Antimicrobial Resistance (AMR) Surveillance Report

Hospital name: **WHO Test Hospital**
Country name: **World Health Organization**

Data from:

01 Jan 1995 to 31 Jan 1995

Contact person: John Stelling
Contact address: Brigham and Women's Hospital
Contact email: jstelling@whonet.org

Generated on: 12 Jan 2021

Generated by

AutoMated tool for Antimicrobial resistance Surveillance System (AMASS)
Version 1.0 (released on February 1, 2019)

The AMASS application is available under the Creative Commons Attribution 4.0 International Public License (CC BY 4.0). The application can be downloaded at: http://www.amass.website

The AMASS application used microbiology_data file that is stored in the same folder as the application (AMASS.bat) used to generate this report.

The goal of the AMASS application is to enable hospitals with microbiology data available in electronic formats to analyze their own data and generate AMR surveillance reports promptly. If hospital admission date data are available, the reports will additionally be stratified by infection origin (community−origin or hospital−origin). If mortality data (such as patient discharge outcome data) are available, a report on mortality involving AMR infection will be added.

This automatically generated report has limitations, and requires users to understand those limitations and use the summary data in the report with careful interpretation.

A valid report could have local implications and much wider benefits if shared with national and international organizations.

This automatically generated report is under the jurisdiction of the hospital to copy, redistribute, and share with any individual or organization.

This automatically generated report contains no patient identifier, similar to standard reports on cumulative antimicrobial susceptibility.

For any query on AMASS, please contact:
Cherry Lim (cherry@tropmedres.ac) and
Direk Limmathurotsakul (direk@tropmedres.ac)

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Introduction

Antimicrobial resistance (AMR) is a global health crisis [1]. The report by Lord Jim O'Neill estimated that 700,000 global deaths could be attributable to AMR in 2015, and projected that the annual death toll could reach 10 million by 2050 [1]. However, data of AMR surveillance from low and middle−income countries (LMICs) are scarce [1,2], and data of mortality associated with AMR infections are rarely available. A recent study estimated that 19,000 deaths are attributable to AMR infections in Thailand annually, using routinely available microbiological and hospital databases [3]. The study also proposed that hospitals in LMICs should utilize routinely available microbiological and hospital admission databases to generate reports on AMR surveillance systematically [3].

Reports on AMR surveillance can have a wide range of benefits [2]; including

- characterization of the frequency of resistance and organisms in different facilities and regions;
- prospective and retrospective information on emerging public health threats;
- evaluation and optimization of local and national standard treatment guidelines;
- evaluation of the impact of interventions beyond antimicrobial guidelines that aim to reduce AMR; and
- data sharing with national and international organizations to support decisions on resource allocation for interventions against AMR and to inform the implementation of action plans at national and global levels.

When reporting AMR surveillance results, it is generally recommended that (a) duplicate results of bacterial isolates are removed, and (b) reports are stratified by infection origin (community−origin or hospital−origin), if possible [2]. Many hospitals in LMICs lack time and resources needed to analyze the data (particularly to deduplicate data and to generate tables and figures), write the reports, and to release the data or reports [4].

AutoMated tool for Antimicrobial resistance Surveillance System (AMASS) was developed as an offline, open−access and easy−to−use application that allows a hospital to perform data analysis independently and generate isolate−based and sample−based surveillance reports stratified by infection origin from routinely collected electronic databases. The application was built in R, which is a free software environment. The application has been placed within a user−friendly interface that only requires the user to double−click on the application icon. The AMASS application can be downloaded at:
http://www.amass.website

Please note that the AMASS application and the automatically−generated report have limitations, and require readers to understand those limitations and review the reports and summary data carefully. We encourage the user of the AMASS application to perform manual validation (such as printing and listing isolates of the species to cross check with the reports), as recommended by Clinical and Laboratory Standards Insitute (CLSI) [5] and European Antimicrobial Resistance Surveillance Network (EUCAST) [6,7]. Moreover, it is important to note that the AMASS is an add−on automatized report generating tool and does not replace WHONET, Laboratory Information System (LIS), quality assurance programme, or antimicrobial surveillance systems (including the WHO GLASS).

References:

[1] O'Neill J. (2014) Antimicrobial resistance: tackling a crisis for the health and wealth of nations. Review on antimicrobial resistance. http://amr−review.org. (accessed on 3 Dec 2018).
[2] World Health Organization (2018) Global Antimicrobial Resistance Surveillance System (GLASS) Report. Early implantation 2016−2017. http://apps.who.int/iris/bitstream/handle/10665/259744/9789241513449−eng.pdf. (accessed on 3 Dec 2018)
[3] Lim C., et al. (2016) Epidemiology and burden of multidrug−resistant bacterial infection in a developing country. Elife 5: e18082.
[4] Ashley EA, Shetty N, Patel J, et al. Harnessing alternative sources of antimicrobial resistance data to support surveillance in low−resource settings. J Antimicrob Chemother. 2019; 74(3):541−546.
[5] Clinical and Laboratory Standards Institute (CLSI). Analysis and Presentation of Cumulative Antimicrobial Susceptibility Test Data, 4th Edition. 2014. (accessed on 21 Jan 2020)
[6] European Antimicrobial Resistance Surveillance Network (EARS−Net). Antimicrobial resistance (AMR) reporting protocol 2018. (accessed on 21 Jan 2020)
[7] European Committee on Antimicrobial Susceptibility Testing (EUCAST). www.eucast.org (accessed on 21 Jan 2020)

Section [1]: Data overview

Introduction
An overview of the data detected by the AMASS application is generated by default. The summary is based on the raw data files saved within the same folder as the application file (AMASS.bat).

Please review and validate this section carefully before proceeds to the next section.

Results
The microbiology_data file (stored in the same folder as the application file) had:

622 specimen data records with collection dates ranging from
01 Jan 1995 to ***31 Jan 1995***

The hospital_admission_data file (stored in the same folder as the application file) had:

NA admission data records with hospital admission dates ranging from
NA to ***NA***

Notes:
[1] If the periods of the data in microbiology_data and hospital_admission_data files are not similar, the automatically−generated report should be interpreted with caution. The AMASS generates the reports based on the available data.

Reporting period by months:
Data was stratified by month to assist detection of missing data, and verification of whether the month distribution of data records in microbiology_data file and hospital_admission_data file reflected the microbiology culture frequency and admission rate of the hospital, respectively. For example if the number of specimens in the microbiology_data file reported below is lower than what is expected, please check the raw data file and data dictionary files.

Month	Number of specimen data records in microbiology_data file	Number of admission data records in hospital_admission_data file
January	*622*	
February	*0*	
March	*0*	
April	*0*	
May	*0*	
June	*0*	
July	*0*	
August	*0*	
September	*0*	
October	*0*	
November	*0*	
December	*0*	
Total:	*622*	*NA*

Note:
[1] Additional general demographic data will be made available in the next version of the AMASS application.

Section [2]: Isolate−based surveillance report

Introduction
An isolate−based surveillance report is generated by default, even if the hospital_ admission_data file is unavailable. This is to enable hospitals with only microbiology data available to utilize the de−duplication and report generation functions of AMASS.
This report is without stratification by origin of infection.

The report generated by the AMASS application version 1.0 includes only blood samples. The next version of AMASS will include other specimen types, including cerebrospinal fluid (CSF), urine, stool, and other specimens.

Organisms under this survey:

- *Staphylococcus aureus*
- *Enterococcus* spp.
- *Streptococcus pneumoniae*
- *Salmonella* spp.
- *Escherichia coli*
- *Klebsiella pneumoniae*
- *Pseudomonas aeruginosa*
- *Acinetobacter* spp.

Results
The microbiology_data file had:

Sample collection dates ranged from ***01 Jan 1995*** to ***31 Jan 1995***

Number of records of blood specimens collected within the above date range:

81 blood specimens records

*Number of records of blood specimens with *negative culture (no growth):*

0 blood specimens records

Number of records of blood specimens with culture positive for a microorganism:

81 blood specimens records

Number of records of blood specimens with culture positive for organism under this survey:

28 blood specimens records

The AMASS application de−duplicated the data by including only the first isolate per patient per specimen type per evaluation period as described in the method. The number of patients with positive samples is as follows:

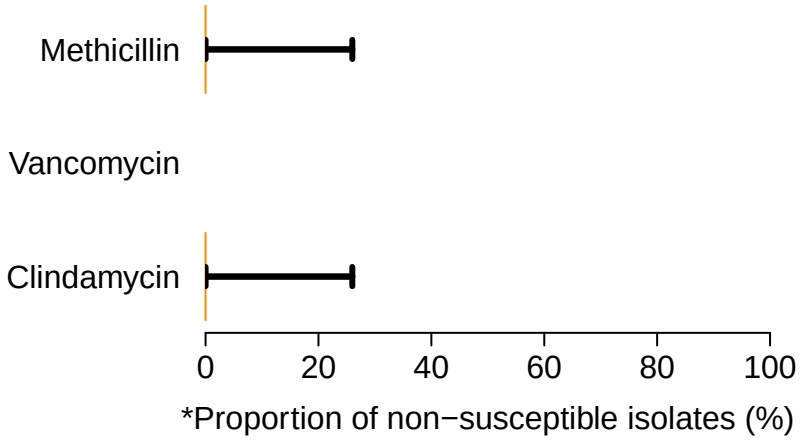
Organism	Number of records of blood specimens culture positive for the organism	**Number of patients with blood culture positive for the organism (de−duplicated)
Staphylococcus aureus	***12***	***11***
***Enterococcus* spp.**	***2***	***2***
Streptococcus pneumoniae	***5***	***5***
***Salmonella* spp.**	***0***	***0***
Escherichia coli	***7***	***6***
Klebsiella pneumoniae	***2***	***2***
Pseudomonas aeruginosa	***0***	***0***
***Acinetobacter* spp.**	***0***	***0***
Total:	***28***	***26***

*The negative culture included data values specified as 'no growth' in the dictionary_for_ microbiology_data file (details on data dictionary files are in the method section) to represent specimens with negative culture for any microorganism.
**Only the first isolate for each patient per specimen type, per pathogen, and per evaluation period was included in the analysis.

The following figures and tables show the proportion of patients with blood culture positive for antimicrobial non−susceptible isolates.

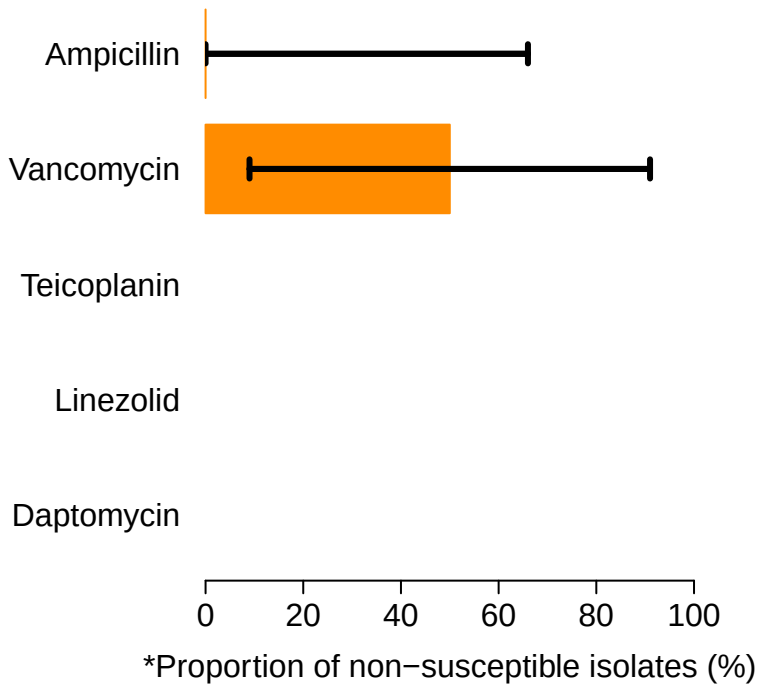
Section [2]: Isolate−based surveillance report

Blood: ***Staphylococcus aureus*** ***(No. of patients = 11)***



Antibiotic agent	% NS (n)	95% CI
Methicillin	0% (0/11)	0%−26%
Vancomycin	NA	−
Clindamycin	0% (0/11)	0%−26%

Blood: ***Enterococcus* spp.** ***(No. of patients = 2)***

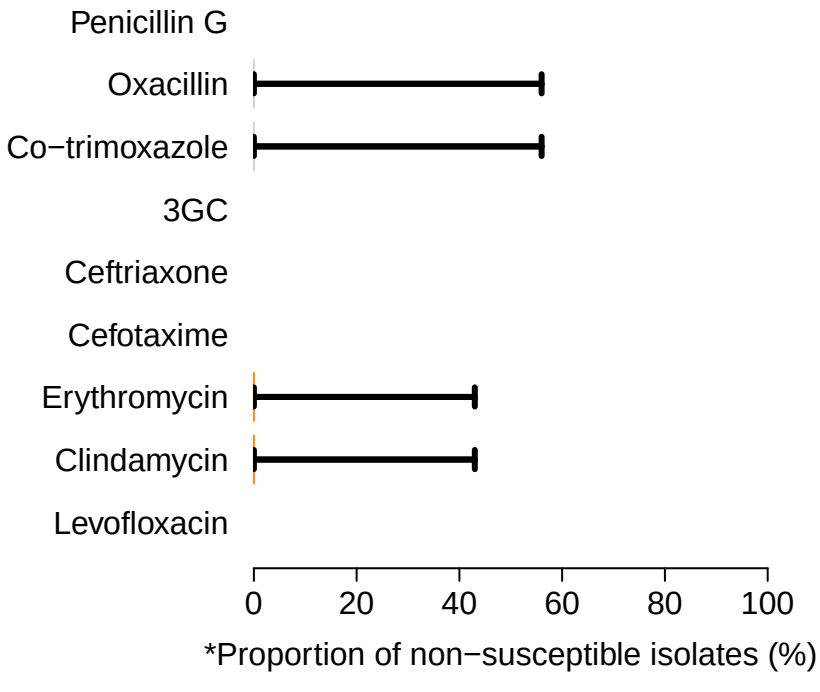


Antibiotic agent	% NS (n)	95% CI
Ampicillin	0% (0/2)	0%−66%
Vancomycin	50% (1/2)	9%−91%
Teicoplanin	NA	−
Linezolid	NA	−
Daptomycin	NA	−

*Proportion of non−susceptible isolates (% NS) represents the number of patients with blood culture positive for non−susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de−duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of patients with blood culture positive for the organism.
CI = confidence interval; NA = Not available/reported/tested; Methicillin: methicillin, oxacillin, or cefoxitin

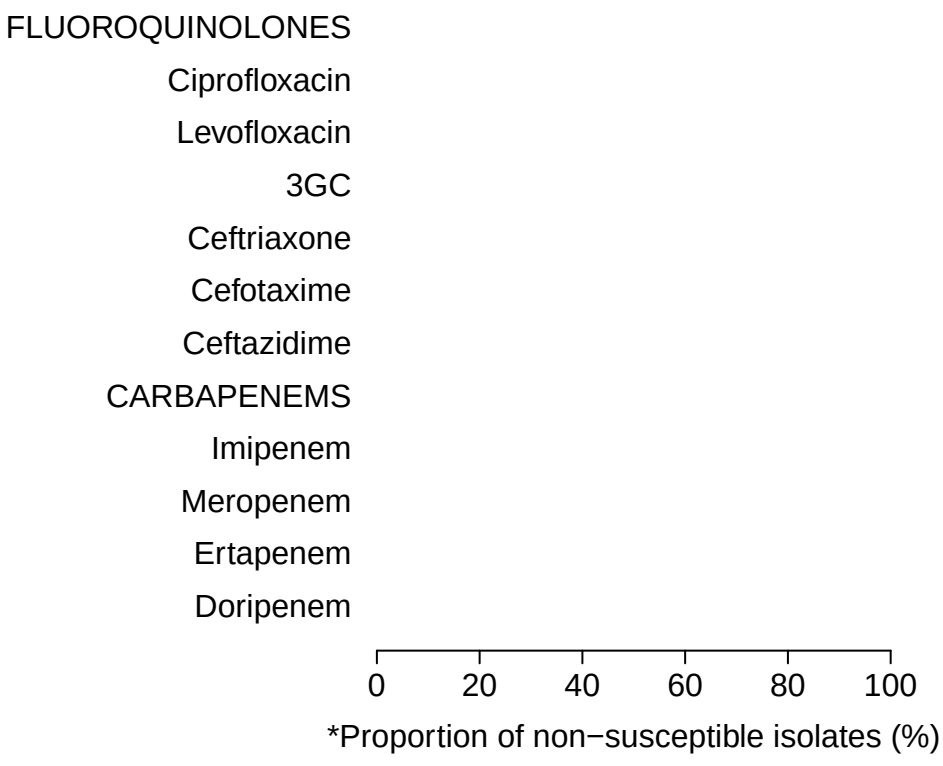
Section [2]: Isolate−based surveillance report

Blood: ***Streptococcus pneumoniae*** ***(No. of patients = 5)***



Antibiotic agent	% NS (n)	95% CI
Penicillin G	NA	−
Oxacillin	0% (0/3)	0%−56%
Co−trimoxazole	0% (0/3)	0%−56%
3GC	NA	−
Ceftriaxone	NA	−
Cefotaxime	NA	−
Erythromycin	0% (0/5)	0%−43%
Clindamycin	0% (0/5)	0%−43%
Levofloxacin	NA	−

Blood: ***Salmonella* spp.** ***(No. of patients = 0)***

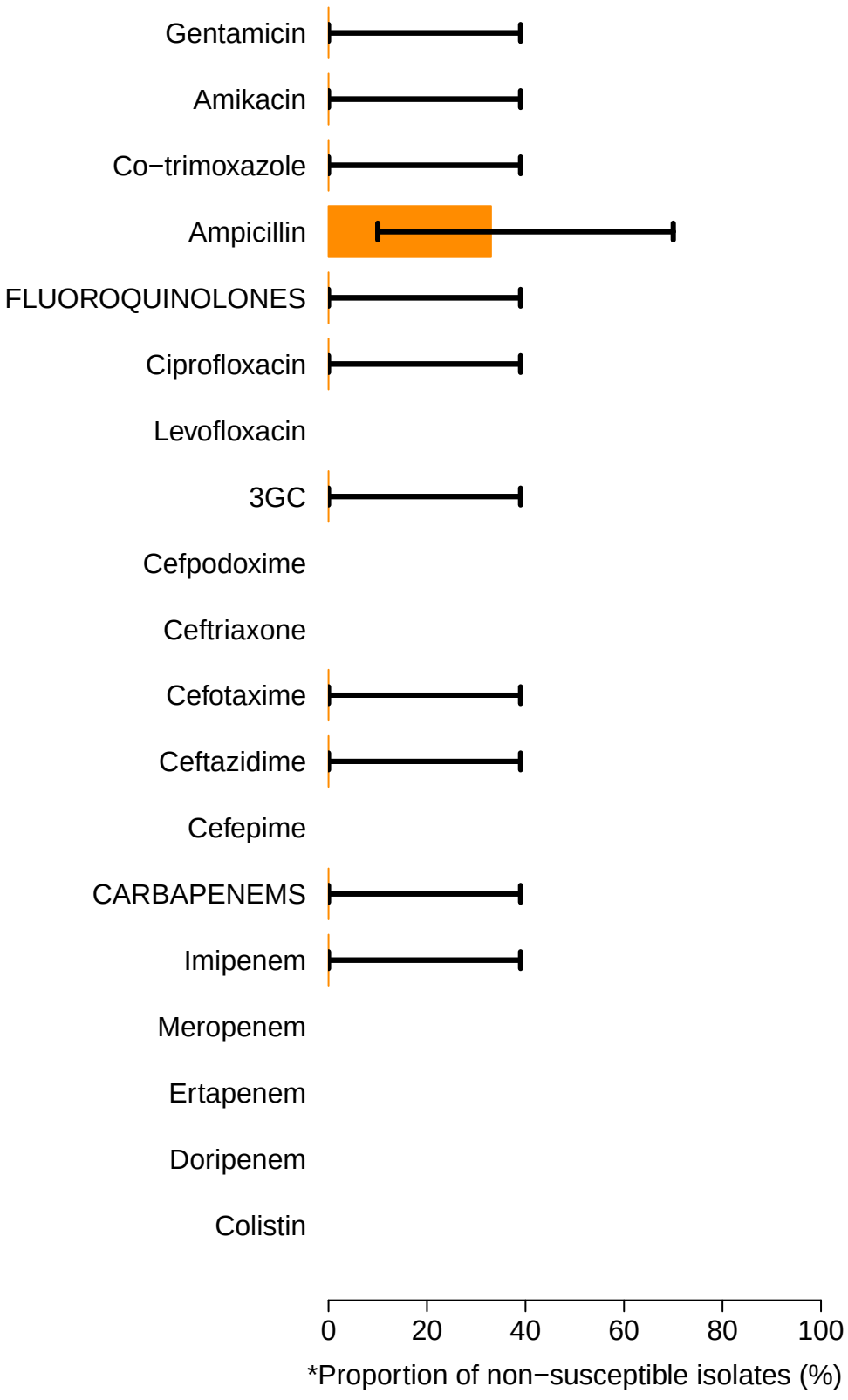


Antibiotic agent	% NS (n)	95% CI
FLUOROQUINOLONES	NA	−
Ciprofloxacin	NA	−
Levofloxacin	NA	−
3GC	NA	−
Ceftriaxone	NA	−
Cefotaxime	NA	−
Ceftazidime	NA	−
CARBAPENEMS	NA	−
Imipenem	NA	−
Meropenem	NA	−
Ertapenem	NA	−
Doripenem	NA	−

*Proportion of non−susceptible isolates (% NS) represents the number of patients with blood culture positive for non−susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de−duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of blood culture positive for the organism.
CI = confidence interval; NA = Not available/reported/tested; 3GC = 3rd−generation cephalosporin;
FLUOROQUINOLONES: ciprofloxacin or levofloxacin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

Section [2]: Isolate−based surveillance report

Blood: ***Escherichia coli*** ***(No. of patients = 6)***

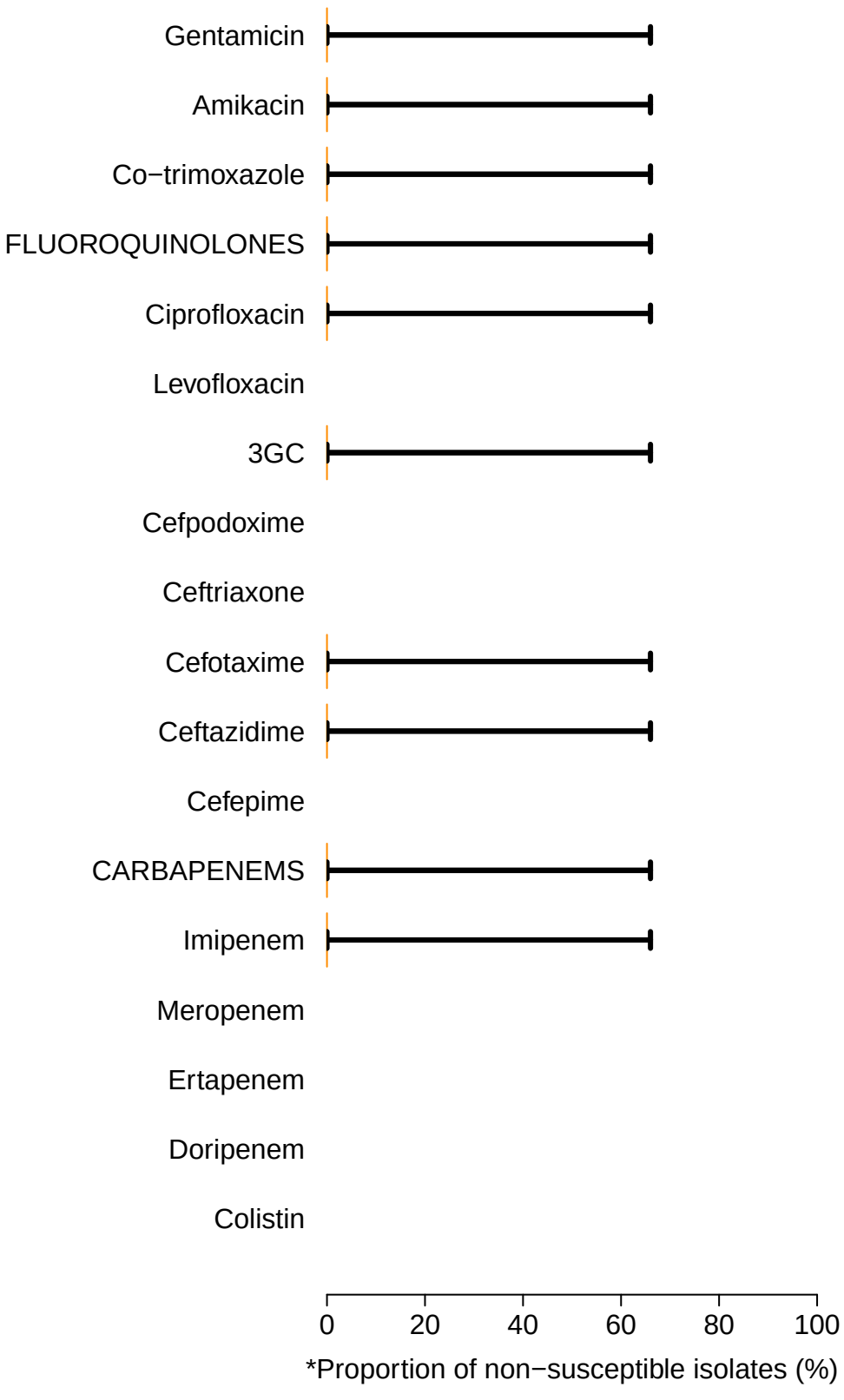


Antibiotic agent	% NS (n)	95% CI
Gentamicin	0% (0/6)	0%−39%
Amikacin	0% (0/6)	0%−39%
Co−trimoxazole	0% (0/6)	0%−39%
Ampicillin	33% (2/6)	10%−70%
FLUOROQUINOLONES	0% (0/6)	0%−39%
Ciprofloxacin	0% (0/6)	0%−39%
Levofloxacin	NA	−
3GC	0% (0/6)	0%−39%
Cefpodoxime	NA	−
Ceftriaxone	NA	−
Cefotaxime	0% (0/6)	0%−39%
Ceftazidime	0% (0/6)	0%−39%
Cefepime	NA	−
CARBAPENEMS	0% (0/6)	0%−39%
Imipenem	0% (0/6)	0%−39%
Meropenem	NA	−
Ertapenem	NA	−
Doripenem	NA	−
Colistin	NA	−

*Proportion of non−susceptible isolates (% NS) represents the number of patients with blood culture positive for non−susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de−duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of blood culture positive for the organism.
CI = confidence interval; NA = Not available/reported/tested; 3GC = 3rd−generation cephalosporin; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

Section [2]: Isolate−based surveillance report

Blood: ***Klebsiella pneumoniae*** ***(No. of patients = 2)***

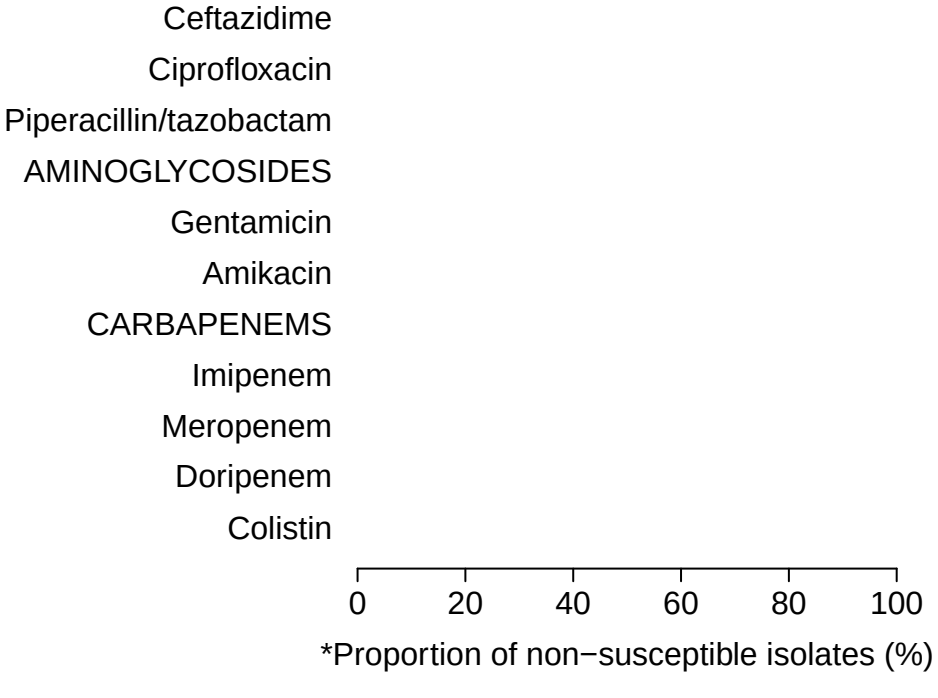


Antibiotic agent	% NS (n)	95% CI
Gentamicin	0% (0/2)	0%−66%
Amikacin	0% (0/2)	0%−66%
Co−trimoxazole	0% (0/2)	0%−66%
FLUOROQUINOLONES	0% (0/2)	0%−66%
Ciprofloxacin	0% (0/2)	0%−66%
Levofloxacin	NA	−
3GC	0% (0/2)	0%−66%
Cefpodoxime	NA	−
Ceftriaxone	NA	−
Cefotaxime	0% (0/2)	0%−66%
Ceftazidime	0% (0/2)	0%−66%
Cefepime	NA	−
CARBAPENEMS	0% (0/2)	0%−66%
Imipenem	0% (0/2)	0%−66%
Meropenem	NA	−
Ertapenem	NA	−
Doripenem	NA	−
Colistin	NA	−

*Proportion of non−susceptible isolates (% NS) represents the number of patients with blood culture positive for non−susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de−duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of blood culture positive for the organism.
CI = confidence interval; NA = Not available/reported/tested; 3GC = 3rd−generation cephalosporin; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

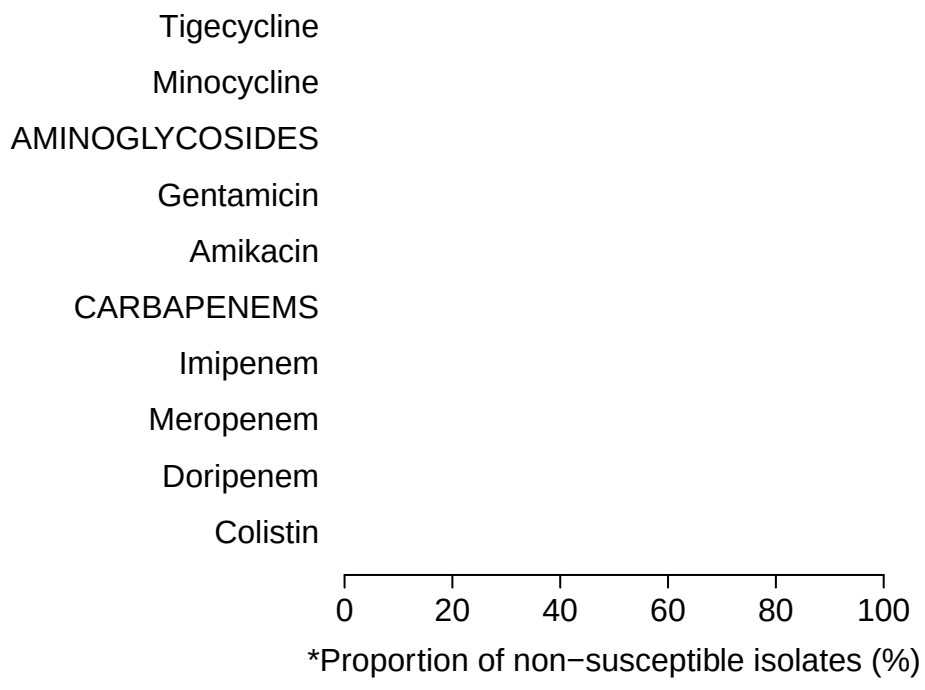
Section [2]: Isolate−based surveillance report

Blood: ***Pseudomonas aeruginosa*** ***(No. of patients = 0)***



Antibiotic agent	% NS (n)	95% CI
Ceftazidime	NA	–
Ciprofloxacin	NA	–
Piperacillin/tazobactam	NA	–
AMINOGLYCOSIDES	NA	–
Gentamicin	NA	–
Amikacin	NA	–
CARBAPENEMS	NA	–
Imipenem	NA	–
Meropenem	NA	–
Doripenem	NA	–
Colistin	NA	–

Blood: ***Acinetobacter* spp.** ***(No. of patients = 0)***



Antibiotic agent	% NS (n)	95% CI
Tigecycline	NA	–
Minocycline	NA	–
AMINOGLYCOSIDES	NA	–
Gentamicin	NA	–
Amikacin	NA	–
CARBAPENEMS	NA	–
Imipenem	NA	–
Meropenem	NA	–
Doripenem	NA	–
Colistin	NA	–

*Proportion of non−susceptible isolates (% NS) represents the number of patients with blood culture positive for non−susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de−duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of blood culture positive for the organism.
CI = confidence interval; NA = Not available/reported/tested; AMINOGLYCOSIDES: either gentamicin or amikacin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

Report [3]: Isolate−based surveillance report with stratification by infection origin

Proportions of antimicrobial−resistance infection stratified by origin of infection is not calculated because hospital admission date data is not available and infection origin variable is not available.

Report [4]: Sample−based surveillance report without stratification by infection origin

Incidence of infections per 100,000 tested population is not calculated because data on blood specimen with no growth is not available.

Report [5]: Sample−based surveillance report with stratification by infection origin

Incidence of infections per 100,000 tested population stratified by infection origin is not calculated because data on blood specimen with no growth is not available, or stratification by origin of infection cannot be done (due to hospital admission date variable is not available).

Report [6] Mortality in AMR antimicrobial−susceptible infections

Not applicable because hospital_admission_data.csv file is not available,
or in−hospital outcome (in hospital_admission_data.csv file) is not available.

Methods used by the AMASS application

Data source:
For each run (double−click on AMASS.bat file), the AMASS application used the microbiology data file (microbiology_data) and the hospital admission data file (hospital_admission_data) that were stored in the same folder as the application file. Hence, if the user would like to update, correct, revise or change the data, the data files in the folder should be updated before the AMASS.bat file is double−clicked again. A new report based on the updated data would then be generated.

Requirements:
− Computer with Microsoft Windows 7 or 10
AMASS may work in other versions of Microsoft Windows and other operating systems. However, thorough testing and adjustment have not been performed.
− AMASS.zip package file
The AMASS application is to be downloaded from http://www.amass.website, and unzipped to generate an AMASS folder that could be stored under any folder in the computer. The AMASS folder contains 4 files (AMASS.bat, z_Rcode.R, dictionary_for_microbiology_data.xlsx, and dictionary_for_hospital_admission_data.xlsx), and 5 folders (Variables, Rprogram, Example_Dataset_1_WHONET, Example_Dataset_2, and ResultData).
− Microbiology data file (microbiology_data in .csv or .xlsx file format)
The user needs to obtain microbiology data, and then copy & paste this data file into the same folder as the AMASS.bat file.
− [Optional] Hospital admission data file (hospital_admission_data)
If available, the user could obtain hospital admission data, and then copy & paste this data file into the same folder as the AMASS.bat file.

Not required:
− Internet to run AMASS application
The AMASS application will run offline. No data are transferred while the application is running and reports are being generated; the reports are in PDF format (do not contain any patient identifier) and can be shared under the user's jurisdiction.
− R
The download package (AMASS.zip) included R portable and R libraries that the AMASS application requires. The user does not need to install any programme before using the AMASS. The user also does not have to uninstall R prgramme if the computer already has the R prgramme installed. The user does not need to know how to use R prgramme.

Note:
[1] Please ensure that the file names of microbiology data file (microbiology_data) and the hospital admission data file (hospital_admission_data) are identical to what is written here. Please make sure that all are lower−cases with an underscore '_' at each space.
[2] Please ensure that both microbiology and hospital admission data files have no empty rows before the row of the variable names (i.e. the variable names are the first row in both files).
[3] For the first run, an user may need to fill the data dictionary files to make sure that the AMASS application understands your variable names and values.

AMASS uses a tier−based approach. In cases when only the microbiology data file with the results of culture positive samples is available, only section one and two would be generated for users. Section three would be generated only when data on admission date are available. This is because these data are required for the stratification by origin of infection. Section four would be generated only when data of specimens with culture negative (no microbial growth) are available in the microbiology data. This is because these are required for the sample−based approach. Section five would be generated only when both data of specimens with culture negative and admission date are available. Section six would be generated only when mortality data are available.

Mortality was calculated from the number of in−hospital deaths (numerator) over the total number of patients with blood culture positive for the organism (denominator). Please note that this is the all−cause mortality calculated using the outcome data in the data file, and may not necessarily represent the mortality directly due to the infections.

How to use data dictionary files
In cases when variable names in the microbiology and hospital admission data files were not the same as the one that AMASS used, the data dictionary files could be edited.
The raw microbiology and hospital admission data files were to be left unchanged.
The data dictionary files provided could be edited and re−used automatically when the microbiology and hospital admission data files were updated and the AMASS.bat were to be double−clicked again (i.e. the data dictionary files would allow the user to re−analyze data files without the need to adjust variable names and data value again every time).

For example:
If variable name for 'hospital number' is written as 'hn' in the raw data file, the user would need to add 'hn' in the cell next to 'hospital_number'. If data value for blood specimens is defined by 'Blood−Hemoculture' in the raw data file, then the user would need to add 'Blood−Hemoculture' in the cell next to 'blood_specimen'.

Dictionary file (dictionary_for_microbiology_data.xlsx) may show up as in the table below:

Variable names used in AMASS	**Variable names used in your microbiology data file**	**Requirements**
Don't change values in this column, but you can add rows with similar values if you need	Change values in this column to represent how variable names are written in your raw microbiology data file	
hospital_number		Required
Values described in AMASS	**Values used in your microbiology data file**	**Requirements**
blood_specimen		Required

Please fill in your variable names as follows:

Variable names used in AMASS	**Variable names used in your microbiology data file**	**Requirements**
Don't change values in this column, but you can add rows with similar values if you need	Change values in this column to represent how variable names are written in your raw microbiology data file	
hospital_number	hn	Required
Values described in AMASS	**Values used in your microbiology data file**	**Requirements**
blood_specimen	Blood−Hemoculture	Required

Then, save the file. For every time the user double−clicked AMASS.bat, the application would know that the variable named 'hn' is similar to 'hospital_number' and represents the patient identifier in the analysis.

Organisms included in this report:

- *Staphylococcus aureus*
- *Enterococcus* spp.
- *Streptococcus pneumoniae*
- *Salmonella* spp.
- *Escherichia coli*
- *Klebsiella pneumoniae*
- *Pseudomonas aeruginosa*
- *Acinetobacter* spp.

The eight organisms and antibiotics included in the report were selected based on the global priority list of antibiotic resistant bacteria and Global Antimicrobial Resistance Surveillance System (GLASS) of WHO [1,2].

Definitions:

The definitions of infection origin proposed by the WHO GLASS was used [1]. In brief, community−origin bloodstream infection (BSI) was defined for patients in the hospital within the first two calendar days of admission when the first blood culture positive specimens were taken. Hospital−origin BSI was defined for patients in the hospital longer than the first calendar days of admission when the first blood culture positive specimens were taken. In cases when the user had additional data on infection origin defined by infection control team or based on referral data, the user could edit the data dictionary file (variable name 'infection_origin') and the AMASS application would use the data of that variable to stratify the data by origin of infection instead of the above definition. However, in cases when data on infection origin were not available (as in many hospitals in LMICs), the above definition would be calculated based on admission date and specimen collection date (with cutoff of 2 calendar days) and used to classify infections as community−origin or hospital−origin.

De−duplication:

When more than one blood culture was collected during patient management, duplicated findings of the same patient were excluded (de−duplicated). Only one result was reported for each patient per sample type (blood) and surveyed organisms (listed above). For example, if two blood cultures from the same patient had *E. coli*, only the first would be included in the report. If there was growth of *E. coli* in one blood culture and of *K. pneumoniae* in the other blood culture, then both results would be reported. One would be for the report on *E. coli* and the other one would be for the report on *K. pneumoniae.*

References:

[1] World Health Organization (2018) Global Antimicrobial Resistance Surveillance System (GLASS) Report. Early implantation 2016−2017. http://apps.who.int/iris/bitstream/handle/10665/259744/9789241513449−eng.pdf. (accessed on 3 Dec 2018)

[2] World Health Organization (2017) Global priority list of antibiotic−resistant bacteria to guide research, discovery, and development of new antibiotics. https://www.who.int/medicines/publications/WHO−PPL−Short_Summary_25Feb−ET_NM_WHO.pdf. (accessed on 3 Dec 2018)

Investigator team

The AMASS application is being developed by Cherry Lim, Clare Ling, Elizabeth Ashley, Paul Turner, Rahul Batra, Rogier van Doorn, Soawapak Hinjoy, Sopon Iamsirithaworn, Susanna Dunachie, Tri Wangrangsimakul, Viriya Hantrakun, William Schilling, John Stelling, Jonathan Edgeworth, Guy Thwaites, Nicholas PJ Day, Ben Cooper and Direk Limmathurotskul.

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