

Antimicrobial Resistance (AMR) Surveillance plus Notifiable Bacterial Diseases Report

Hospital name: **Kantharalak Hospital**
Country name: **Thailand**

Data from:
01 Jan 2021 to 31 Dec 2021

Contact person: **Punya Jiramahasan**
Contact address: **Kantharalak Hospital**
Contact email: **cd_ktlhos@hotmail.com**
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M-Lab

Generated by

AutoMated tool for Antimicrobial resistance Surveillance System plus (AMASSplus)
Beta version (released on 25 March 2021)

The AMASSplus application is an extension of AMASS Version 1.1 that was released on 12 January 2021.

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 and hospital_admission_data files that are stored in the same folder as the application (AMASS.bat) 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.

If you have any queries about AMASS or AMASSplus, please contact:
Chalida Rangsiwutisak (chalida@tropmedres.ac),
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 Institute (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).

The AMASSplus is the AMASS application with an additional report on selected notifiable bacterial diseases. The AMASSplus allows users to generate summary reports on patients with selected notifiable bacterial diseases; including melioidosis, brucellosis, diphtheria, gonorrhea, meningococcal, typhoid, paratyphoid, salmonellosis, shigellosis, *Streptococcus suis* infection and vibriosis based on bacterial culture results. Please note that the additional report of the AMASSplus also require readers to understand the limitations and review the reports and summary data carefully.

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:

5493 specimen data records with collection dates ranging from
01 Jan 2021 to **31 Dec 2021**

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

19736 admission data records with hospital admission dates ranging from
01 Jan 2021 to **31 Dec 2021**

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	469	1336
February	494	1380
March	513	1614
April	432	1475
May	315	1222
June	495	1292
July	472	1642
August	439	2205
September	471	1642
October	529	1609
November	429	2668
December	435	1651
Total:	5493	19736

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 2021** to **31 Dec 2021***

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

1095 blood specimens records

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

78 blood specimens records

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

1017 blood specimens records

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

335 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)
<i>Staphylococcus aureus</i>	37	34
<i>Enterococcus</i> spp.	11	10
<i>Streptococcus pneumoniae</i>	3	3
<i>Salmonella</i> spp.	11	10
<i>Escherichia coli</i>	169	158
<i>Klebsiella pneumoniae</i>	70	64
<i>Pseudomonas aeruginosa</i>	10	9
<i>Acinetobacter</i> spp.	24	22
Total:	335	310

*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.

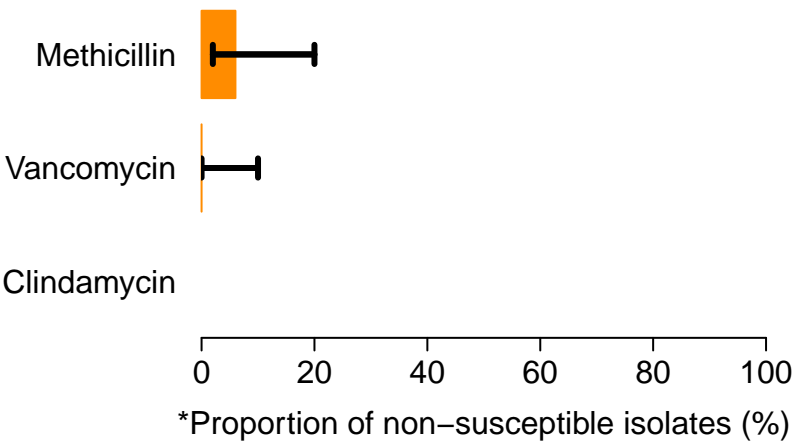
**Only the first isolate for each patient per specimen type, per pathogen, and per evaluation period was included in the analysis.

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*

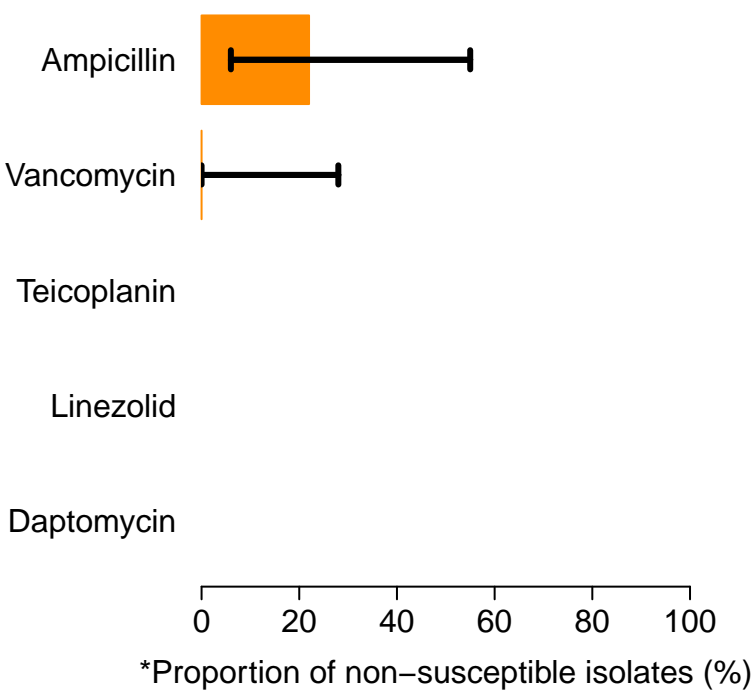
(No. of patients = 34)



Antibiotic agent	% NS (n)	95% CI
Methicillin	6% (2/32)	2%–20%
Vancomycin	0% (0/34)	0%–10%
Clindamycin	NA	–

Blood: *Enterococcus* spp.

(No. of patients = 10)



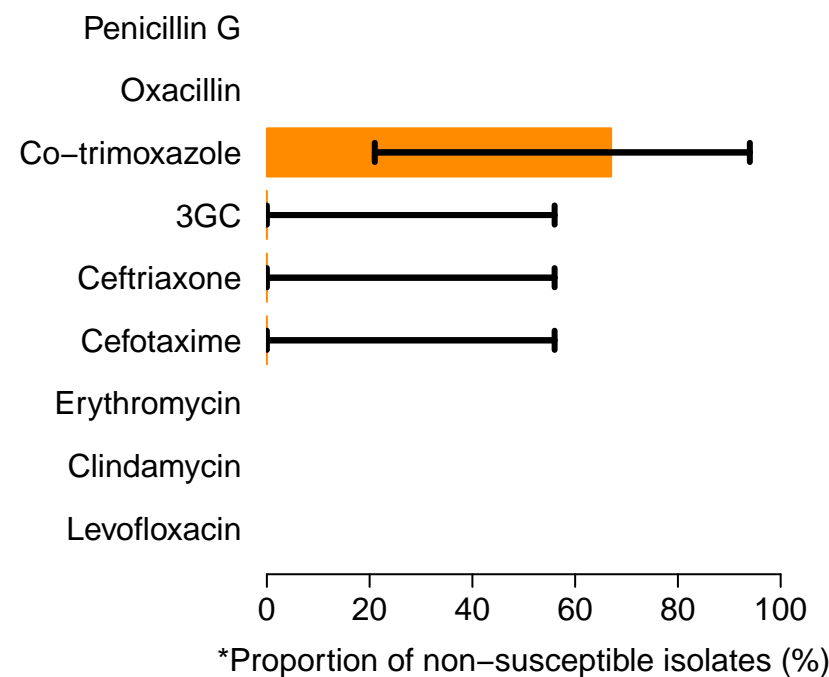
Antibiotic agent	% NS (n)	95% CI
Ampicillin	22% (2/9)	6%–55%
Vancomycin	0% (0/10)	0%–28%
Teicoplanin	NA	–
Linezolid	NA	–
Daptomycin	NA	–

*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 ceftioxin

Section [2]: Isolate-based surveillance report

Blood: *Streptococcus pneumoniae*

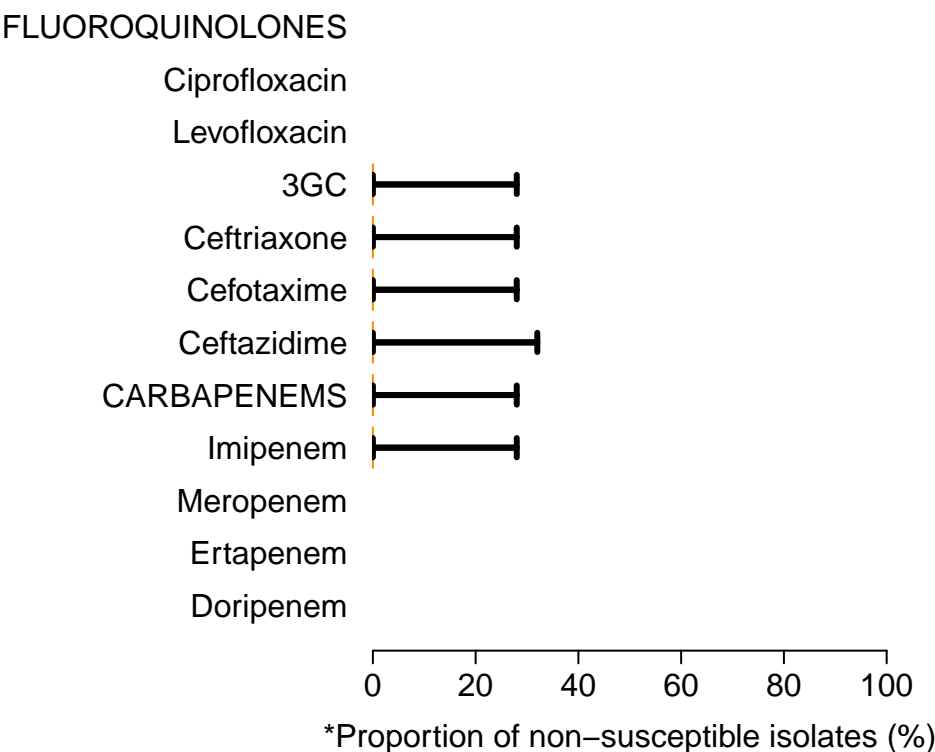
(No. of patients = 3)



Antibiotic agent	% NS (n)	95% CI
Penicillin G	NA	–
Oxacillin	NA	–
Co-trimoxazole	67% (2/3)	21%–94%
3GC	0% (0/3)	0%–56%
Ceftriaxone	0% (0/3)	0%–56%
Cefotaxime	0% (0/3)	0%–56%
Erythromycin	NA	–
Clindamycin	NA	–
Levofloxacin	NA	–

Blood: *Salmonella* spp.

(No. of patients = 10)



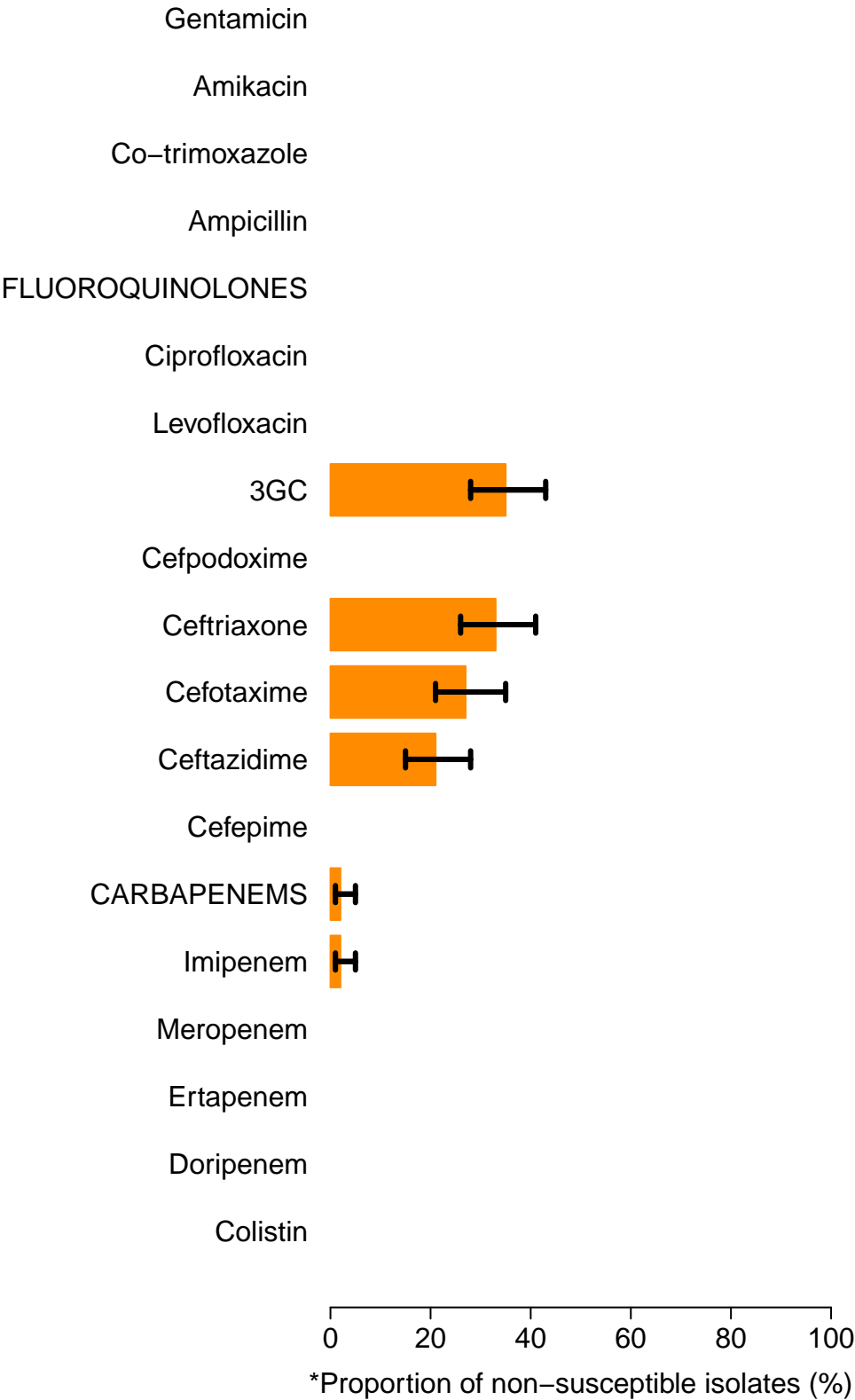
Antibiotic agent	% NS (n)	95% CI
FLUOROQUINOLONES	NA	–
Ciprofloxacin	NA	–
Levofloxacin	NA	–
3GC	0% (0/10)	0%–28%
Ceftriaxone	0% (0/10)	0%–28%
Cefotaxime	0% (0/10)	0%–28%
Ceftazidime	0% (0/8)	0%–32%
CARBAPENEMS	0% (0/10)	0%–28%
Imipenem	0% (0/10)	0%–28%
Meropenem	NA	–
Ertapenem	NA	–
Doripenem	NA	–

*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 = 158)

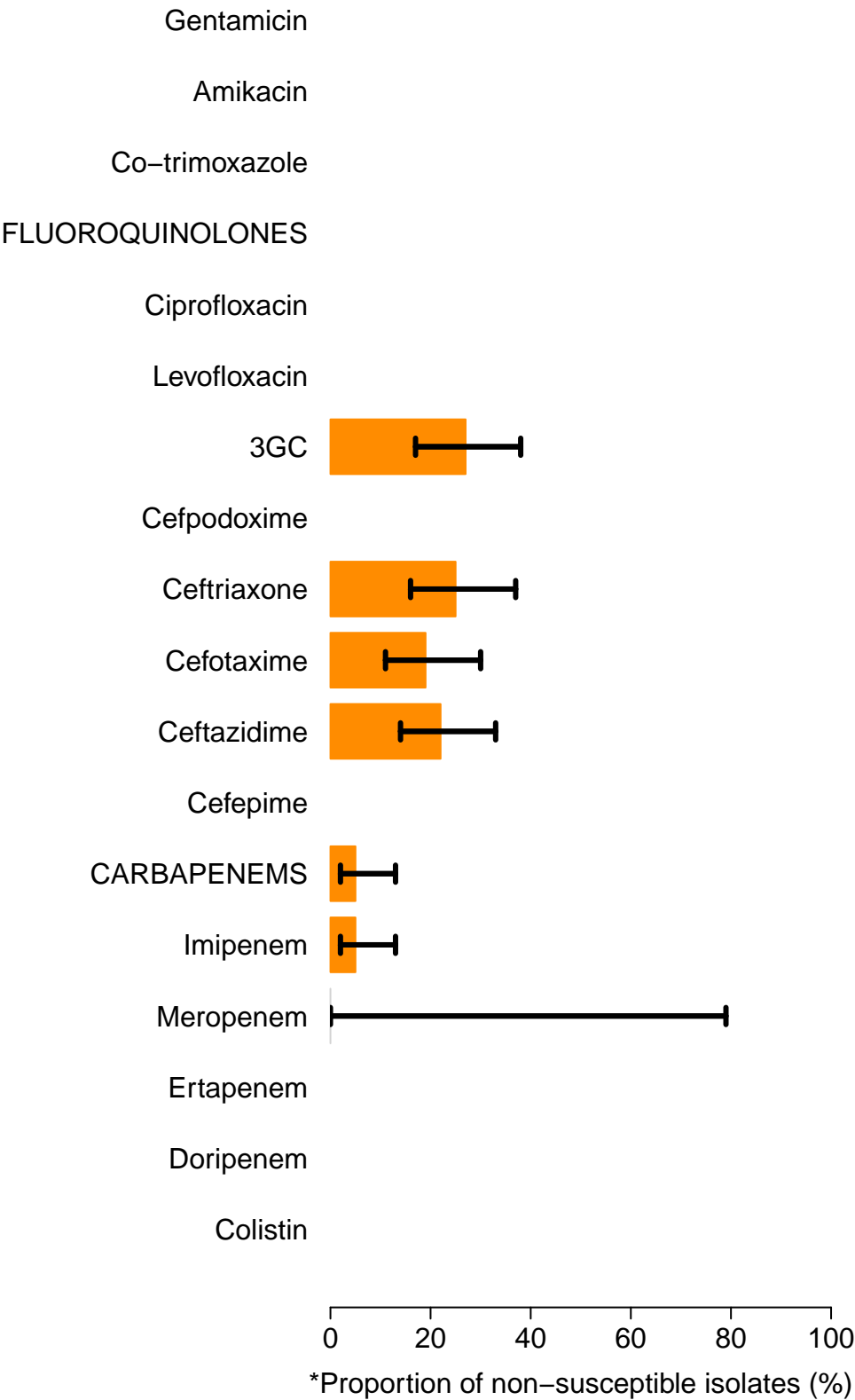


Antibiotic agent	% NS (n)	95% CI
Gentamicin	NA	–
Amikacin	NA	–
Co-trimoxazole	NA	–
Ampicillin	NA	–
FLUOROQUINOLONES	NA	–
Ciprofloxacin	NA	–
Levofloxacin	NA	–
3GC	35% (55/158)	28%–43%
Cefpodoxime	NA	–
Ceftriaxone	33% (52/158)	26%–41%
Cefotaxime	27% (43/158)	21%–35%
Ceftazidime	21% (33/158)	15%–28%
Cefepime	NA	–
CARBAPENEMS	2% (3/158)	1%–5%
Imipenem	2% (3/158)	1%–5%
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 = 64)

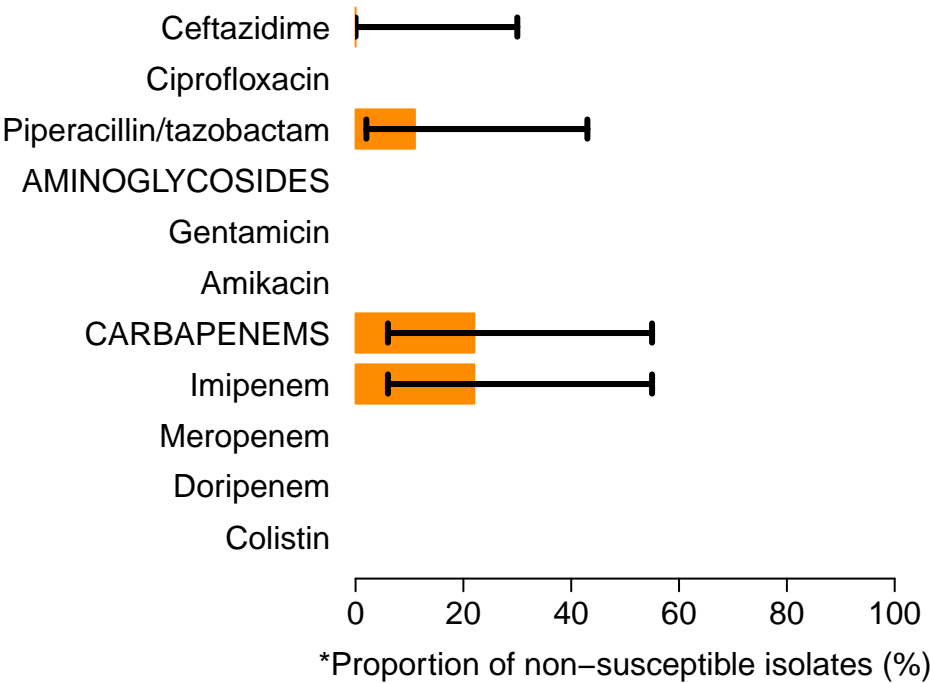


*Proportion of non-susceptible isolates (% NS) represents the number of patients with blood culture positive for non-susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). 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*

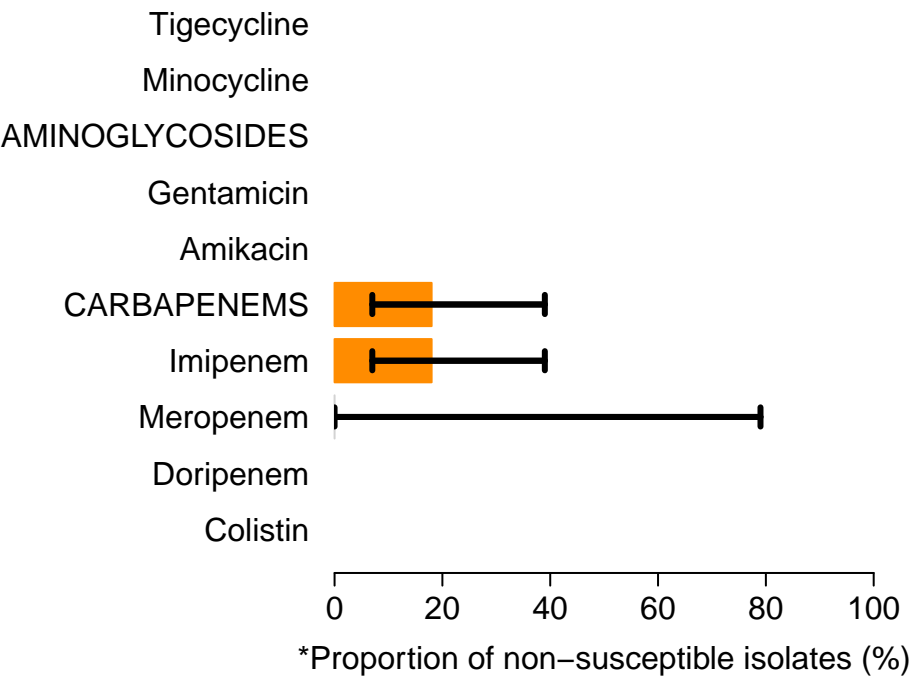
(No. of patients = 9)



Antibiotic agent	% NS (n)	95% CI
Ceftazidime	0% (0/9)	0%–30%
Ciprofloxacin	NA	–
Piperacillin/tazobactam	11% (1/9)	2%–43%
AMINOGLYCOSIDES	NA	–
Gentamicin	NA	–
Amikacin	NA	–
CARBAPENEMS	22% (2/9)	6%–55%
Imipenem	22% (2/9)	6%–55%
Meropenem	NA	–
Doripenem	NA	–
Colistin	NA	–

Blood: *Acinetobacter* spp.

(No. of patients = 22)



Antibiotic agent	% NS (n)	95% CI
Tigecycline	NA	–
Minocycline	NA	–
AMINOGLYCOSIDES	NA	–
Gentamicin	NA	–
Amikacin	NA	–
CARBAPENEMS	18% (4/22)	7%–39%
Imipenem	18% (4/22)	7%–39%
Meropenem	0% (0/1)	0%–79%
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

Section [3]: Isolate–based surveillance report with stratification by infection origin

Introduction

An isolate–based surveillance report with stratification by origin of infection is generated only if admission date data are available in the raw data file(s) with the appropriate specification in the data dictionaries.

Stratification by origin of infection is used as a proxy to define where the bloodstream infection (BSI) was contracted (hospital versus community).

The definitions of infection origin proposed by the WHO GLASS are used. In brief, community–origin BSI is defined as patients in the hospital for less than or equal to two calendar days when the first specimen culture positive for the pathogen was taken. Hospital–origin BSI is defined as patients admitted for more than two calendar days when the first specimen culture positive for the pathogen was taken.

Results:

The data included in the analysis to generate the report had:

*Sample collection dates ranged from **01 Jan 2021** to **31 Dec 2021***

**Number of patients with blood culture positive for pathogen under the survey:*

310 patients

***Number of patients with community–origin BSI:*

173 patients

***Number of patients with hospital–origin BSI:*

88 patients

****Number of patients with unknown infection of origin status:*

49 patients

Organism	Number of patients with blood culture positive for the organism	Community –origin**	Hospital –origin**	Unknown origin***
<i>Staphylococcus aureus</i>	34	17	10	7
<i>Enterococcus</i> spp.	10	1	5	4
<i>Streptococcus pneumoniae</i>	3	3	0	0
<i>Salmonella</i> spp.	10	5	5	0
<i>Escherichia coli</i>	158	102	34	22
<i>Klebsiella pneumoniae</i>	64	34	20	10
<i>Pseudomonas aeruginosa</i>	9	2	5	2
<i>Acinetobacter</i> spp.	22	9	9	4
Total:	310	173	88	49

Note:

NA= Not applicable (hospital admission date or infection origin data are not available)

*Only the first isolate for each patient per specimen type per pathogen under the reporting period is included in the analysis. Please refer to Section [2] for details on how this number was calculated from the raw microbiology_data file.

**The definitions of infection origin proposed by the WHO GLASS is used. In brief, community–origin BSI was defined as patients in the hospital for less than or equal to two calendar days when the first blood culture positive for the pathogen was taken. Hospital–origin BSI was defined as patients admitted for more than two calendar days when the first specimen culture positive for the pathogen was taken.

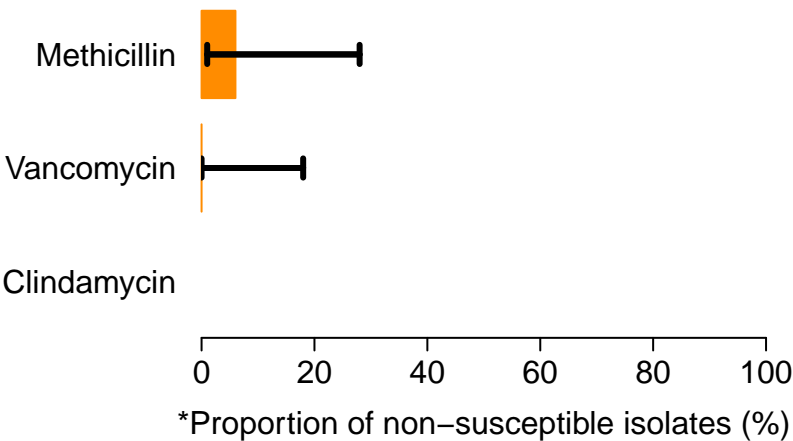
Please refer to the 'Methods' section for more details on the definitions used.

***Unknown origin could be because admission date data are not available or the patient was not hospitalised.

The following figures and tables below show the proportion of patients with blood culture positive for antimicrobial non–susceptible isolates stratified by infection of origin.

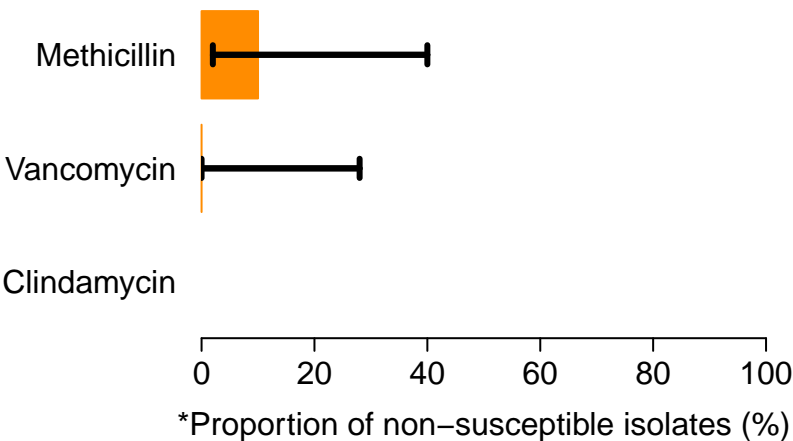
Section [3]: Isolate-based surveillance report
with stratification by infection origin

Blood: *Staphylococcus aureus* Community-origin (No. of patients = 17)



Antibiotic agent	% NS (n)	95% CI
Methicillin	6% (1/16)	1%–28%
Vancomycin	0% (0/17)	0%–18%
Clindamycin	NA	–

Blood: *Staphylococcus aureus* Hospital-origin (No. of patients = 10)



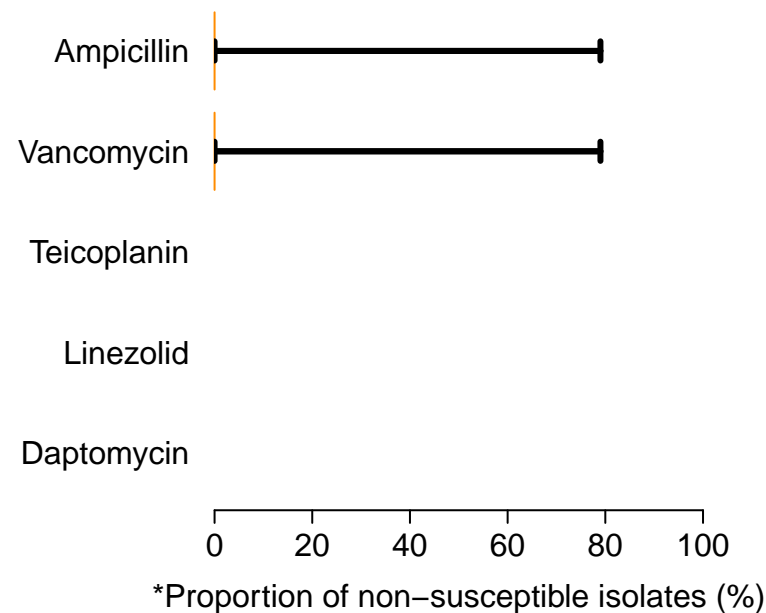
Antibiotic agent	% NS (n)	95% CI
Methicillin	10% (1/10)	2%–40%
Vancomycin	0% (0/10)	0%–28%
Clindamycin	NA	–

*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 [3]: Isolate–based surveillance report
with stratification by infection origin

Blood: *Enterococcus* spp.

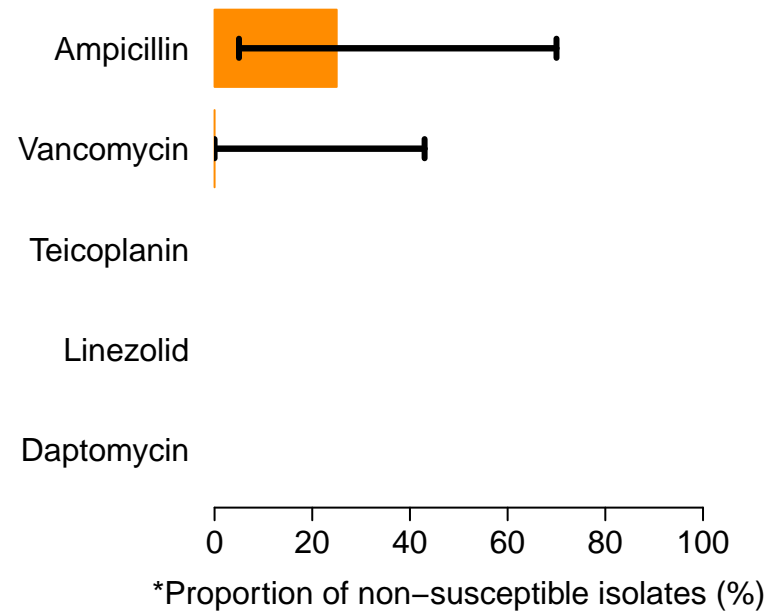
Community–origin (*No. of patients = 1*)



Antibiotic agent	% NS (n)	95% CI
Ampicillin	0% (0/1)	0%–79%
Vancomycin	0% (0/1)	0%–79%
Teicoplanin	NA	–
Linezolid	NA	–
Daptomycin	NA	–

Blood: *Enterococcus* spp.

Hospital–origin (*No. of patients = 5*)

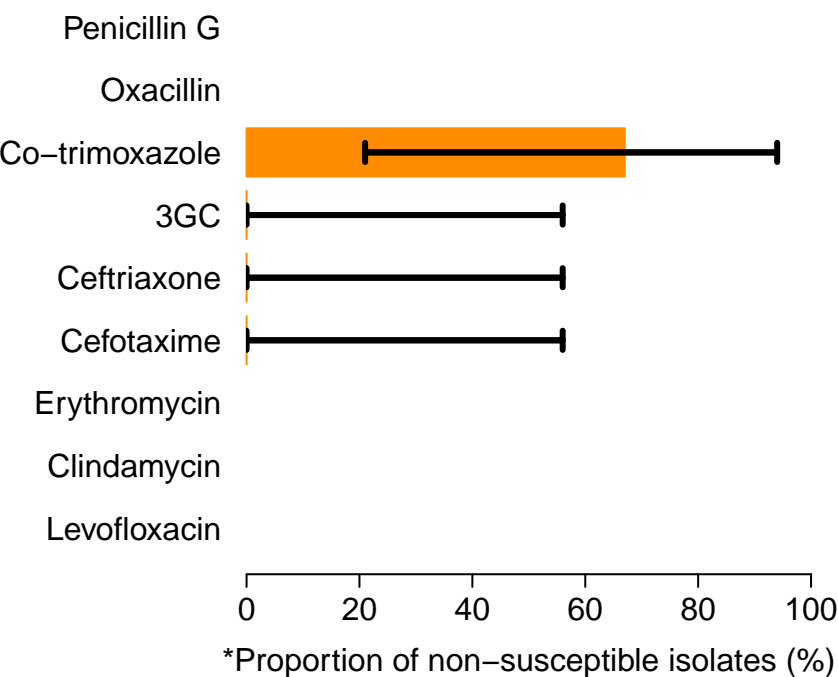


Antibiotic agent	% NS (n)	95% CI
Ampicillin	25% (1/4)	5%–70%
Vancomycin	0% (0/5)	0%–43%
Teicoplanin	NA	–
Linezolid	NA	–
Daptomycin	NA	–

*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

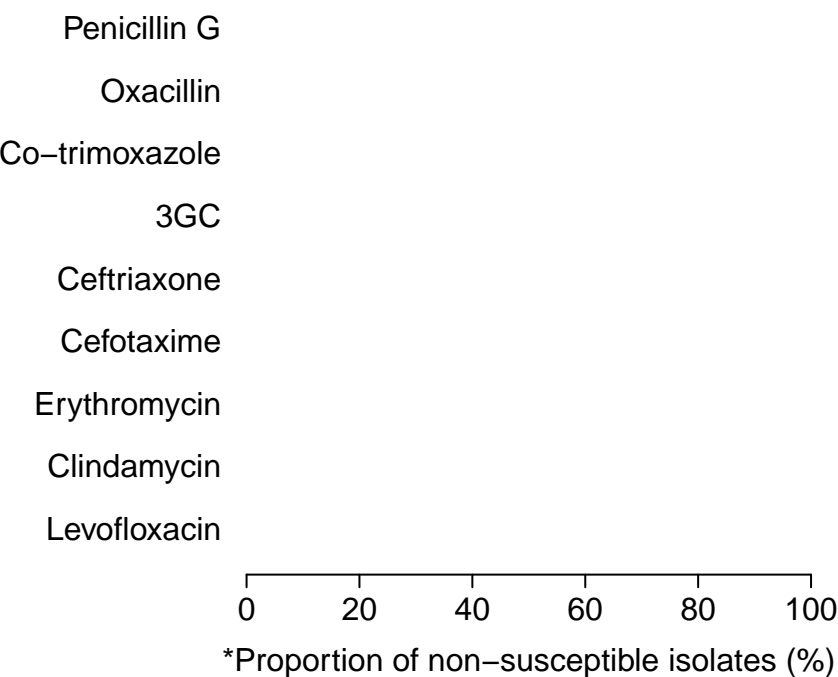
Section [3]: Isolate-based surveillance report with stratification by infection origin

Blood: Streptococcus pneumoniae Community-origin (No. of patients = 3)



Antibiotic agent	% NS (n)	95% CI
Penicillin G	NA	–
Oxacillin	NA	–
Co-trimoxazole	67% (2/3)	21%–94%
3GC	0% (0/3)	0%–56%
Ceftriaxone	0% (0/3)	0%–56%
Cefotaxime	0% (0/3)	0%–56%
Erythromycin	NA	–
Clindamycin	NA	–
Levofloxacin	NA	–

Blood: Streptococcus pneumoniae Hospital-origin (No. of patients = 0)

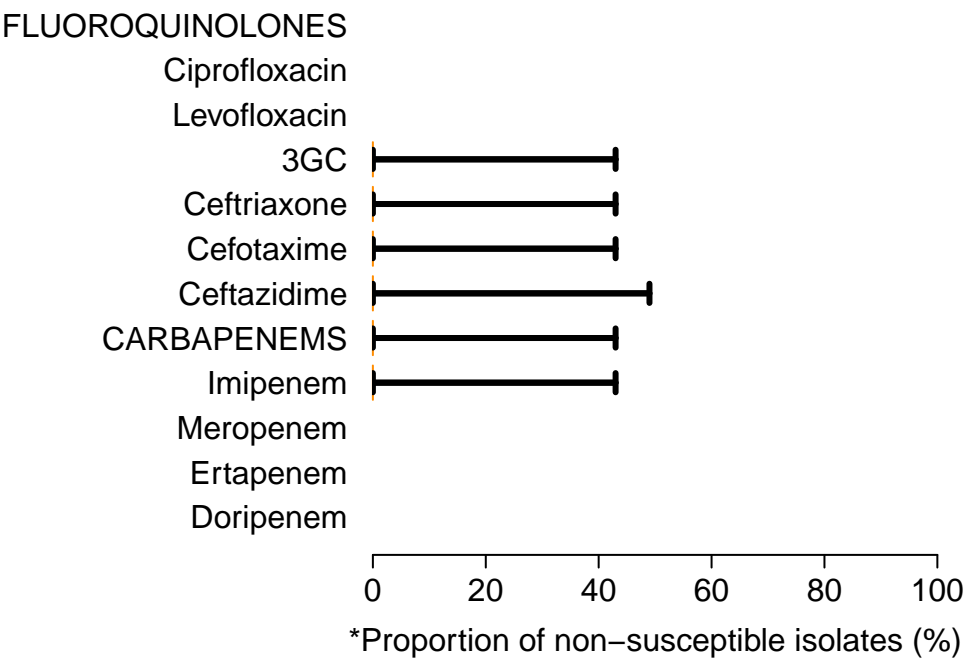


Antibiotic agent	% NS (n)	95% CI
Penicillin G	NA	–
Oxacillin	NA	–
Co-trimoxazole	NA	–
3GC	NA	–
Ceftriaxone	NA	–
Cefotaxime	NA	–
Erythromycin	NA	–
Clindamycin	NA	–
Levofloxacin	NA	–

*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 [3]: Isolate–based surveillance report
with stratification by infection origin

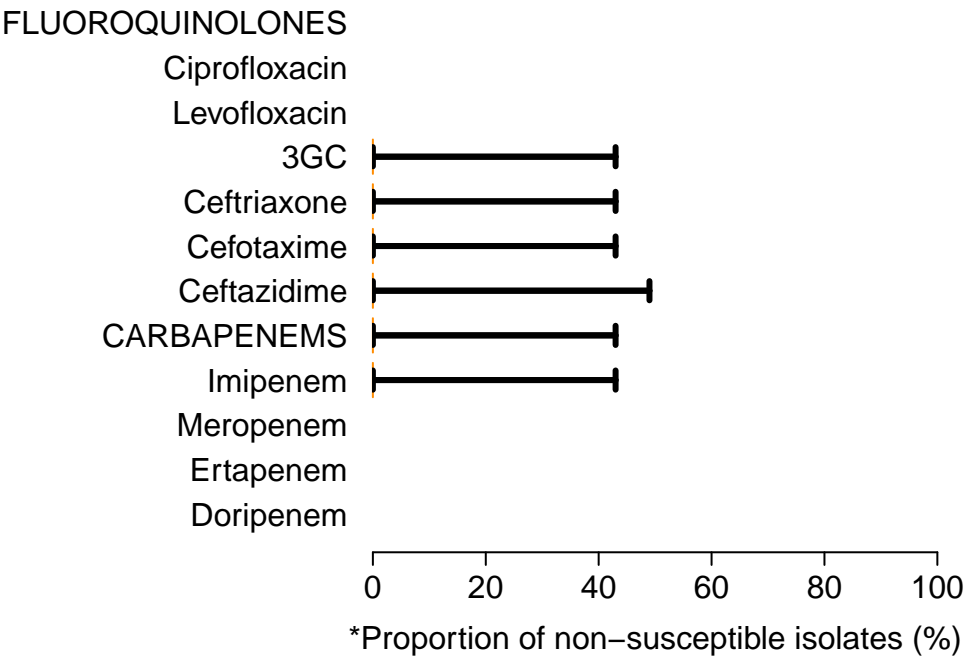
Blood: *Salmonella* spp.



Community–origin (*No. of patients = 5*)

Antibiotic agent	% NS (n)	95% CI
FLUOROQUINOLONES	NA	–
Ciprofloxacin	NA	–
Levofloxacin	NA	–
3GC	0% (0/5)	0%–43%
Ceftriaxone	0% (0/5)	0%–43%
Cefotaxime	0% (0/5)	0%–43%
Ceftazidime	0% (0/4)	0%–49%
CARBAPENEMS	0% (0/5)	0%–43%
Imipenem	0% (0/5)	0%–43%
Meropenem	NA	–
Ertapenem	NA	–
Doripenem	NA	–

Blood: *Salmonella* spp.



Hospital–origin (*No. of patients = 5*)

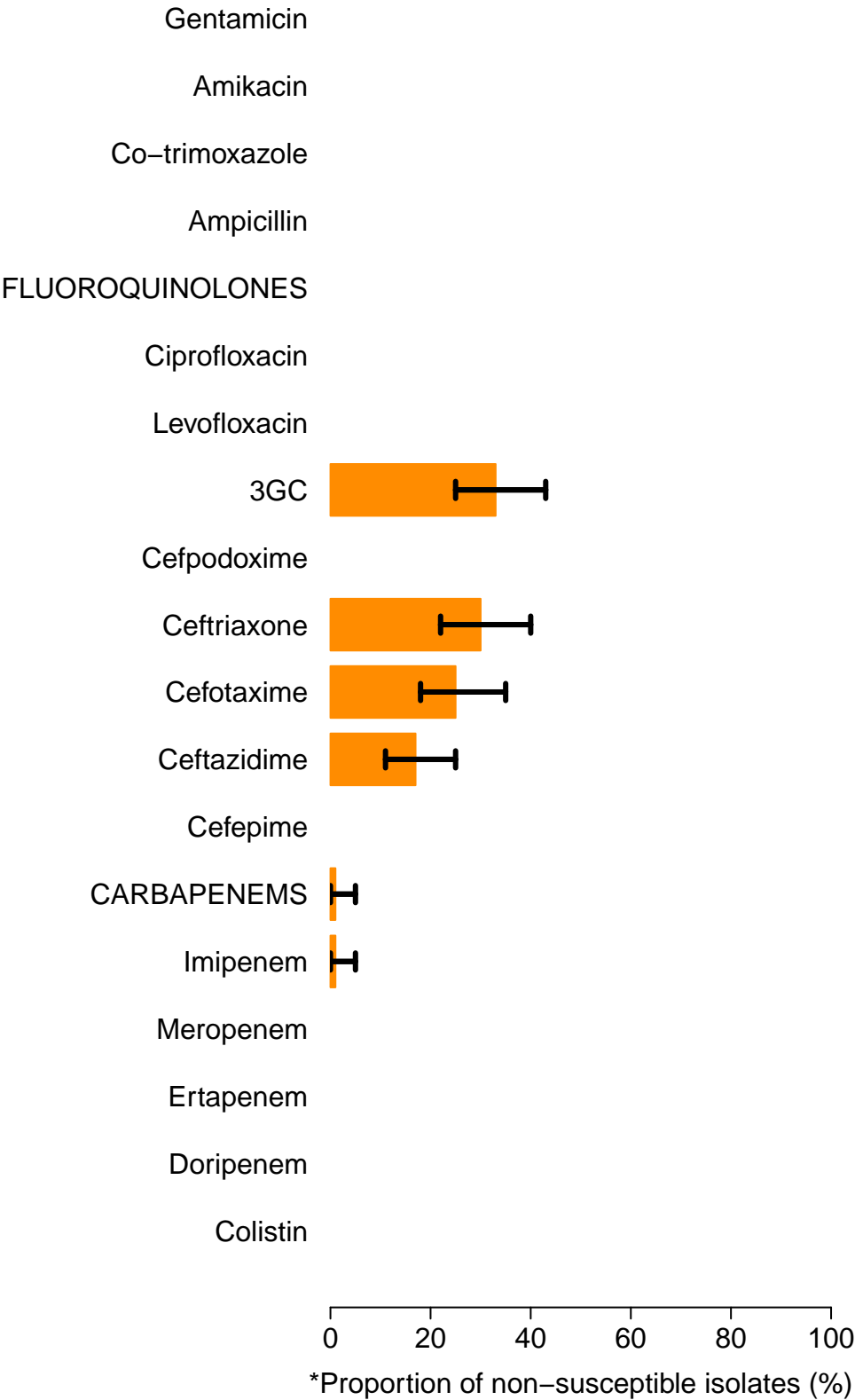
Antibiotic agent	% NS (n)	95% CI
FLUOROQUINOLONES	NA	–
Ciprofloxacin	NA	–
Levofloxacin	NA	–
3GC	0% (0/5)	0%–43%
Ceftriaxone	0% (0/5)	0%–43%
Cefotaxime	0% (0/5)	0%–43%
Ceftazidime	0% (0/4)	0%–49%
CARBAPENEMS	0% (0/5)	0%–43%
Imipenem	0% (0/5)	0%–43%
Meropenem	NA	–
Ertapenem	NA	–
Doripenem	NA	–

*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 [3]: Isolate-based surveillance report
with stratification by infection origin

Blood: *Escherichia coli*

Community-origin (*No. of patients = 102*)

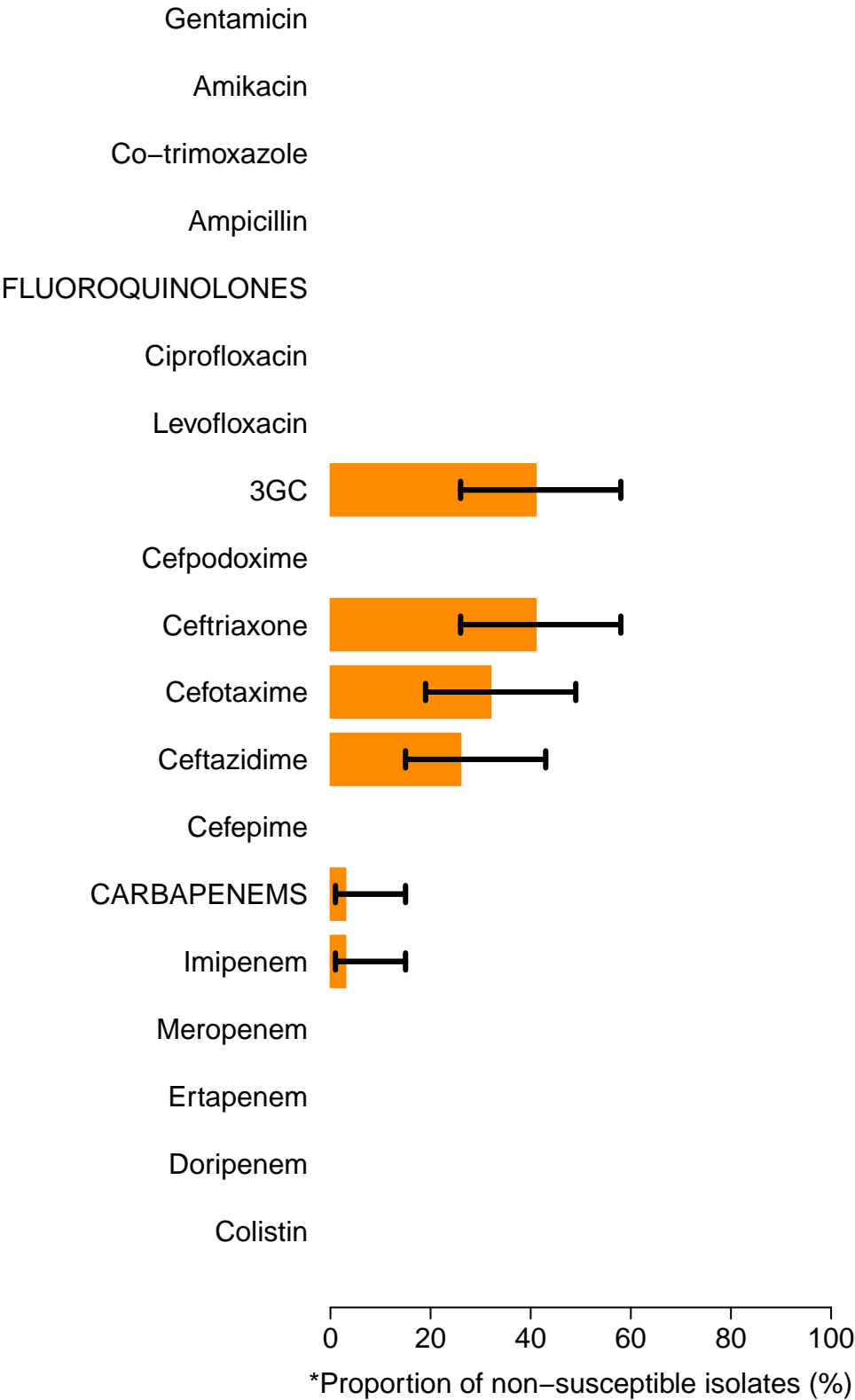


Antibiotic agent	% NS (n)	95% CI
Gentamicin	NA	–
Amikacin	NA	–
Co-trimoxazole	NA	–
Ampicillin	NA	–
FLUOROQUINOLONES	NA	–
Ciprofloxacin	NA	–
Levofloxacin	NA	–
3GC	33% (34/102)	25%–43%
Cefpodoxime	NA	–
Ceftriaxone	30% (31/102)	22%–40%
Cefotaxime	25% (26/102)	18%–35%
Ceftazidime	17% (17/102)	11%–25%
Cefepime	NA	–
CARBAPENEMS	1% (1/102)	0%–5%
Imipenem	1% (1/102)	0%–5%
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 [3]: Isolate-based surveillance report
with stratification by infection origin

Blood: *Escherichia coli* Hospital-origin (No. of patients = 34)



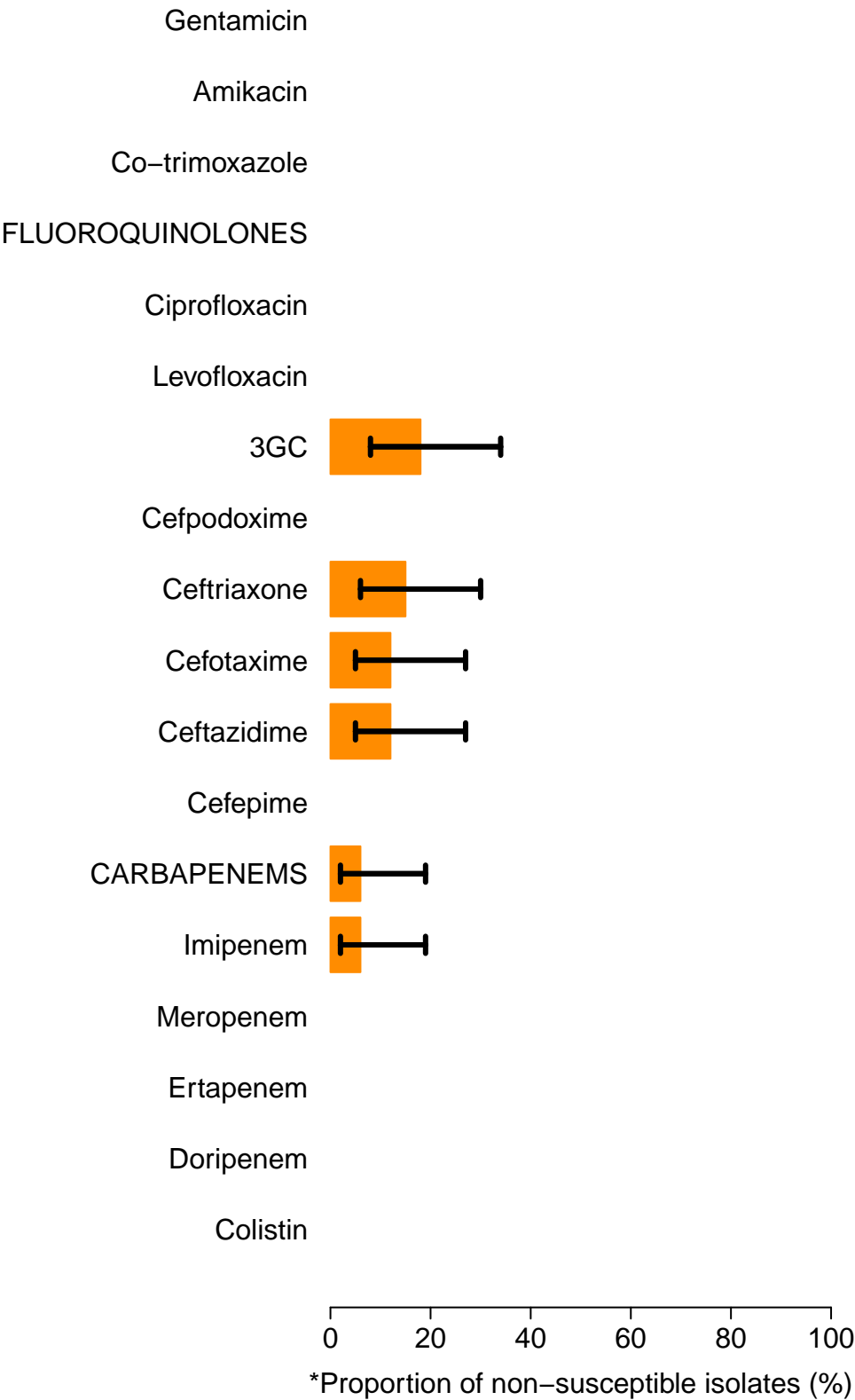
Antibiotic agent	% NS (n)	95% CI
Gentamicin	NA	–
Amikacin	NA	–
Co-trimoxazole	NA	–
Ampicillin	NA	–
FLUOROQUINOLONES	NA	–
Ciprofloxacin	NA	–
Levofloxacin	NA	–
3GC	41% (14/34)	26%–58%
Cefpodoxime	NA	–
Ceftriaxone	41% (14/34)	26%–58%
Cefotaxime	32% (11/34)	19%–49%
Ceftazidime	26% (9/34)	15%–43%
Cefepime	NA	–
CARBAPENEMS	3% (1/34)	1%–15%
Imipenem	3% (1/34)	1%–15%
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 [3]: Isolate-based surveillance report
with stratification by infection origin

Blood: *Klebsiella pneumoniae*

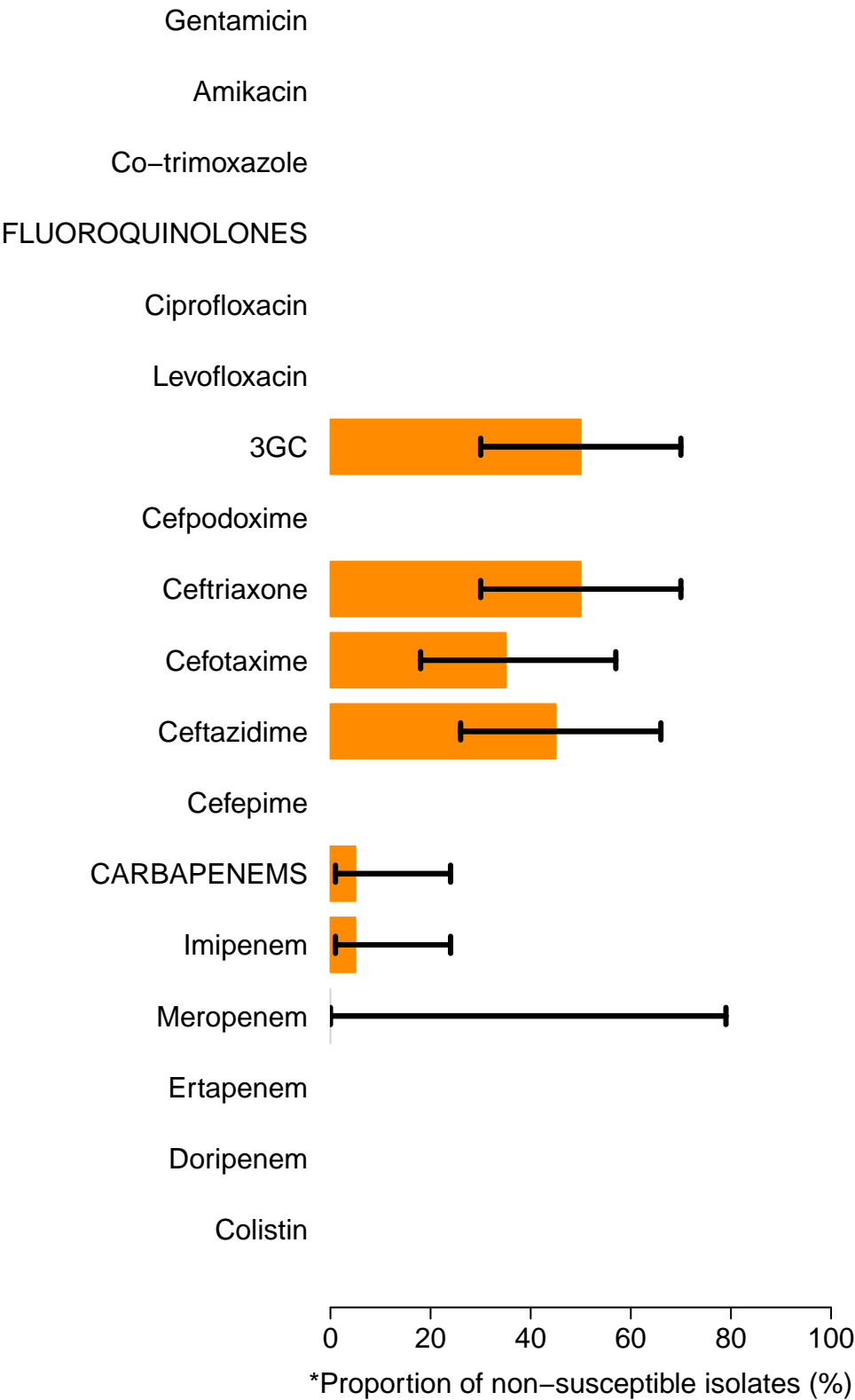
Community-origin (*No. of patients = 34*)



*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 [3]: Isolate-based surveillance report
with stratification by infection origin

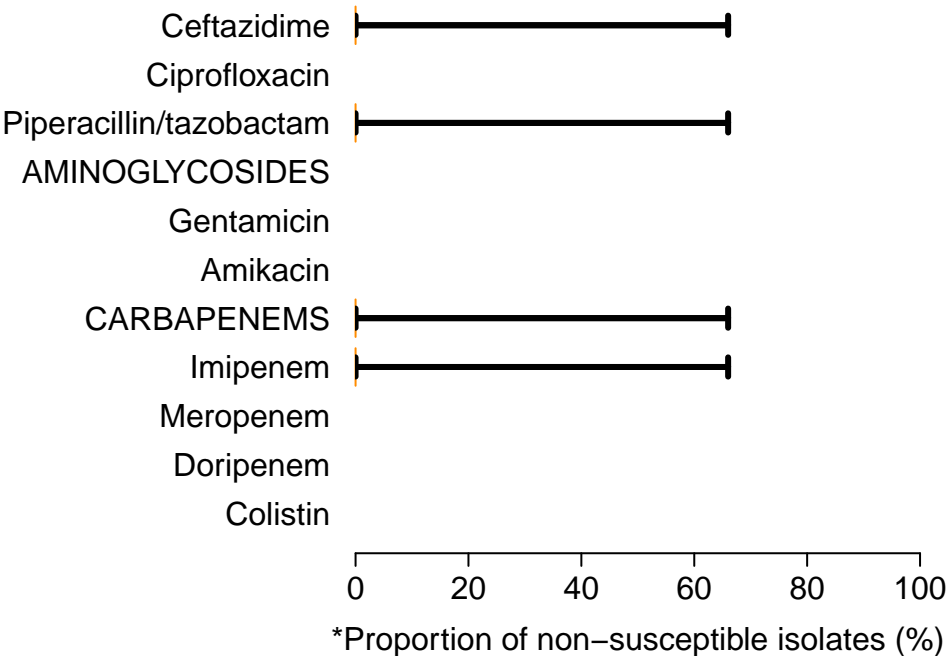
Blood: *Klebsiella pneumoniae* Hospital-origin (No. of patients = 20)



*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

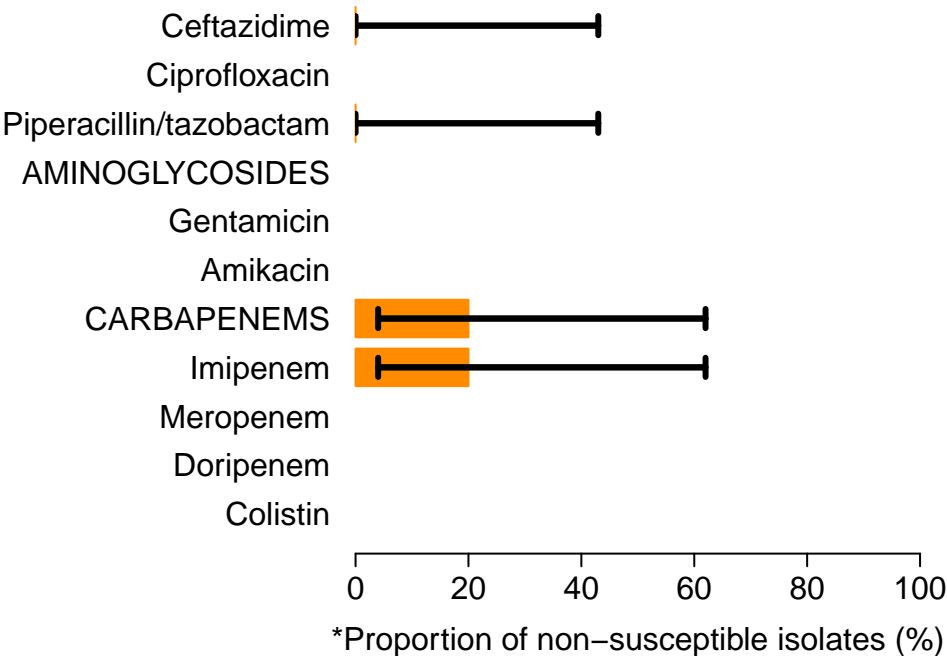
Section [3]: Isolate-based surveillance report
with stratification by infection origin

Blood: *Pseudomonas aeruginosa* Community-origin (No. of patients = 2)



Antibiotic agent	% NS (n)	95% CI
Ceftazidime	0% (0/2)	0%–66%
Ciprofloxacin	NA	–
Piperacillin/tazobactam	0% (0/2)	0%–66%
AMINOGLYCOSIDES	NA	–
Gentamicin	NA	–
Amikacin	NA	–
CARBAPENEMS	0% (0/2)	0%–66%
Imipenem	0% (0/2)	0%–66%
Meropenem	NA	–
Doripenem	NA	–
Colistin	NA	–

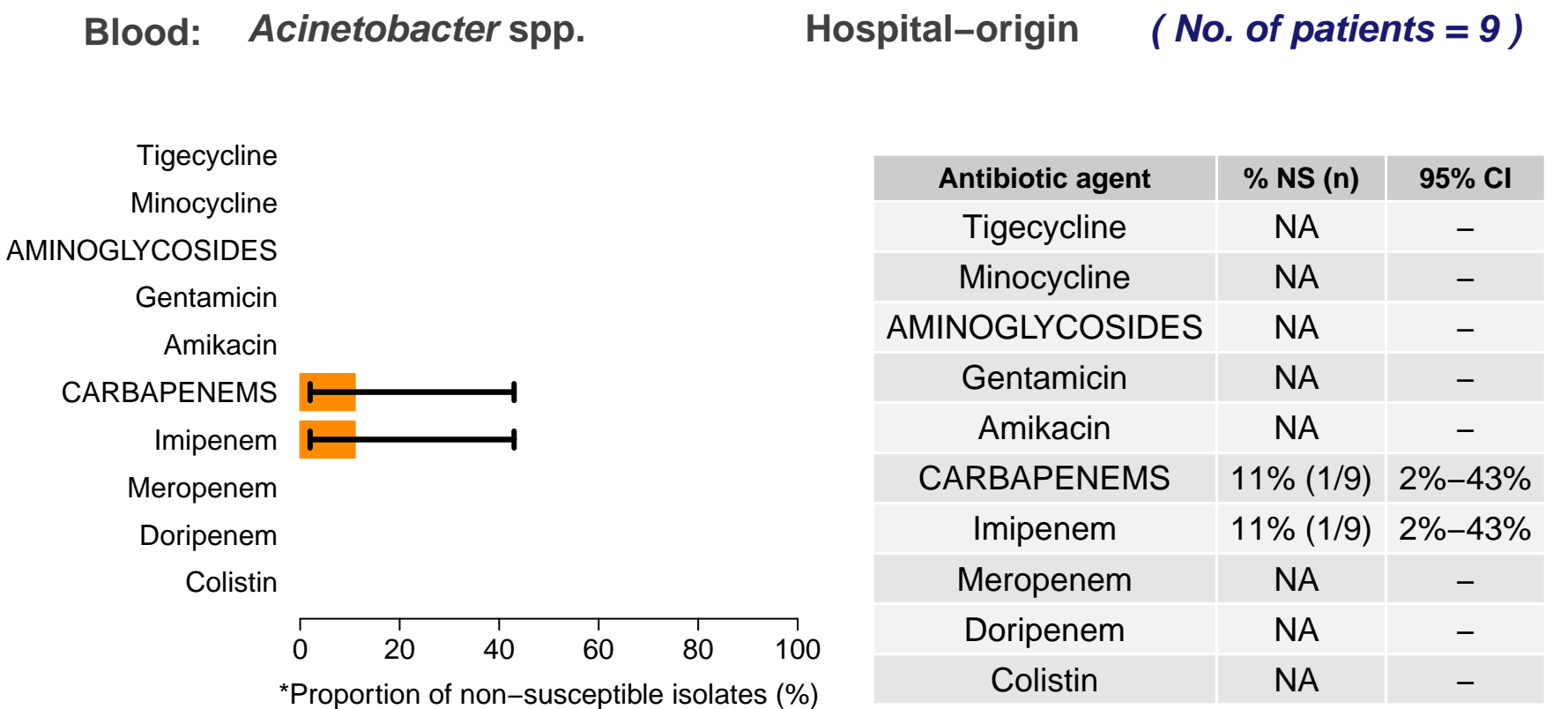
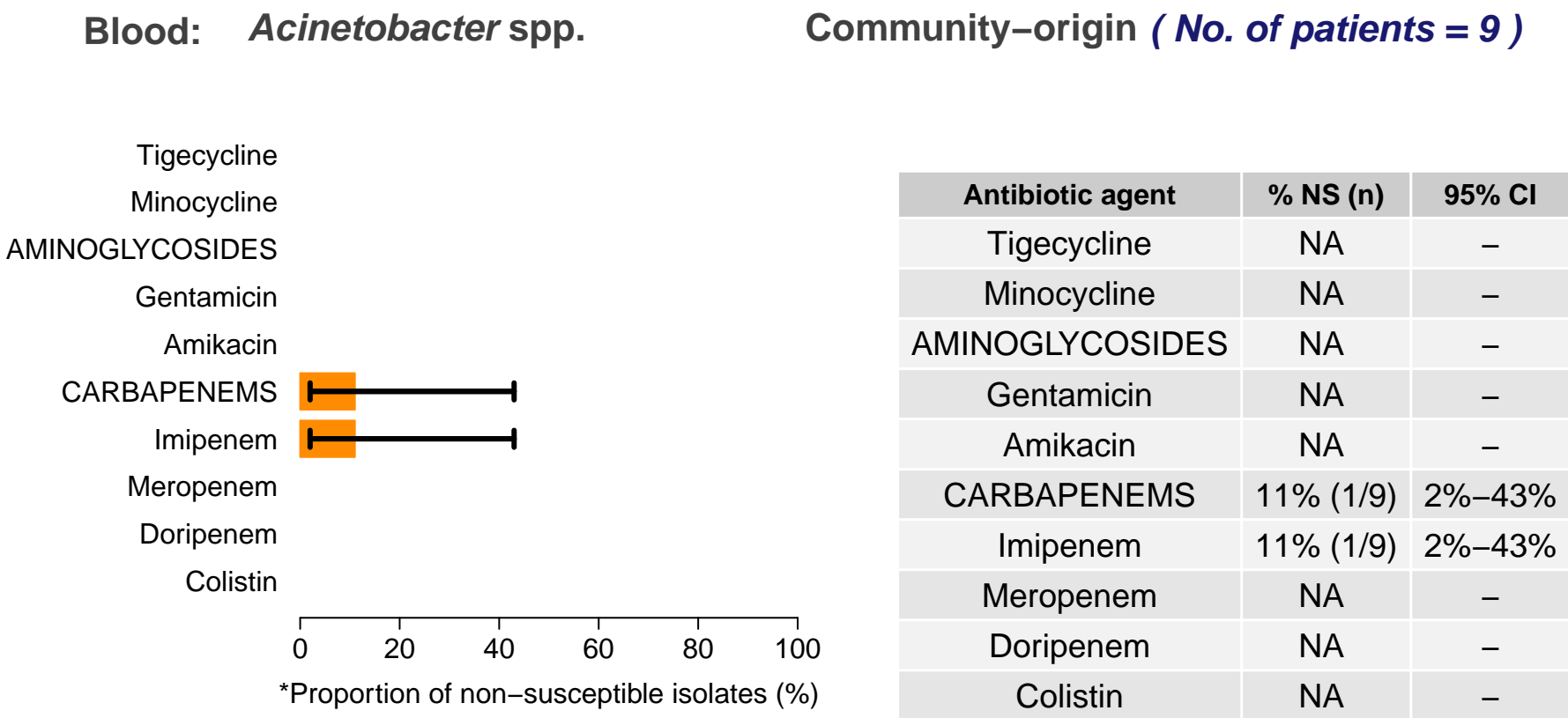
Blood: *Pseudomonas aeruginosa* Hospital-origin (No. of patients = 5)



Antibiotic agent	% NS (n)	95% CI
Ceftazidime	0% (0/5)	0%–43%
Ciprofloxacin	NA	–
Piperacillin/tazobactam	0% (0/5)	0%–43%
AMINOGLYCOSIDES	NA	–
Gentamicin	NA	–
Amikacin	NA	–
CARBAPENEMS	20% (1/5)	4%–62%
Imipenem	20% (1/5)	4%–62%
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

Section [3]: Isolate-based surveillance report
with stratification by infection origin



*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

Section [4]: Sample-based surveillance report

Introduction

A sample-based surveillance report is generated if data of culture negative is available.

The sample-based approach involves the collection of data on all blood samples taken for microbiological testing and includes information on the number of positive blood samples for a specific specimen type (both pathogens under the survey and other bacteria) as well as number of negative (no microbial growth) samples. After removal of duplicate results and assuming that routine blood culture testing is applied systematically, we can use the number of tested patients as a proxy for a number of patients with new cases of bloodstream infection (BSI).

Results:

The microbiology_data file had:

Specimen collection dates ranged from **01 Jan 2021 to 31 Dec 2021**

Number of records on blood specimen collected within the above date range:

1095 blood specimen records

**Number of patients sampled for blood culture within the above date range:*

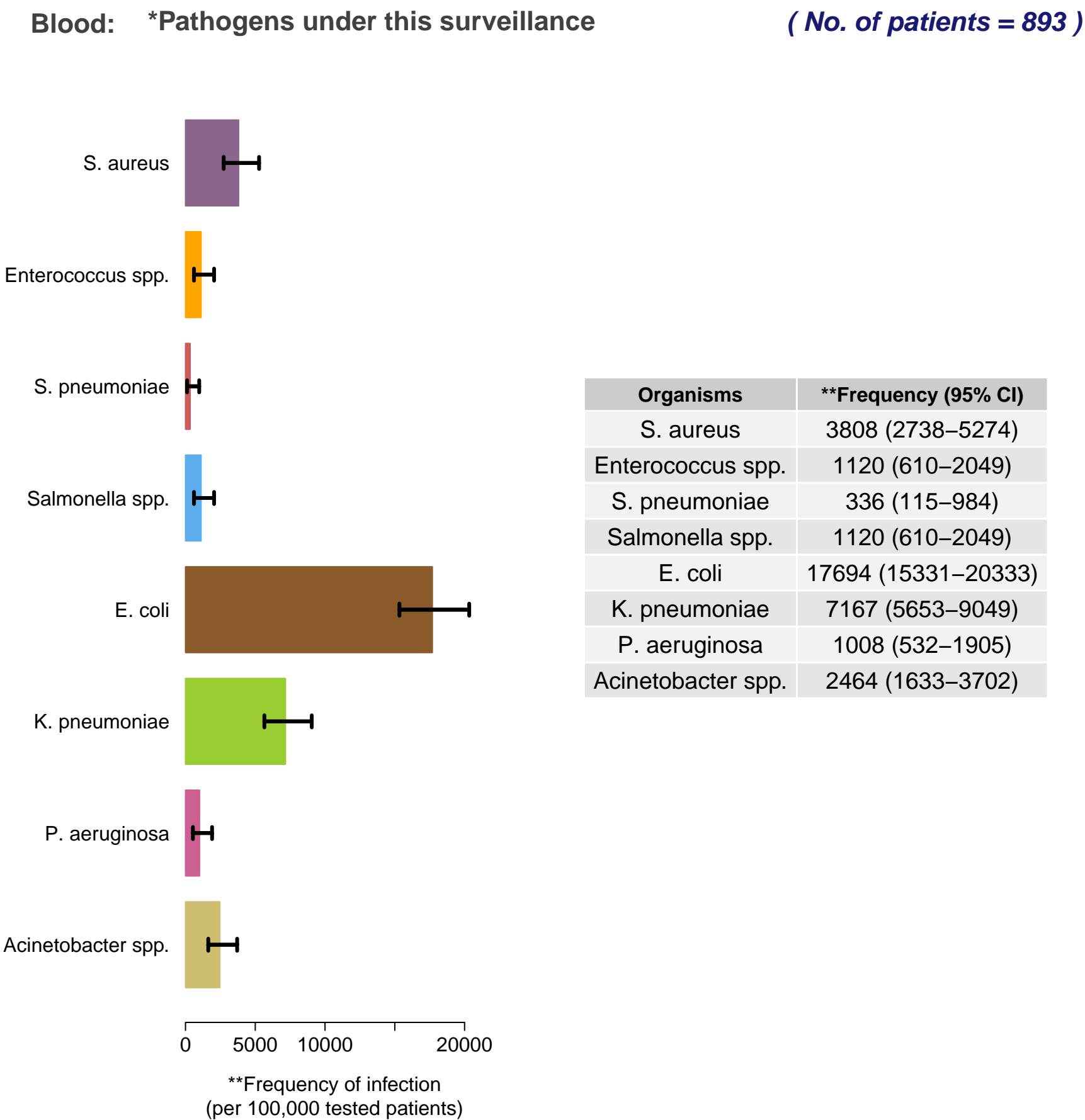
893 patients sampled for blood culture

Note:

*Number of patients sampled for blood culture is used as denominator to estimate the frequency of infections per 100,000 tested patients

The following figures show the frequency of infections for patients with blood culture tested.

Section [4]: Sample-based surveillance report



*We apologise that the bacteria name in the table and in the figure are not written in italic. This is because of the R command we used. We will improve this in the next version.

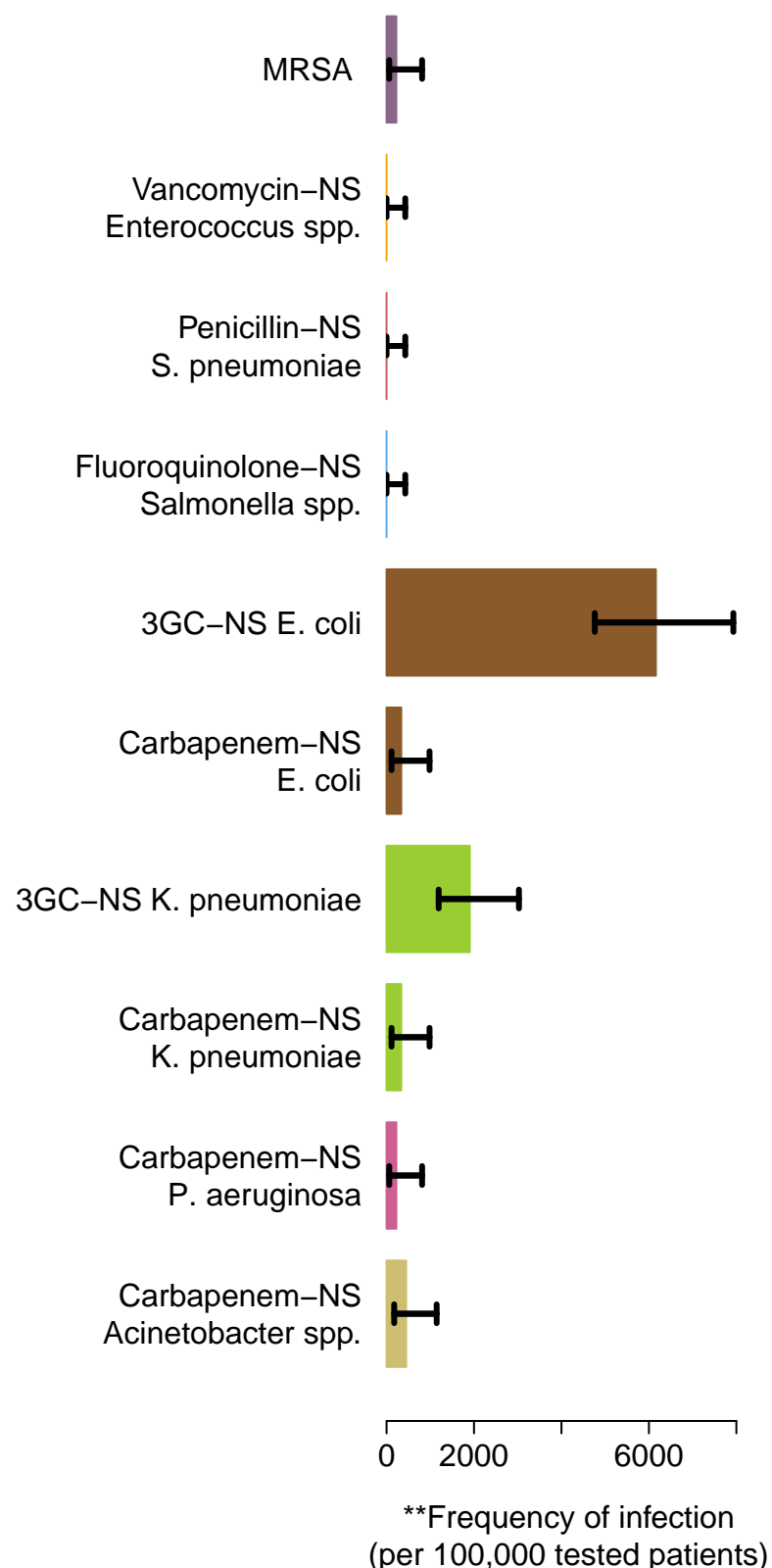
**Frequency of infection per 100,000 tested patients represents the number of patients with blood culture positive for a pathogen (numerator) over the total number of tested patients (denominator). The AMASS application de-duplicates the data by included only the first isolate of each patient per specimen type per reporting period.

CI = confidence interval; NS = non-susceptible; NA = Not available/reported/tested; 3GC = 3rd-generation cephalosporin

Section [4]: Sample-based surveillance report

Blood: *AMR pathogens under this surveillance

(No. of patients = 893)



Organism	**Frequency (95% CI)
MRSA	224 (62–813)
Vancomycin–NS Enterococcus spp.	0 (0–429)
Penicillin–NS S. pneumoniae	0 (0–429)
Fluoroquinolone–NS Salmonella spp.	0 (0–429)
3GC–NS E. coli	6160 (4763–7932)
Carbapenem–NS E. coli	336 (115–984)
3GC–NS K. pneumoniae	1904 (1192–3028)
Carbapenem–NS K. pneumoniae	336 (115–984)
Carbapenem–NS P. aeruginosa	224 (62–813)
Carbapenem–NS Acinetobacter spp.	448 (175–1147)

*We apologise that the bacteria name in the table and in the figure are not written in italic. This is because of the R command we used. We will improve this in the next version.

**Frequency of infection per 100,000 tested patients represents the number of patients with blood culture positive for a pathogen (numerator) over the total number of tested patients (denominator). The AMASS application de-duplicates the data by included only the first isolate of each patient per specimen type per reporting period.

CI = confidence interval; NS = non-susceptible; NA = Not available/reported/tested; 3GC = 3rd-generation cephalosporin

Section [5]: Sample-based surveillance report with stratification by infection origin

Introduction

A sample-based surveillance report with stratification by origin of infection is generated only if data of culture negative is available and admission date or a variable containing the classification is available in the raw data file with the appropriate specification in the data dictionaries.

Results:

The data included in the analysis had:

Specimen collection dates ranged from **01 Jan 2021 to 31 Dec 2021**

Number of records on blood specimen collected within the above date range:

1095 blood specimen records

Number of patients sampled for blood culture within the above date range:

893 patients sampled for blood culture

401 patients had at least one admission having the first blood culture drawn within first 2 calendar days of hospital admission.

This parameter is used as a denominators for frequency of community-origin bacteraemia (per 100,000 patients tested for blood culture on admission).

332 patients had at least one admission having the first blood culture drawn after 2 calendar days of hospital admission.

This parameter is used as a denominators for frequency of hospital-origin bacteraemia (per 100,000 patients tested for blood culture for HAI).

175 patients had a blood drawn for culture and with unknown origin of infection. Validation of this statistics is highly recommended.

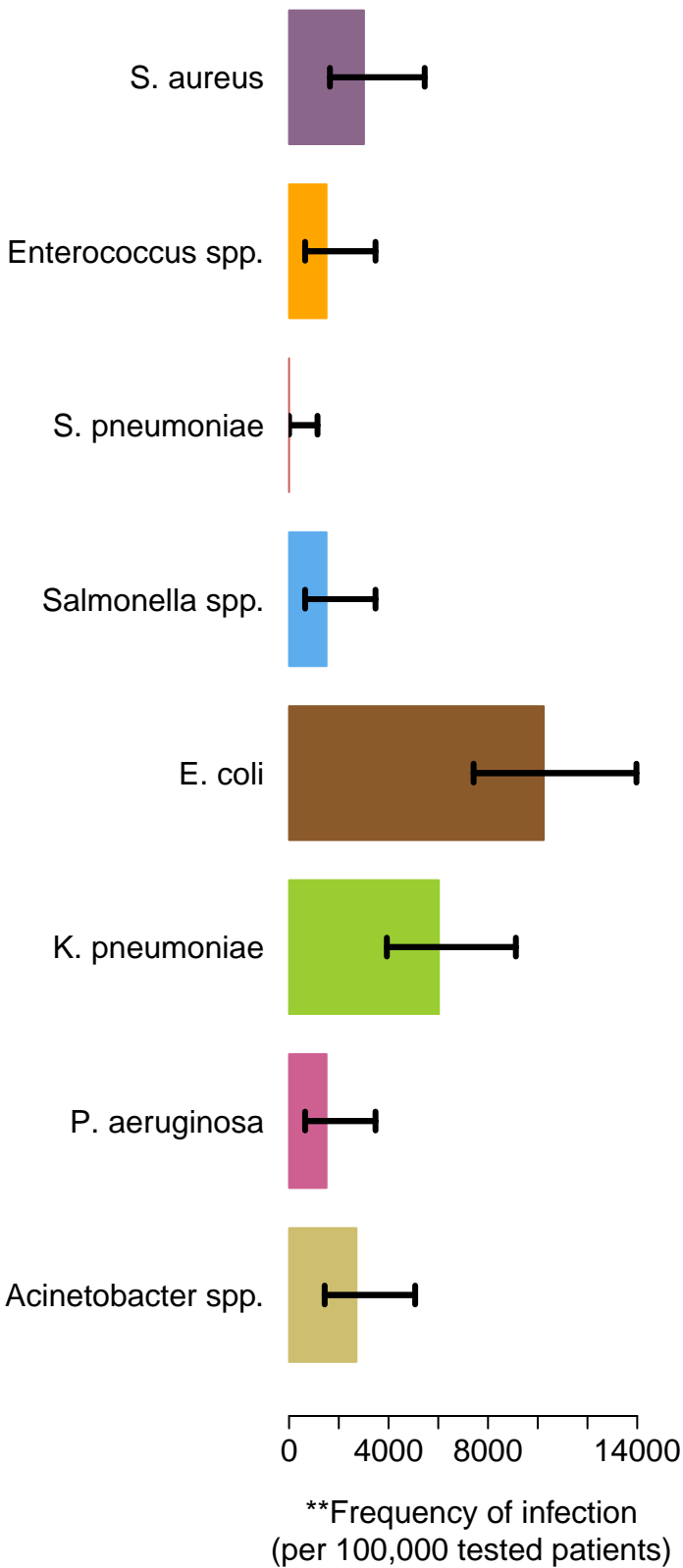
Note:

15 patients had more than one admissions, of which at least one admission had the first blood culture drawn within the first 2 calendar days of hospital admission AND at least one admission had the first blood culture drawn after 2 calendar days of hospital admission.

The following figures show the frequency of infections for patients with blood culture tested and stratified by infection origin, under this surveillance.

Section [5]: Sample-based surveillance report with stratification by infection origin

Blood: *Pathogens Hospital-origin (No. of patients = 332)



Organism	**Frequency (95% CI)
S. aureus	3013 (1645–5455)
Enterococcus spp.	1507 (645–3477)
S. pneumoniae	0 (0–1144)
Salmonella spp.	1507 (645–3477)
E. coli	10241 (7422–13971)
K. pneumoniae	6025 (3934–9122)
P. aeruginosa	1507 (645–3477)
Acinetobacter spp.	2711 (1433–5071)

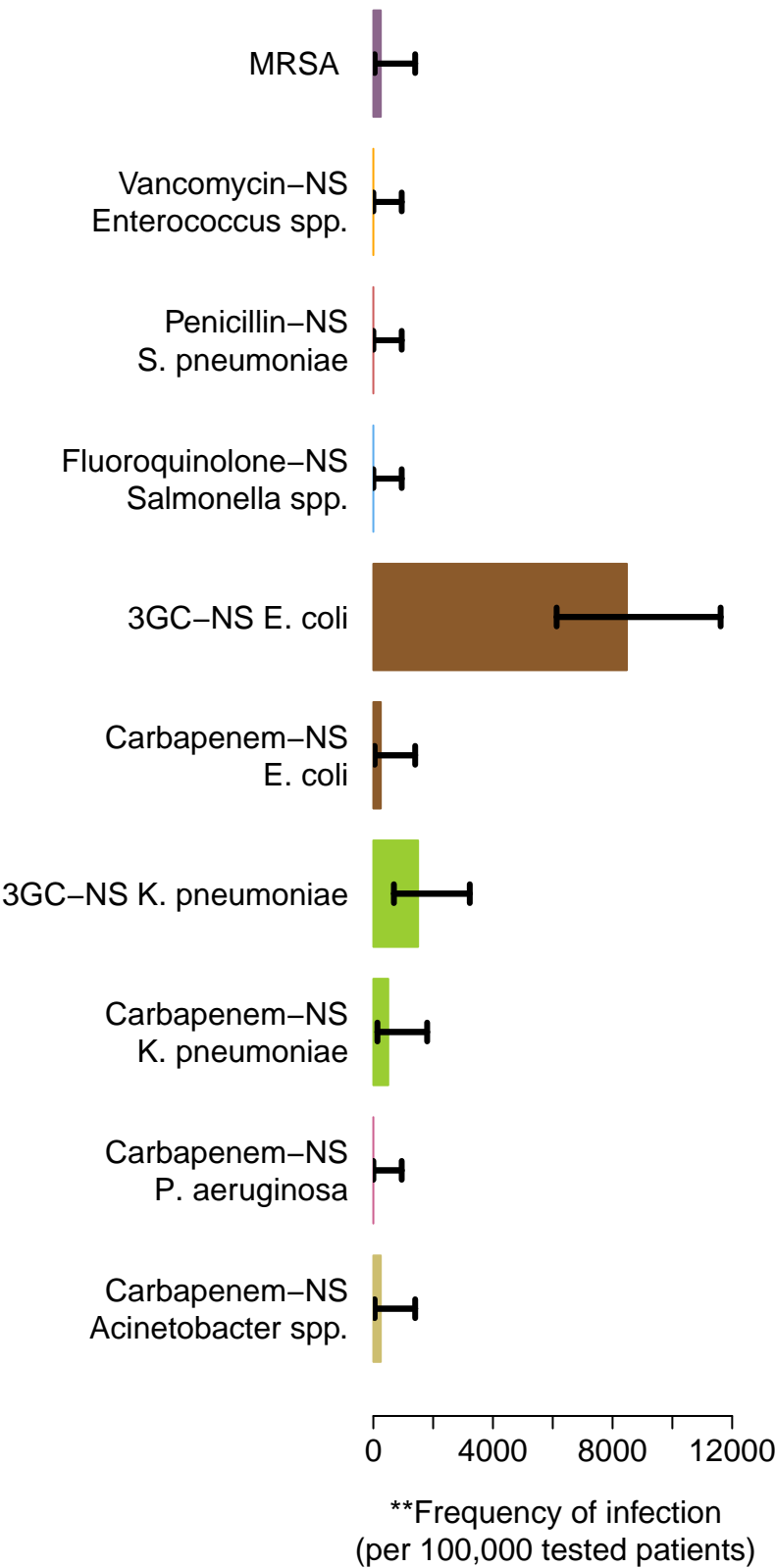
*We apologise that the bacteria name in the table and in the figure are not written in italic. This is because of the R command we used. We will improve this in the next version.

**Frequency of infection per 100,000 tested population at risk of HAI represents the number of patients with blood culture positive for a pathogen (numerator) over the total number of tested population at risk of HAI (denominator). The AMASS application de-duplicates the data by included only the first isolate of each patient per specimen type per reporting period.

CI = confidence interval; NS = non-susceptible; NA = Not available/reported/tested; 3GC = 3rd-generation cephalosporin

Section [5]: Sample-based surveillance report with stratification by infection origin

Blood: *AMR pathogens Community-origin (No. of patients = 401)



Organism	**Frequency (95% CI)
MRSA	250 (45–1399)
Vancomycin-NS Enterococcus spp.	0 (0–949)
Penicillin-NS S. pneumoniae	0 (0–949)
Fluoroquinolone-NS Salmonella spp.	0 (0–949)
3GC-NS E. coli	8479 (6131–11615)
Carbapenem-NS E. coli	250 (45–1399)
3GC-NS K. pneumoniae	1497 (688–3226)
Carbapenem-NS K. pneumoniae	499 (137–1801)
Carbapenem-NS P. aeruginosa	0 (0–949)
Carbapenem-NS Acinetobacter spp.	250 (45–1399)

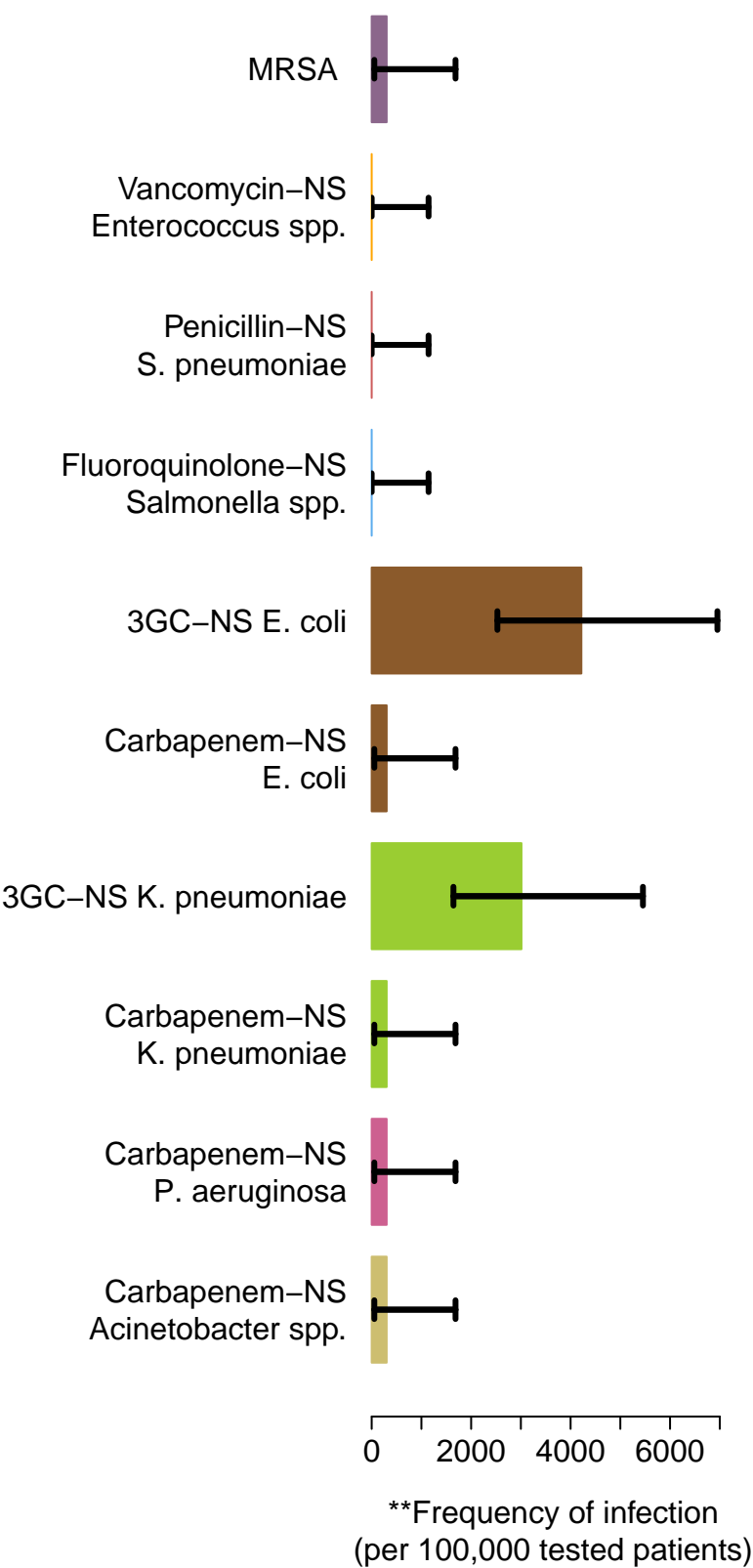
*We apologise that the bacteria name in the table and in the figure are not written in italic. This is because of the R command we used. We will improve this in the next version.

**Frequency of infection per 100,000 tested patients represents the number of patients with blood culture positive for a pathogen (numerator) over the total number of tested patients (denominator). The AMASS application de-duplicates the data by included only the first isolate of each patient per specimen type per reporting period.

CI = confidence interval; NS = non-susceptible; NA = Not available/reported/tested; 3GC = 3rd-generation cephalosporin

Section [5]: Sample-based surveillance report
with stratification by infection origin

Blood: *AMR pathogens Hospital-origin (No. of patients = 332)



Organism	**Frequency (95% CI)
MRSA	302 (54–1687)
Vancomycin–NS Enterococcus spp.	0 (0–1144)
Penicillin–NS S. pneumoniae	0 (0–1144)
Fluoroquinolone–NS Salmonella spp.	0 (0–1144)
3GC–NS E. coli	4217 (2529–6953)
Carbapenem–NS E. coli	302 (54–1687)
3GC–NS K. pneumoniae	3013 (1645–5455)
Carbapenem–NS K. pneumoniae	302 (54–1687)
Carbapenem–NS P. aeruginosa	302 (54–1687)
Carbapenem–NS Acinetobacter spp.	302 (54–1687)

*We apologise that the bacteria name in the table and in the figure are not written in italic. This is because of the R command we used. We will improve this in the next version.

**Frequency of infection per 100,000 tested patients represents the number of patients with blood culture positive for a pathogen (numerator) over the total number of tested patients (denominator). The AMASS application de-duplicates the data by included only the first isolate of each patient per specimen type per reporting period.

CI = confidence interval; NS = non-susceptible; NA = Not available/reported/tested; 3GC = 3rd-generation cephalosporin

Section [6] Mortality involving AMR and antimicrobial–susceptible infections

Introduction

A surveillance report on mortality involving AMR infections and antimicrobial–susceptible infections with stratification by origin of infection is generated only if data on patient outcomes (i.e. discharge status) are available. Antimicrobial–resistant infection is a threat to modern health care, and the impact of the infection on patient outcomes is largely unknown. Performing analyses and generating reports on mortality often takes time and resources.

The term 'mortality involving AMR and antimicrobial–susceptible infections' was used because the mortality reported was all–cause mortality. This measure of mortality included deaths caused by or related to other underlying and intermediate causes.

Here, AMASS summarized the overall mortality of patients with antimicrobial–resistant and antimicrobial–susceptible bacteria bloodstream infections (BSI).

Results:

The data included in the analysis had:

Sample collection dates ranged from **01 Jan 2021** to **31 Dec 2021**

Number of patients with blood culture positive for the organism under the survey:

310 patients

Number of patients with community–origin BSI:

173 patients

Number of patients with hospital–origin BSI:

88 patients

The hospital admission data file had:

Hospital admission dates ranging from **01 Jan 2021** to **31 Dec 2021**

Number of records in the raw hospital admission data:

19736 records

Number of patients included in the analysis (de–duplicated):

16298 patients

Number of patients had death as outcome in any admission data records:

148 patients

Overall mortality:

1% (148/16298)

The AMASS application merged the microbiology data file and hospital admission data file. The merged dataset was then de-duplicated so that only the first isolate per patient per specimen per reporting period was included in the analysis. The de-duplicated data was stratified by infection origin (community-origin infection or hospital-origin infection).

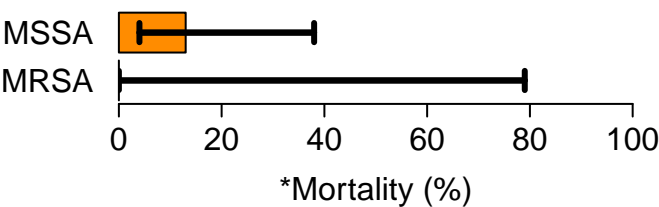
Organism	Mortality in patients with Community-origin BSI	Mortality in patients with Hospital-origin BSI
<i>Staphylococcus aureus</i>	12% (2/17)	0% (0/10)
<i>Enterococcus</i> spp.	0% (0/1)	0% (0/5)
<i>Streptococcus pneumoniae</i>	67% (2/3)	NaN% (0/0)
<i>Salmonella</i> spp.	20% (1/5)	0% (0/5)
<i>Escherichia coli</i>	2% (2/102)	15% (5/34)
<i>Klebsiella pneumoniae</i>	12% (4/34)	10% (2/20)
<i>Pseudomonas aeruginosa</i>	0% (0/2)	0% (0/5)
<i>Acinetobacter</i> spp.	22% (2/9)	0% (0/9)
Total:	8% (13/173)	8% (7/88)

The following figures and tables show the mortality of patients who were blood culture positive for antimicrobial non-susceptible and susceptible isolates.

Section [6] Mortality involving AMR and antimicrobial-susceptible infections

Staphylococcus aureus

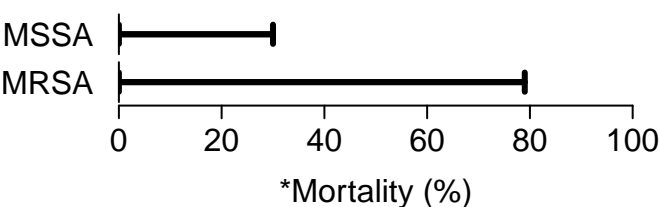
Community-origin (No. of patients = 17)



Type of pathogen	Mortality (n)	95% CI
MRSA	0% (0/1)	0%–79%
MSSA	13% (2/15)	4%–38%

Staphylococcus aureus

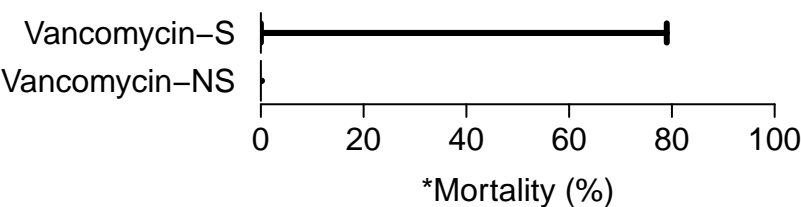
Hospital-origin (No. of patients = 10)



Type of pathogen	Mortality (n)	95% CI
MRSA	0% (0/1)	0%–79%
MSSA	0% (0/9)	0%–30%

Enterococcus spp.

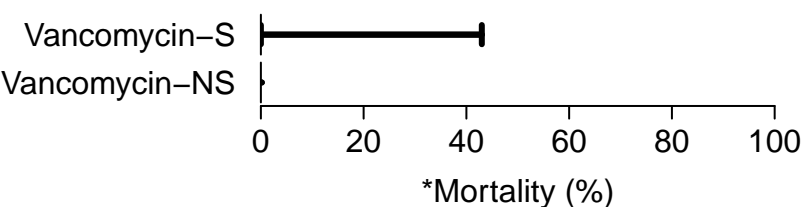
Community-origin (No. of patients = 1)



Type of pathogen	Mortality (n)	95% CI
Vancomycin-NS	NA	–
Vancomycin-S	0% (0/1)	0%–79%

Enterococcus spp.

Hospital-origin (No. of patients = 5)



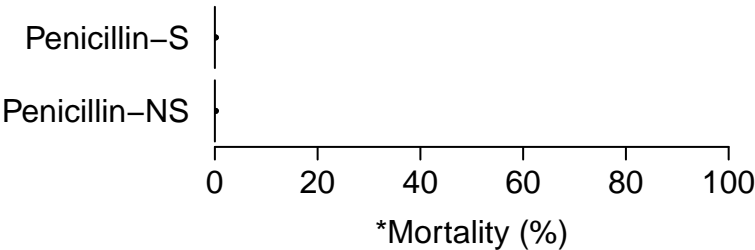
Type of pathogen	Mortality (n)	95% CI
Vancomycin-NS	NA	–
Vancomycin-S	0% (0/5)	0%–43%

*Mortality is the proportion (%) of in-hospital deaths (all-cause deaths). This represents the number of in-hospital deaths (numerator) over the total number of patients with blood culture positive for the organism and the type of pathogen (denominator). The AMASS application de-duplicates the data by included only the first isolate per patient per specimen type per evaluation period. NS = non-susceptible; S = susceptible; CI = confidence interval; Fluoroquinolone-NS = NS to any fluoroquinolone tested; 3GC-NS = NS to any 3rd-generation cephalosporin and susceptible to carbapenem

Section [6] Mortality involving AMR and antimicrobial-susceptible infections

Streptococcus pneumoniae

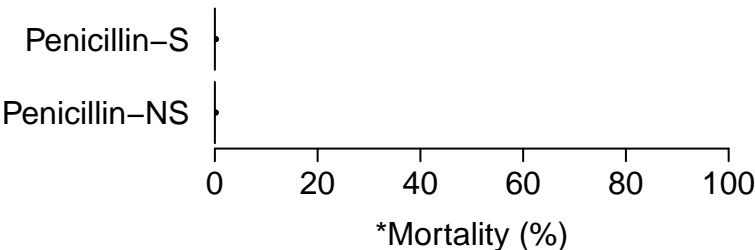
Community-origin (No. of patients = 3)



Mortality	Mortality (n)	95% CI
Penicillin-NS	NA	–
Penicillin-S	NA	–

Streptococcus pneumoniae

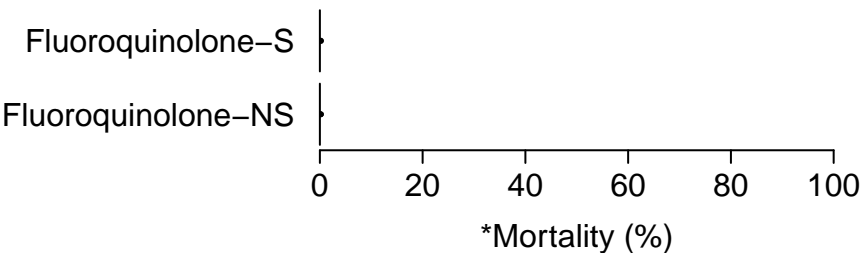
Hospital-origin (No. of patients = 0)



Type of pathogen	Mortality (n)	95% CI
Penicillin-NS	NA	–
Penicillin-S	NA	–

Salmonella spp.

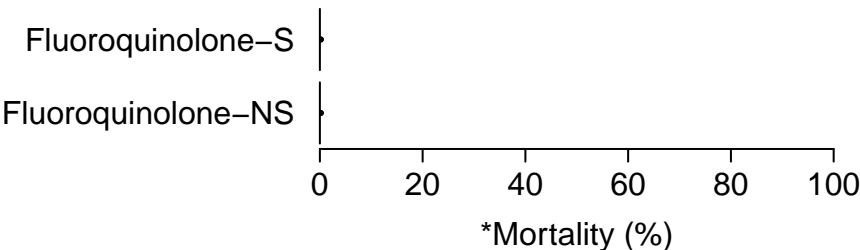
Community-origin (No. of patients = 5)



Type of pathogen	Mortality (n)	95% CI
Fluoroquinolone-NS	NA	–
Fluoroquinolone-S	NA	–

Salmonella spp.

Hospital-origin (No. of patients = 5)

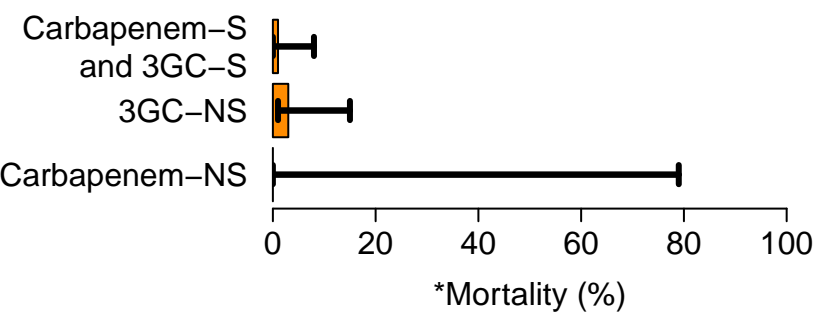


Type of pathogen	Mortality (n)	95% CI
Fluoroquinolone-NS	NA	–
Fluoroquinolone-S	NA	–

*Mortality is the proportion (%) of in-hospital deaths (all-cause deaths). This represents the number of in-hospital deaths (numerator) over the total number of patients with blood culture positive for the organism and the type of pathogen (denominator). The AMASS application de-duplicates the data by included only the first isolate per patient per specimen type per evaluation period. NS = non-susceptible; S = susceptible; CI = confidence interval; Fluoroquinolone-NS = NS to any fluoroquinolone tested; 3GC-NS = NS to any 3rd-generation cephalosporin and susceptible to carbapenem

Section [6] Mortality involving AMR and antimicrobial-susceptible infections

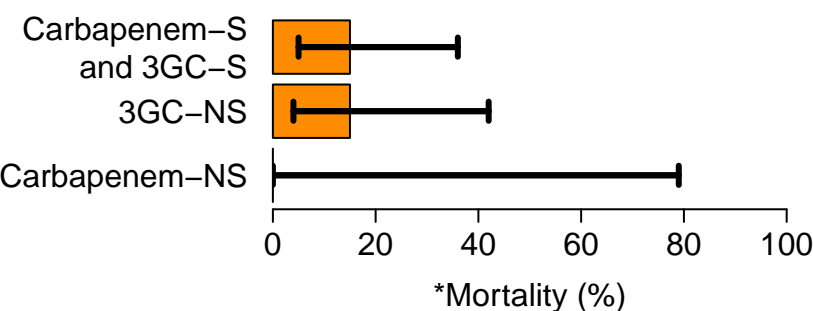
Escherichia coli



Community-origin (No. of patients = 102)

Type of pathogen	Mortality (n)	95% CI
Carbapenem-NS	0% (0/1)	0%–79%
3GC-NS	3% (1/33)	1%–15%
Carbapenem-S and 3GC-S	1% (1/68)	0%–8%

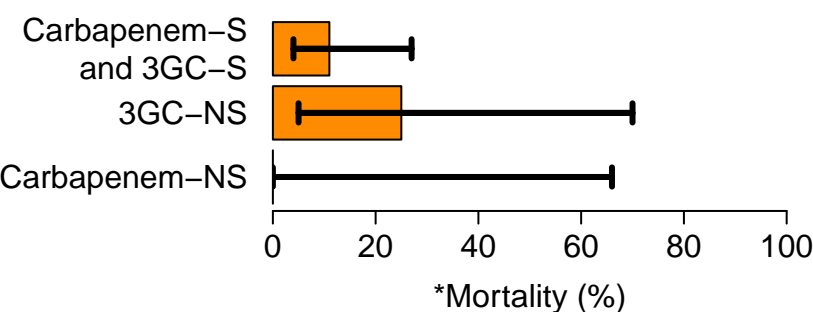
Escherichia coli



Hospital-origin (No. of patients = 34)

Type of pathogen	Mortality (n)	95% CI
Carbapenem-NS	0% (0/1)	0%–79%
3GC-NS	15% (2/13)	4%–42%
Carbapenem-S and 3GC-S	15% (3/20)	5%–36%

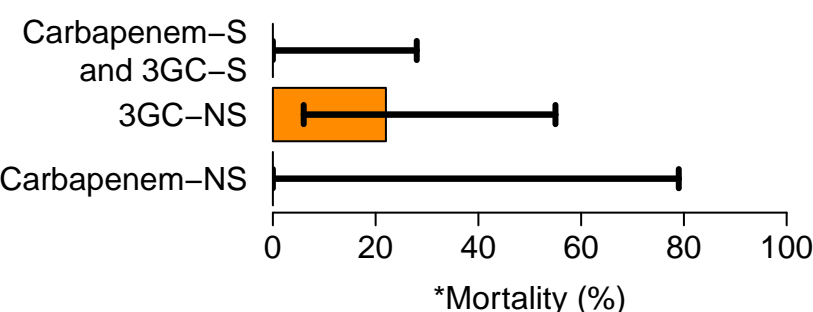
Klebsiella pneumoniae



Community-origin (No. of patients = 34)

Type of pathogen	Mortality (n)	95% CI
Carbapenem-NS	0% (0/2)	0%–66%
3GC-NS	25% (1/4)	5%–70%
Carbapenem-S and 3GC-S	11% (3/28)	4%–27%

Klebsiella pneumoniae



Hospital-origin (No. of patients = 20)

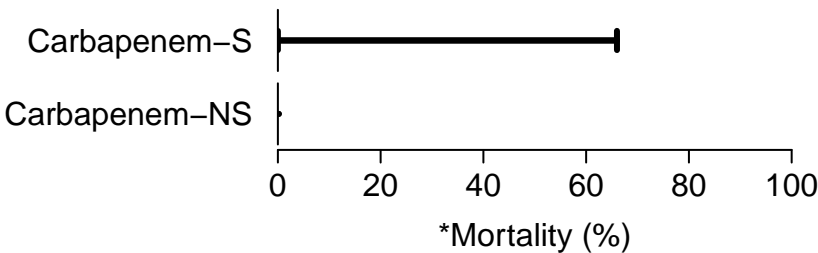
Type of pathogen	Mortality (n)	95% CI
Carbapenem-NS	0% (0/1)	0%–79%
3GC-NS	22% (2/9)	6%–55%
Carbapenem-S and 3GC-S	0% (0/10)	0%–28%

*Mortality is the proportion (%) of in-hospital deaths (all-cause deaths). This represents the number of in-hospital deaths (numerator) over the total number of patients with blood culture positive for the organism and the type of pathogen (denominator). The AMASS application de-duplicates the data by including only the first isolate per patient per specimen type per evaluation period. NS = non-susceptible; S = susceptible; CI = confidence interval; Carbapenem-NS = NS to any carbapenems tested; 3GC-NS = NS to any 3rd-generation cephalosporin and susceptible to carbapenem

Section [6] Mortality involving AMR and antimicrobial-susceptible infections

Pseudomonas aeruginosa

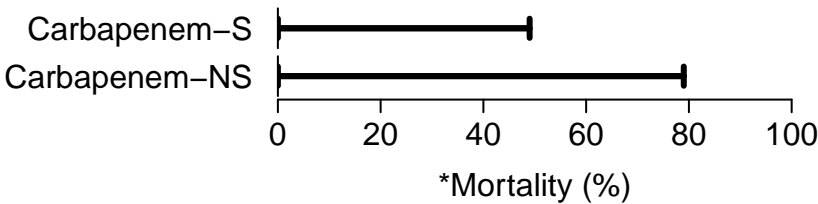
Community-origin (No. of patients = 2)



Type of pathogen	Mortality (n)	95% CI
Carbapenem-NS	NA	–
Carbapenem-S	0% (0/2)	0%–66%

Pseudomonas aeruginosa

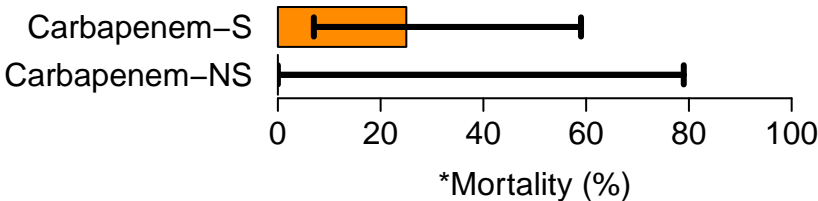
Hospital-origin (No. of patients = 5)



Type of pathogen	Mortality (n)	95% CI
Carbapenem-NS	0% (0/1)	0%–79%
Carbapenem-S	0% (0/4)	0%–49%

Acinetobacter spp.

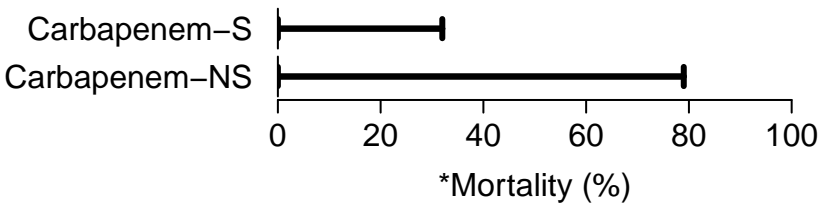
Community-origin (No. of patients = 9)



Type of pathogen	Mortality (n)	95% CI
Carbapenem-NS	0% (0/1)	0%–79%
Carbapenem-S	25% (2/8)	7%–59%

Acinetobacter spp.

Hospital-origin (No. of patients = 9)



Type of pathogen	Mortality (n)	95% CI
Carbapenem-NS	0% (0/1)	0%–79%
Carbapenem-S	0% (0/8)	0%–32%

*Mortality is the proportion (%) of in-hospital deaths (all-cause deaths). This represents the number of in-hospital deaths (numerator) over the total number of patients with blood culture positive for the organism and the type of pathogen (denominator). The AMASS application de-duplicates the data by including only the first isolate per patient per specimen type per evaluation period. NS = non-susceptible; S = susceptible; CI = confidence interval; Carbapenem-NS = NS to any carbapenems tested; 3GC-NS = NS to any 3rd-generation cephalosporin and susceptible to carbapenem

Section [7]: Report on notifiable bacterial diseases

Introduction

This is a report generated from AMASSplus using microbiology_data as the default for reporting the selected notifiable bacterial diseases, even if the hospital_admission_data file is unavailable. This is to provide the report for hospitals with only microbiology_data available.

The report generated by AMASSplus contains various type of specimens including blood, cerebrospinal fluid(CSF), respiratory tract specimens, urine, genital swab, stool and others or unknown sample types. The microorganisms in this report were initially selected from common notifiable bacterial diseases in Thailand.

Notifiable bacteria under the survey

- | | |
|--|--|
| – <i>Burkholderia pseudomallei</i> | – <i>Salmonella enterica</i> serotype <i>typhi</i> |
| – <i>Brucella</i> spp. | – Non-typhoidal <i>Salmonella</i> spp. |
| – <i>Corynebacterium diphtheriae</i> | – <i>Shigella</i> spp. |
| – <i>Neisseria gonorrhoeae</i> | – <i>Streptococcus suis</i> |
| – <i>Neisseria meningitidis</i> | – <i>Vibrio</i> spp. |
| – <i>Salmonella enterica</i> serotype <i>paratyphi</i> | |

Results

The data included in the analysis had:

Sample collection dates ranged from **01 Jan 2021 to 31 Dec 2021**

Number of records of clinical specimens with culture positive for a notifiable organism under this survey:

49 specimen records (**41, 0, 0, 1, 2, 4, and 1** were blood, CSF, genital swab, respiratory tract specimens, stool, urine, and other or unknown sample types, respectively)

Number of patients with a clinical specimen culture positive for a notifiable organism under this survey from the microbiology data (de-duplicated) :

40 patients

Section [7]: Report on notifiable bacterial diseases

In cases when hospital admission data is available, the AMASSplus application would merge the microbiology_data and hospital_admission_data. The number of patients with a clinical specimen culture positive for the notifiable organism under the survey are as follows:

Organism	Total number of patients*	Blood**	CSF**	Genital swab**	RTS**	Stool**	Urine**	Others**
B. pseudomallei	22	20	0	0	1	0	2	0
Brucella spp	0	0	0	0	0	0	0	0
C. diphtheriae	0	0	0	0	0	0	0	0
N. gonorrhoeae	0	0	0	0	0	0	0	0
N. meningitidis	0	0	0	0	0	0	0	0
Salmonella enterica serotype paratyphi	0	0	0	0	0	0	0	0
Salmonella enterica serotype typhi	0	0	0	0	0	0	0	0
Non-typhoidal Salmonella spp	14	10	0	0	0	2	1	1
Shigella spp	0	0	0	0	0	0	0	0
S. suis	4	4	0	0	0	0	0	0
Vibrio spp	0	0	0	0	0	0	0	0
Total	40	34	0	0	1	2	3	1

Note: Some patients may have more than one type of clinical specimen culture positive for the notifiable organism under the survey, and some may have more than one notifiable organism per evaluation period.

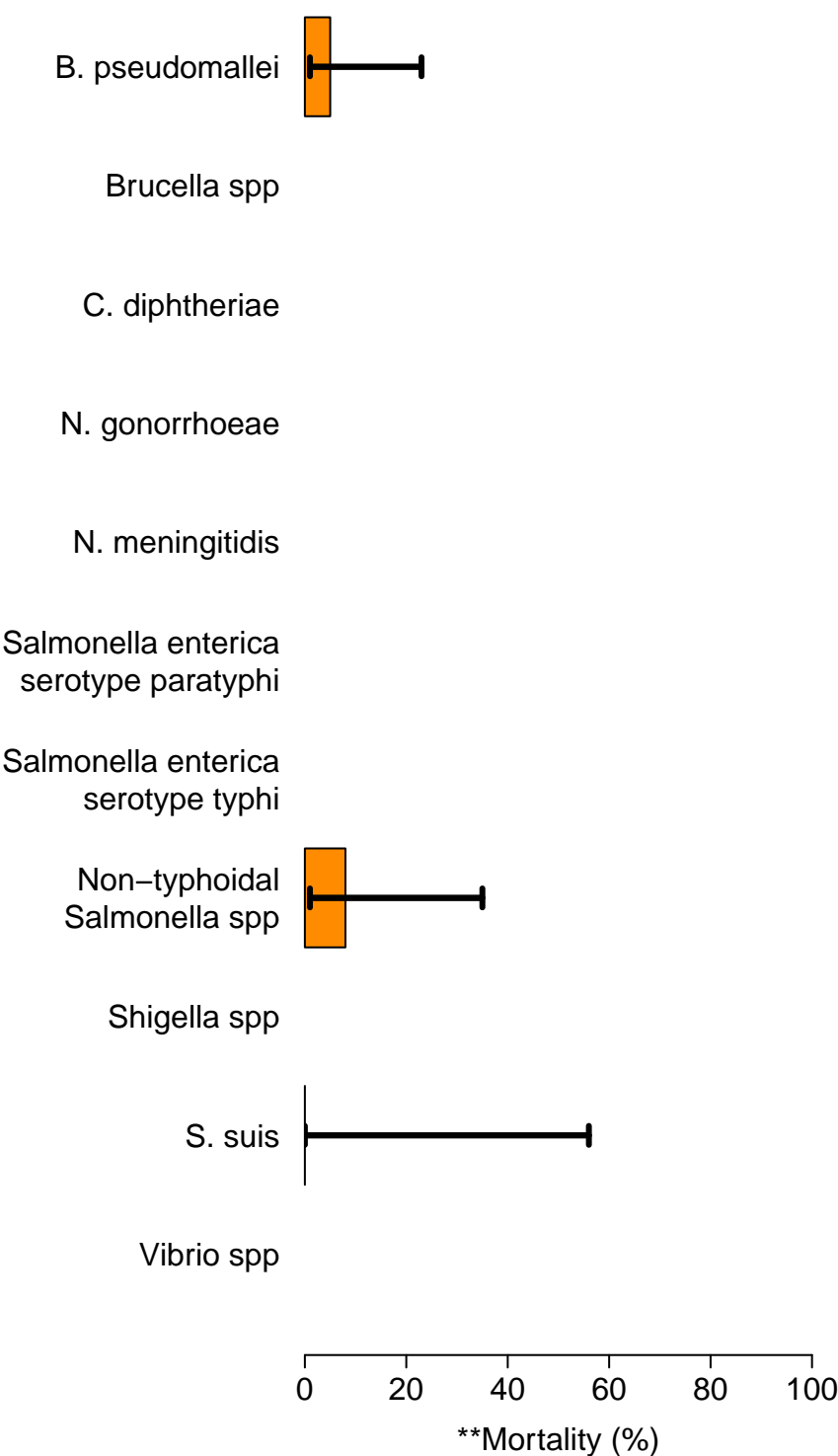
*Total number of patients are de-duplicated. One patient per organism was counted in the calculation.

**Only the first isolate per patient per specimen type per evaluation period was counted in the calculation.

RTS = Respiratory tract specimens; Others = Others or unknown sample types

Section [7]: Report on notifiable bacterial diseases

Mortality involving the notifiable bacterial diseases*



Organism	Mortality (n)	95% CI
B. pseudomallei	5% (1/21)	1% – 23%
Brucella spp	NA	–
C. diphtheriae	NA	–
N. gonorrhoeae	NA	–
N. meningitidis	NA	–
Salmonella enterica serotype paratyphi	NA	–
Salmonella enterica serotype typhi	NA	–
Non-typhoidal Salmonella spp	8% (1/12)	1% – 35%
Shigella spp	NA	–
S. suis	0% (0/3)	0% – 56%
Vibrio spp	NA	–

*We apologise that the bacteria name in the table and in the figure are not written in italic. This is because of the R command we used. We will improve this in the next version.

**Mortality is the proportion (%) of in-hospital deaths (all-cause deaths). This represents the number of in-hospital deaths (numerator) over the total number of patients with culture positive for each type of pathogen (denominator).
The AMASSplus application de-duplicates the data by including only the first isolate per patient per specimen type per evaluation period. CI = confidence interval

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_plus.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 programme if the computer already has the R programme installed. The user does not need to know how to use R programme.

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 for the AMR Surveillance 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].

Organisms included for the Notifiable Bacterial Diseases Report:

- *Burkholderia pseudomallei*
- *Brucella* spp.
- *Corynebacterium diphtheriae*
- *Neisseria gonorrhoeae*
- *Neisseria meningitidis*
- *Salmonella enterica* serotype *paratyphi*
- *Salmonella enterica* serotype *typhi*
- Non-typhoidal *Salmonella* spp.
- *Shigella* spp.
- *Streptococcus suis*
- *Vibrio* spp.

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.

The AMASSplus application is being developed by Chalida Rangsiwutisak, Cherry Lim, and Direk Limmathurotsakul.

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If you have any queries about AMASS or AMASSplus, please contact:

For technical information:

Chalida Rangsiwutisak (chalida@tropmedes.ac),
Cherry Lim (cherry@tropmedres.ac), and
Direk Limmathurotsakul (direk@tropmedres.ac)

For implementation of AMASSplus at your hospitals in Thailand:

Preeyarach Klaytong (preeyarach@tropmedres.ac), and
Viriya Hantrakun (viriya@tropmedres.ac)

