC01	N/A
Itraconazole	J02AC02	N/A
Voriconazole	J02AC03	N/A
Posaconazole	J02AC04	N/A
Isavuconazole	J02AC05	N/A
Flucytosine	J02AX01	N/A
Caspofungin	J02AX04	N/A
Micafungin	J02AX05	N/A
Anidulafungin	J02AX06	N/A

Key - A: Access W: Watch R: Reserve U: Uncategorised

Appendix 4: Key AMC specific variables

	Variables	Mandatory or Optional
	Antimicrobial consumption specific	
1	Site Name /Pharmacy name	Mandatory
2	Date of transaction	Mandatory
3	Antibiotic Name	Mandatory
4	Antibiotic Identification Number	Optional
5	Antibiotic strength	Mandatory
6	Antibiotic Strength Units	Mandatory
7	Form	Mandatory
8	Pack size	Mandatory
10	Brand	Mandatory
11	Quantity Issued IN/OUT	Mandatory
12	Balance (after a transaction is complete)	Mandatory
13	Date of data entry (data capture date by data collectors)	Optional
14	Date of data review (data review date by data manager or regional coordinator)	Optional
15	Recipient facility	Optional
16	Recipient unit	Optional

Appendix 5: Data collection process flowchart



**CENAME: National Centre for the Supply of Drugs and Essential Consumables - Cameroon*

Appendix 6: Description of AMC analysis methodology

Defined Daily Dose (DDD) AMC Analysis:
DDD's were calculated as follows:

$$\text{Number of DDDs} = \frac{\text{Total milligrams used}}{\text{DDD value in milligrams*}}$$

***WHO approved DDDs for antibiotics:**

Where total grams of the antimicrobial used is determined by summing the amount of active ingredient across the various formulations (different strengths of tablets, or capsules, syrup formulations) and pack sizes.

Once AMC is converted to standard DDDs, the data is further analysed into the below standard units: DDDs/1000 inhabitants/day (DID): used to calculate total AMC for the Cameroon population at a national level; includes all age and gender groups and used the known population numbers as the denominator (obtained from the Worldometer Population Database). The below formula summarises how this calculation was done:

The below formula summarises how this calculation was done:

DDD/1000 Inhabitants/day =

$$\frac{\text{Utilisation in DDDs} \times 1000}{(\text{Number of inhabitants*}) \times (\text{Number of days in the period of data collection})}$$

*Cameroon population estimated for 2017-2019 obtained from: https://www.worldometers.info/world-population/cameroon-population/

DDD equivalent: used to calculate AMC at site level (presented as a percentage) and used WHO DDD as the denominator. The below formulas indicate how this was done:

DDD equivalent (%) =

$$\frac{\text{Total milligrams consumed/purchased} \times 100}{\text{WHO DDD*}}$$

*WHO approved DDDs for antibiotics:

WHO Anatomical Therapeutic Chemical (ATC) classification

Definition of the classification of the medicines in groups at five different levels:

Level 1: Indicates the anatomical main group, it is represented by a letter. For antimicrobials, the main group is 'J', which represented Anti-infectives for systemic use. It should be noted that there are antimicrobials that are classified in other main groups.

Level 2: Indicates the therapeutic subgroups and is represented by a number. For example: J01 groups together Antibacterial for systemic use.

Level 3: Classifies the pharmacological subgroup, e.g., J01C is Beta (β)-lactam antibacterial, Penicillins and J01F lists Macrolides, Lincosamides and Streptogramins

Level 4: Further defines the group by pharmacological subgroup, e.g., J01CA is Penicillins with extended spectrum and J01FA is Macrolides

Level 5: Is the chemical substance, e.g., J01CA01 is ampicillin and J01FA10 s azithromycin

WHO Access, Watch and Reserve (AWaRe) AMC Analysis:

Description of the AWaRe categories below:

'Access': This group includes antibiotics that generally have a narrow spectrum of activity against microbes and are active against a wide range of common infections. The Access group represent first and second choice antibiotics for the empiric treatment of most common infectious syndromes. They offer the best therapeutic value, while minimizing the potential for resistance. The distribution of antibiotics in this group includes Beta (β)–lactam (52.63%), followed by aminoglycosides (15.78%), macrolides (5.26%), and tetracyclines (5.26%). Access group compromises of 48 antibiotics; 19 of which are included in the WHO's EML.

'Watch': These antibiotics generally have a broader spectrum of activity against microbes and are to be used sparingly as first or second choice treatment options for specified infectious syndromes; they are indicated for specific, limited number of infective syndromes or patient groups. These medicines are also preferred over access antibiotics in serious infections. β-lactams (54.54%) constitute the larger share of the watch group antibiotics followed by macrolides (18.18%), aminoglycosides (9.09%), and carbapenems (9.09%). Watch group compromises of 110 antibiotics; 11 of which are included in the WHO's EML. Watch group antibiotics should be prioritised as key targets of stewardship programmes and monitoring.

'Reserve' group antibiotics: Should strictly be considered as the last-resort option. They should be used only in the most severe circumstances when all other alternatives have failed i.e., in life-threatening infections due to multi-drug resistant bacteria. The reserve group is majorly constituted of polymyxin (28.57%) followed by β-lactams (14.28%) and aminoglycosides (14.28%). Reserve group compromises of 22 antibiotics; 7 of which are included in the WHO's EML. The use of antibiotics in this group should be closely monitored and prioritised as targets for AMS to ensure their continued effectiveness.

Appendix 7: National AMC by Antimicrobial molecules

ATC Class Rank	AWaRe category	Molecule	2017	2018	2019	Mean DDD/1000 inhabitant-days
			DDD/1000 inhabitant-days (%*)			
J01 Class		Total	5.96 (100)	4.21 (100)	4.18 (100)	4.78
1	Access	Sulfamethoxazole/ Trimethoprim	2.93 (49.2)	0.69 (16.4)	0.73 (17.5)	1.45
2	Access	Amoxicillin/Clavulanic Acid	0.86 (14.5)	0.69 (16.4)	0.81 (19.4)	0.79
3	Access	Doxycycline	0.52 (8.7)	0.65 (15.5)	0.56 (13.4)	0.58
4	Access	Amoxicillin	0.33 (5.6)	0.59 (13.9)	0.42 (10.1)	0.45
5	Watch	Ciprofloxacin	0.14 (2.4)	0.19 (4.5)	0.20 (4.7)	0.18
6	Watch	Cefixime	0.13 (2.2)	0.18 (4.2)	0.21 (5.1)	0.17
7	Watch	Azithromycin	0.14 (2.4)	0.15 (3.6)	0.19 (4.5)	0.16
8	Access	Flucloxacillin	0.16 (2.8)	0.15 (3.6)	0.13 (3.2)	0.15
9	Watch	Ofloxacin	0.13 (2.2)	0.14 (3.3)	0.13 (3.1)	0.13
10	Watch	Levofloxacin	0.08 (1.4)	0.09 (2.2)	0.09 (2.2)	0.09
11	Access	Cloxacillin	0.004 (0.1)	0.13 (3.2)	0.11 (2.7)	0.08
12	Watch	Erythromycin	0.06 (1.1)	0.06 (1.6)	0.08 (2)	0.07
13	Watch	Clarithromycin	0.05 (0.8)	0.06 (1.5)	0.06 (1.5)	0.06
14	Watch	Spiramycin	0.05 (0.9)	0.05 (1.2)	0.05 (1.2)	0.05
15	Access	Phenoxymethylpenicillin	0.04 (0.7)	0.04 (1)	0.04 (1)	0.04
16	Access	Thiamphenicol	0.03 (0.5)	0.03 (0.8)	0.03 (0.7)	0.03
17	Watch	Cefuroxime	0.03 (0.5)	0.03 (0.7)	0.03 (0.7)	0.03
18	Watch	Ceftriaxone	0.01 (0.2)	0.04 (1.1)	0.03 (0.7)	0.03
19	Watch	Lincomycin	0.02 (0.3)	0.03 (0.7)	0.03 (0.7)	0.02
20	Access	Oxacillin	0.02 (0.4)	0.02 (0.5)	0.02 (0.6)	0.02
21	Uncategorised	Ofloxacin/Ornidazole	0.02 (0.3)	0.02 (0.4)	0.02 (0.5)	0.02
22	Access	Gentamicin	0.005 (0.1)	0.01 (0.2)	0.04 (1)	0.02
23	Watch	Spiramycin/Metronidazole	0.02 (0.3)	0.02 (0.4)	0.02 (0.4)	0.02
24	Uncategorised	Amoxicillin/Metronidazole	0.01 (0.2)	0.02 (0.4)	0.02 (0.4)	0.01
25	Access	Cefadroxil	0.02 (0.3)	0.01 (0.3)	0.004 (0.1)	0.01
26	Uncategorised	Ampicillin/Cloxacillin	0.01 (0.2)	0.01 (0.3)	0.01 (0.2)	0.01
27	Watch	Cefpodoxime proxetil	0.01 (0.2)	0.01 (0.2)	0.01 (0.2)	0.01
28	Watch	Josamycin	0.01 (0.2)	0.01 (0.2)	0.01 (0.2)	0.01
29	Access	Benzylpenicillin	0.01 (0.2)	0.01 (0.2)	0.01 (0.2)	0.01
30	Watch	Roxithromycin	0.01 (0.2)	0.01 (0.2)	0.01 (0.3)	0.01
31	Uncategorised	Ciprofloxacin/Tinidazole	0.01 (0.1)	0.01 (0.2)	0.01 (0.3)	0.01
32	Watch	Minocycline	0.01 (0.2)	0.01 (0.2)	0.01 (0.2)	0.01
33	Access	Ampicillin	0.01 (0.1)	0.01 (0.2)	0.01 (0.2)	0.01
34	Watch	Norfloxacin	0.01 (0.1)	0.007 (0.2)	0.01 (0.1)	0.01

35	Watch	Sparfloxacin	0.01 (0.1)	0.005 (0.1)	0.004 (0.1)	0.005
36	Access	Cefalexin	0.004 (0.1)	0.005 (0.1)	0.005 (0.1)	0.005
37	Watch	Fusidic Acid	0.004 (0.1)	0.004 (0.1)	0.004 (0.1)	0.004
38	Watch	Streptomycin	0.006 (0.1)	0.004 (0.1)	0 (0)	0.003 3
39	Watch	Cefepime	0.003 (0.1)	0.002 (0.1)	0.002 (0.1)	0.002
40	Uncategorised	Ofloxacin/Tinidazole	0 (0)	0.002 (0.1)	0.004 (0.1)	0.002
41	Access	Pivmecillinam	0.002 (0)	0.002 (0)	0.001 (0)	0.002
42	Uncategorised	Ceftriaxone/Sulbactam	0.001 (0)	0.002 (0)	0.002 (0.1)	0.002
43	Watch	Imipenem/Cilastatin	0.001 (0)	0.001 (0)	0.001 (0)	0.001
44	Watch	Pristinamycin	0.002 (0)	0 (0)	0 (0)	0.0007
45	Watch	Ceftazidime	0.0005 (0)	0.0004 (0)	0.0005 (0)	0.0005
46	Watch	Flumequine	0.0006 (0)	0.0004 (0)	0.0001 (0)	0.0004
47	Uncategorised	Cefuroxime/ Clavulanic Acid	0.0006 (0)	0.0002 (0)	0 (0)	0.0003
48	Watch	Meropenem	0.0002 (0)	0.0002 (0)	0.0003 (0)	0.0002
49	Uncategorised	Cefixime/Clavulanic Acid	0.0005 (0)	0.00007 (0)	0 (0)	0.0002
50	Access	Clindamycin	0.0001 (0)	0 (0)	0.0004 (0)	0.0002
51	Watch	Cefotaxime	0 (0)	0.0001 (0)	0.0003 (0)	0.0002
52	Watch	Moxifloxacin	0.0002 (0)	0.00005 (0)	0 (0)	0.0001
53	Uncategorised	Cefpodoxime proxetil/ Clavulanic Acid	0.0002 (0)	0.00004 (0)	0 (0)	0.0001
54	Uncategorised	Amoxicillin/Cloxacillin	0.00005 (0)	0.00004 (0)	0.0001 (0)	0.00005
55	Uncategorised	Amoxicillin/Pivsulbactam	0.00006 (0)	0 (0)	0 (0)	0.00002
56	Uncategorised	Cefadroxil/Clavulanic Acid	0.00004 (0)	0.00001 (0)	0 (0)	0.00002
57	Watch	Piperacillin/Tazobactam	0 (0)	0 (0)	0.00003 (0)	0.00001
58	Access	Benzathine benzylpeni-cillin	0 (0)	0.00001 (0)	0.00001 (0)	0.00001
59	Watch	Cefoperazone	0 (0)	0 (0)	0.00002 (0)	0.00001
60	Access	Cefradine	0 (0)	0 (0)	0 (0)	0
61	Watch	Cefaclor	0 (0)	0 (0)	0 (0)	0
62	Uncategorised	Amoxicillin/Sulbactam	0 (0)	0 (0)	0 (0)	0
J02 Class		**Total**	**0.29 (100)**	**0.29 (100)**	**0.29 (100)**	**0.29**
1	Uncategorised	Fluconazole	0.22 (78.5)	0.23 (79.8)	0.23 (80.6)	0.23
2	Uncategorised	Ketoconazole	0.06 (21.1)	0.06 (19.8)	0.06 (19)	0.06
3	Uncategrised	Itraconazole	0.001 (0.4)	0.001 (0.4)	0.001 (0.4)	0.002
P01AB Class		**Total**	**0.05 (100)**	**0.06 (100)**	**0.06 (100)**	**0.055**
1	Uncategrised	Metronidazole/ Diloxanide	0.04 (81.5)	0.05 (82)	0.048 (82.3)	0.04
2	Uncategrised	Tinidazole	0.005 (10.2)	0.006 (10)	0.005 (8.8)	0.005
3	Uncategrised	Secnidazole	0.004 (8.3)	0.004 (8)	0.005 (9)	0.005

Appendix 8: Breakdown of national AMC by ATC classes

	% consumption		
ATC class	2017	2018	2019
Combinations of sulfonamides and trimethoprim, incl. derivatives	46.5%	15.2%	16.1%
Combinations of penicillins, incl. beta-lactamase inhibitors	13.9%	15.4%	18.1%
Tetracyclines	8.4%	14.5%	12.5%
Penicillins with extended spectrum	5.5%	13.1%	9.5%
Fluoroquinolones	5.9%	9.5%	9.5%
Macrolides	5.3%	7.6%	8.9%
Beta-lactamase resistant penicillins	3.1%	6.8%	6.0%
Triazole derivatives	3.6%	5.0%	5.2%
Third-generation cephalosporins	2.6%	5.1%	5.6%
Combinations of antibacterials	0.9%	1.4%	1.7%
Imidazole derivatives	1.0%	1.2%	1.2%
Beta-lactamase sensitive penicillins	0.8%	1.1%	1.2%
Nitroimidazole derivatives	0.7%	1.1%	1.2%
Amphenicols	0.5%	0.7%	0.7%
Second-generation cephalosporins	0.5%	0.7%	0.7%
Lincosamides	0.3%	0.6%	0.6%
Aminoglycosides	0.2%	0.2%	0.9%
First-generation cephalosporins	0.4%	0.4%	0.2%
Steroid antibacterials	0.1%	0.1%	0.1%
Fourth-generation cephalosporins	<0.1%	0.1%	0.1%
Carbapenems	<0.1%	<0.1%	<0.1%
Streptogramins	<0.1%	0.0%	0.0%
Other quinolones	<0.1%	<0.1%	<0.1%
First-generation cephalosporins and beta-lactamase inhibitors	<0.1%	<0.1%	0.0%

Appendix 9: Breakdown of antibiotic documented and their inclusion in the WHO EML and National EML

Standardised Molecule Name	WHO AWaRe Categorisation	WHO ATC Code	WHO EML	National EML	Documented Data
Amikacin	Access	J01GB06	Y	Y	Y
Amoxicillin	Access	J01CA04	Y	Y	Y
Amoxicillin/Clavulanic Acid	Access	J01CR02	Y	Y	Y
Amoxicillin/Cloxacillin		J01CR50	N	N	Y
Amoxicillin/Metronidazole		J01RA--	N	N	Y
Amoxicillin/Pivsulbactam		J01CR02	N	N	Y
Amoxicillin/Sulbactam		J01CR02	N	N	Y
Amphotericin-B		J02AA01	N	Y	N
Ampicillin	Access	J01CA01	Y	Y	Y
Ampicillin/Cloxacillin		J01CR50	N	N	Y
Azithromycin	Watch	J01FA10	Y	Y	Y
Benzathine benzylpenicillin	Access	J01CE08	Y	Y	Y
Benzylpenicillin	Access	J01CE01	Y	Y	Y
Cefaclor	Watch	J01DC04	N	N	Y
Cefadroxil	Access	J01DB05	N	N	Y
Cefadroxil/Clavulanic Acid		J01DB--	N	N	Y
Cefalexin	Access	J01DB01	Y	N	Y
Cefazolin	Access	J01DB04	Y	Y	Y
Cefepime	Watch	J01DE01	N	N	Y
Cefiderocol	Reserve	J01DI04	Y	N	N
Cefixime	Watch	J01DD08	Y	Y	Y
Cefixime/Clavulanic Acid		J01DD--	N	N	Y
Cefoperazone	Watch	J01DD12	N	N	Y
Cefotaxime	Watch	J01DD01	Y	Y	Y
Cefpodoxime proxetil	Watch	J01DD13	N	N	Y
Cefpodoxime proxe-til/Clavulanic Acid		J01DD64	N	N	Y
Cefradine	Access	J01DB09	N	N	Y
Ceftazidime	Watch	J01DD02	Y	N	Y
Ceftazidime/avibactam	Reserve	J01DD52	Y	N	N
Ceftriaxone	Watch	J01DD04	Y	Y	Y
Ceftriaxone/Sulbactam		J01DD63	N	N	Y
Cefuroxime	Watch	J01DC02	Y	Y	Y
Cefuroxime/Clavulanic Acid		J01DC--	N	N	Y
Chloramphenicol	Access	J01BA01	Y	N	N
Ciprofloxacin	Watch	J01MA02	Y	Y	Y
Ciprofloxacin/Tinidazole		J01RA11	N	N	Y
Clarithromycin	Watch	J01FA09	Y	Y	Y
Clindamycin	Access	J01FF01	Y	N	Y
Cloxacillin	Access	J01CF02	Y	Y	Y
Colistin	Reserve	J01XB01	Y	N	N
Doxycycline	Access	J01AA02	Y	Y	Y
Erythromycin	Watch	J01FA01	N	Y	Y
Flucloxacillin	Access	J01CF05	N	N	Y

Fluconazole		J02AC01	N	Y	Y
Flumequine	Watch	J01MB07	N	N	Y
Fosfomycin (IV)	Reserve	J01XX01	Y	N	N
Fosfomycin (oral)	Watch	J01XX01	N	N	Y
Fusidic Acid	Watch	J01XC01	N	Y	Y
Gentamicin	Access	J01GB03	Y	Y	Y
Imipenem/Cilastatin	Watch	J01DH51	N	N	Y
Itraconazole		J02AC02	N	Y	Y
Josamycin	Watch	J01FA07	N	N	Y
Kanamycin	Watch	J01GB04	N	Y	N
Ketoconazole		J02AB02	N	Y	Y
Levofloxacin	Watch	J01MA12	N	Y	Y
Lincomycin	Watch	J01FF02	N	N	Y
Linezolid	Reserve	J01XX08	Y	Y	N
Meropenem	Watch	J01DH02	Y	N	Y
Meropenem/vaborbactam	Reserve	J01DH52	Y	N	N
Metronidazole	Access	P01AB01	Y	Y	Y
Metronidazole/Diloxanide		P01AB51	N	N	Y
Minocycline	Watch	J01AA08	N	N	Y
Moxifloxacin	Watch	J01MA14	N	N	Y
Netilimicin		J01GB07	N	Y	N
Nitrofurantoin	Access	J01XE01	Y	N	Y
Norfloxacin	Watch	J01MA06	N	N	Y
Ofloxacin	Watch	J01MA01	N	Y	Y
Ofloxacin/Ornidazole		J01RA09	N	N	Y
Ofloxacin/Tinidazole		J01RA--	N	N	Y
Oxacillin	Access	J01CF04	N	N	Y
Phenoxymethylpenicillin	Access	J01CE02	Y	Y	Y
Piperacillin/Tazobactam	Watch	J01CR05	Y	N	Y
Pivmecillinam	Access	J01CA08	N	N	Y
Plazomicin	Reserve	J01GB14	Y	N	N
Polymyxin-B	Reserve	J01XB02	Y	N	N
Pristinamycin	Watch	J01FG01	N	N	Y
Procaine benzylpenicillin	Access	J01CE09	Y	N	N
Roxithromycin	Watch	J01FA06	N	N	Y
Secnidazole		P01AB07	N	N	Y
Sparfloxacin	Watch	J01MA09	N	N	Y
Spectinomycin	Access	J01XX04	Y	N	N
Spiramycin	Watch	J01FA02	N	Y	Y
Spiramycin/Metronidazole	Watch	J01RA04	N	N	Y
Streptomycin	Watch	J01GA01	N	Y	Y
Sulfamethoxa-zole/Trimethoprim	Access	J01EE01	Y	Y	Y
Thiamphenicol	Access	J01BA02	N	Y	Y
Tinidazole		P01AB02	N	Y	Y
Tobramycin	Watch	J01GA01	N	N	Y
Trimethoprim	Access	J01EA01	Y	N	N
Vancomycin	Watch	J01XA01	Y	Y	Y

Appendix 10: AMC data collection and expired drug and losses tool

AMC Data Collection Tool

Product Name
Pack Size_Value
Pack Size_Unit
Strength Num_Value
Strength Num_Unit
Strength Denom_Value
Strength Denom_Unit
ATC5
Combi-nation
Route
Salt
Volume

Expired Drug and Losses Tool

Country
Pharmacy Name
Date of Transaction
Antibiotic Name
Strength Value
Strength Unit
Form
Pack Size
Brand
Quantity

MAAP
Mapping AMR & AMU Partnership

The Fleming Fund
Regional Grants

UKaid
from the British people

African Union

AFRICA CDC
Centres for Disease Control and Prevention
Safeguarding Africa's Health

ASLM
AFRICAN SOCIETY FOR LABORATORY MEDICINE

ECOWAS

ECSA
HEALTH COMMUNITY

InSTEDD
Innovative Support To Emergencies Diseases and Disasters

IQVIA

ONEHEALTH
TRUST