Human AMR surveillance – where are we now and where should we be heading?

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Hosted by Jane Barnett
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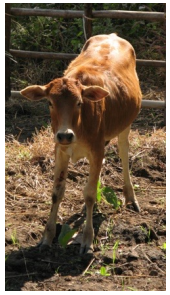
Outline

- An overview of AMR surveillance
- Snapshot of the situation in Southeast Asia
- What are the barriers to overcome?
- Better AMR surveillance moving forwards
- Questions

AMR surveillance takes all sorts…



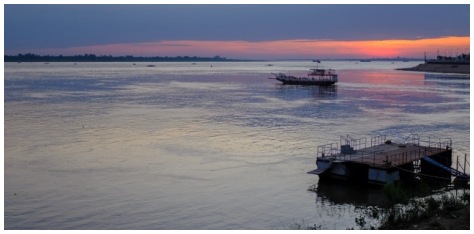


Image credit:
https://www.sanger.ac.uk/news_item/2014-04-29-two-human-genomes-per-hour/

Why do **human** AMR surveillance?

The Fleming Fund

A Summary of Phase One

Surveillance is the solution

> *It is time for us all to step up and speak out against the 'silent pandemic' of AMR.*

Professor Dame Sally Davies, *UK Government Special Envoy on Antimicrobial Resistance*

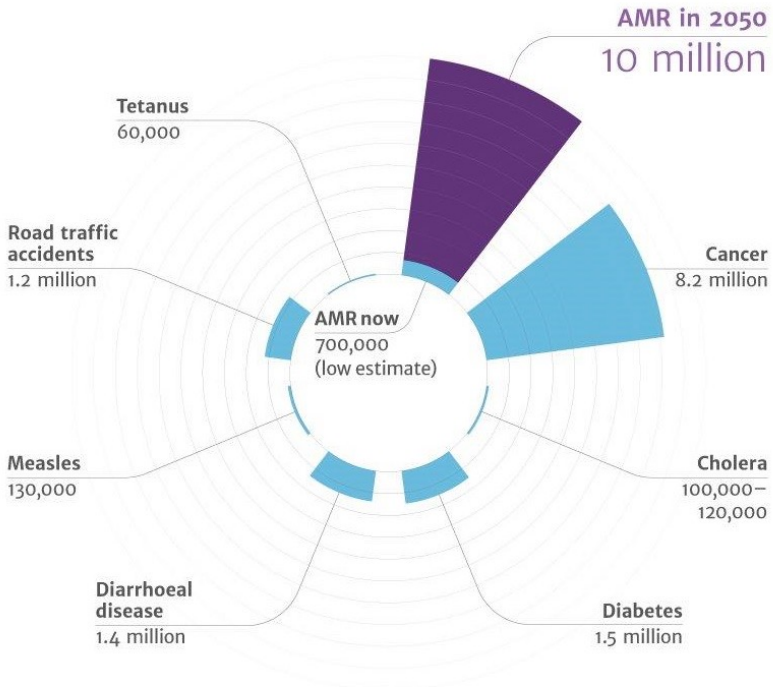
https://www.flemingfund.org/

Why do human AMR surveillance?

- To estimate burden of disease
- To characterise trends in space and time
- To serve as benchmark to measure the impact of interventions
- To provide local evidence for empiric treatment guidelines and clinical decision making

Burden of AMR:
What do we know already?

How much AMR is there and what impact does it have?



PLOS | MEDICINE

ESSAY

Will 10 Million People Die a Year due to Antimicrobial Resistance by 2050?

Marlieke E. A. de Kraker[1]*, Andrew J. Stewardson[2], Stephan Harbarth[1]

1 Infection Control Program, Geneva University Hospitals and Faculty of Medicine, Geneva, Switzerland,
2 Infectious Diseases Department, Austin Health, Heidelberg, Australia

- Current global estimates of the burden of AMR are not very informative; we need detailed, reliable data to be able to improve AMR control measures, preferably based on comprehensive, population-based surveillance data from low-, middle-, and high-income countries.

PLoS Med. 2016;13(11):e1002184

O'Neill report (2016)

Improving the estimation of the global burden of antimicrobial resistant infections

Direk Limmathurotsakul, Susanna Dunachie, Keiji Fukuda, Nicholas A Feasey, Iruka N Okeke, Alison H Holmes, Catrin E Moore, Christiane Dolecek, H Rogier van Doorn, Nandini Shetty, Alan D Lopez, Sharon J Peacock, Surveillance and Epidemiology of Drug Resistant Infections Consortium (SEDRIC)

***Panel*: Key actions to improve the estimation of the global burden of AMR infections**

Strengthen health systems

- Increase country capability and capacity to:
  - Reliably detect the global priority list of AMR bacteria reported by WHO
  - Document clinical outcomes and link to laboratory data

Lancet Infect Dis. 2019;19(11):e392-e8

Is there any good data?

- Recent review of 286 studies
- Mostly:
  - High income countries
  - Retrospective
  - Single centre
  - Methodologically sub-optimal
- Conclusion:
  - Need better studies / data urgently
  - Policy makers are unable to act until burden is clear

Contents lists available at ScienceDirect

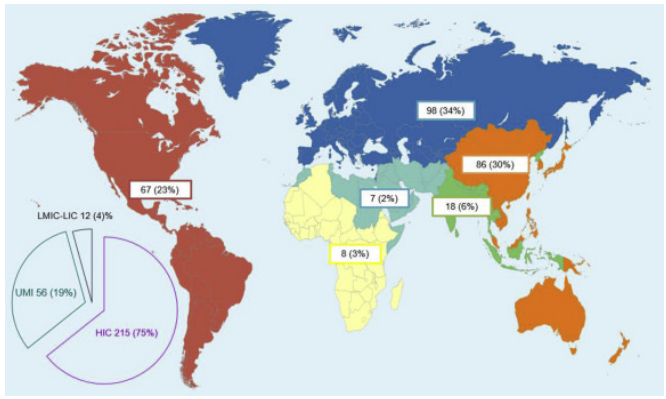
Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com

Systematic review

Methodological quality of studies evaluating the burden of drug-resistant infections in humans due to the WHO Global Antimicrobial Resistance Surveillance System target bacteria

Maria Diletta Pezzani [1,*], Barbara Tornimbene [2], Carmem Pessoa-Silva [2], Marlieke de Kraker [3], Sebastiano Rizzardo [1], Nicola Duccio Salerno [1], Stephan Harbarth [3], Evelina Tacconelli [1,4]



Clin Microbiol Infect. 2021. 10.1016/j.cmi.2021.01.004

JAC Antimicrob Resist
doi:10.1093/jacamr/dlaa130

JAC-Antimicrobial Resistance

Mortality attributable to third-generation cephalosporin resistance in Gram-negative bloodstream infections in African hospitals: a multi-site retrospective study

Angela Dramowski[1], Gerald Ong'ayo[2], Andrea M. Rehman [3], Andrew Whitelaw[4], Appiah-Korang Labi[5], Noah Obeng-Nkrumah[6], Awa Ndir[7], Marcelyn T. Magwenzi[8], Kenneth Onyedibe[9], Martin Wolkewitz[10], Marlieke E. A. de Kraker [11], J. Anthony G. Scott[2,3] and Alexander M. Aiken [3]* on behalf of the MBIRA study collaborators†

Table 3. Impact of third-generation cephalosporin resistance on in-hospital mortality, discharge and length of stay in *E. coli* and *K. pneumoniae* BSI

	HR (95% CI)			
Comparison	Cox model (death)	Cox model (discharge alive)	Fine + Gray model (death)	Excess LOS, days (95% CI)
R-*E. coli* versus matched controls	2.82 (2.10–3.79)	0.51 (0.44–0.59)	4.10 (3.06–5.48)	1.9 (−1.4 to 5.1)
S-*E. coli* versus matched controls	2.73 (2.29–3.24)	0.54 (0.50–0.58)	3.81 (3.21–4.51)	4.5 (3.1–5.8)
R-*E. coli* versus S-*E. coli*[a]	1.03 (0.73–1.46)	0.94 (0.79–1.11)	1.08 (0.77–1.51)	0.80 (0.59–1.09)
R-*K. pneumoniae* versus matched controls	2.89 (2.38–3.50)	0.47 (0.43–0.51)	4.55 (3.77–5.49)	6.2 (4.5–7.8)
S-*K. pneumoniae* versus matched controls	2.61 (2.03–3.37)	0.51 (0.46–0.57)	3.99 (3.11–5.12)	6.0 (3.9–8.2)
R-*K. pneumoniae* versus S-*K. pneumoniae*[a]	1.10 (0.80–1.52)	0.92 (0.80–1.06)	1.14 (0.83–1.55)	1.01 (0.84–1.21)

"…there did not appear to be an impact of 3GC-resistance on mortality in *E. coli* or *K. pneumoniae* BSI in African hospitals, as compared with susceptible BSI with equivalent species"

Mortality associated with third-generation cephalosporin resistance in Enterobacterales bloodstream infections at eight sub-Saharan African hospitals (MBIRA): a prospective cohort study

*Alexander M Aiken, Andrea M Rehman, Marlieke E A de Kraker, Lola Madrid, Meron Kebede, Appiah-Korang Labi, Noah Obeng-Nkrumah, Brian Nyamwaya, Eunice Kagucia, Derek Cocker, Kondwani Kawaza, Rebecca Lester, Kenneth C Iregbu, Nubwa Medugu, Philip I Nwajiobi-Princewill, Angela Dramowski, Tolbert Sonda, Asia Hemed, Sombo Fwoloshi, David Ojok, J Anthony G Scott, Andrew Whitelaw, for the MBIRA study collaborators**

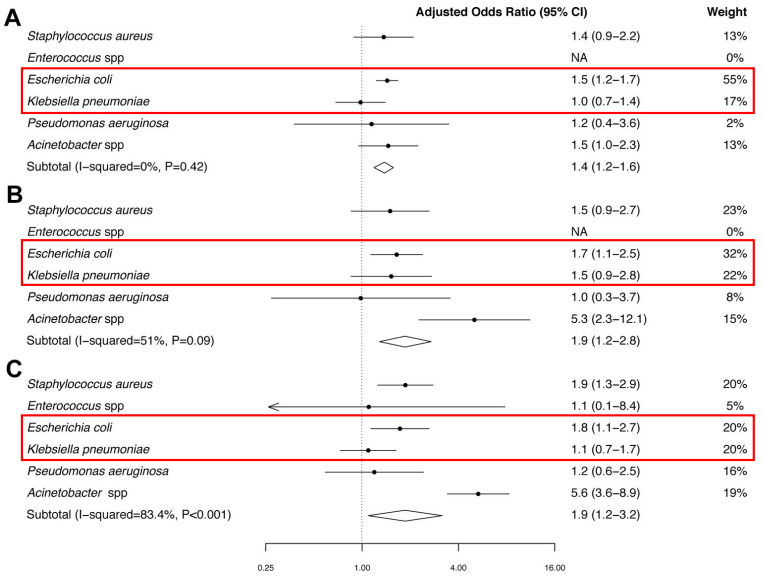
Same result

Lancet Infect Dis. 2023. DOI: 10.1016/S1473-3099(23)00233-5

Epidemiology and burden of multidrug-resistant bacterial infection in a developing country

Cherry Lim[1†], Emi Takahashi[1†], Maliwan Hongsuwan[1], Vanaporn Wuthiekanun[1], Visanu Thamlikitkul[2], Soawapak Hinjoy[3], Nicholas PJ Day[1,4], Sharon J Peacock[1,5,6], Direk Limmathurotsakul[1,4,7*]

Elife. 2016;5



"We estimate that 43% deaths in patients with hospital-acquired infection due to MDR bacteria in Thailand in 2010 represented excess mortality caused by MDR"

Standardised protocols:
This is a step in the right direction

…but it will take a while for data to be generated

IHME – Oxford – GRAM to the rescue?

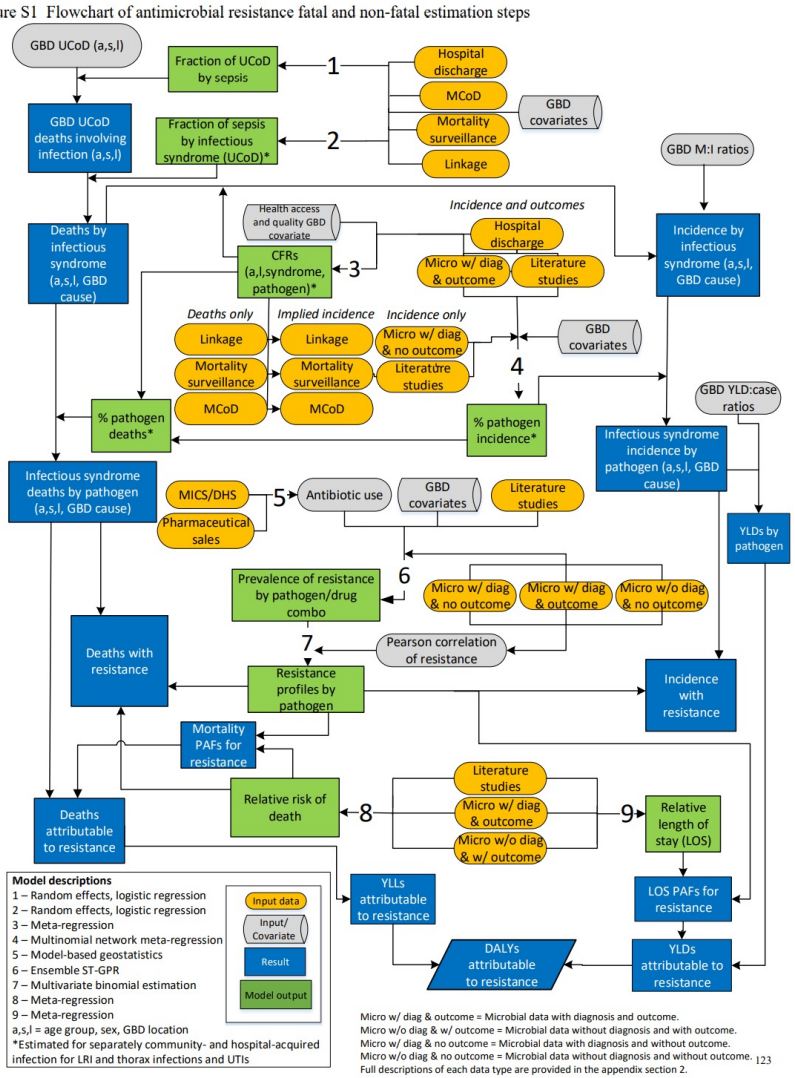
Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis

*Antimicrobial Resistance Collaborators**

Global mortality associated with 33 bacterial pathogens in 2019: a systematic analysis for the Global Burden of Disease Study 2019

*GBD 2019 Antimicrobial Resistance Collaborators**

The model…

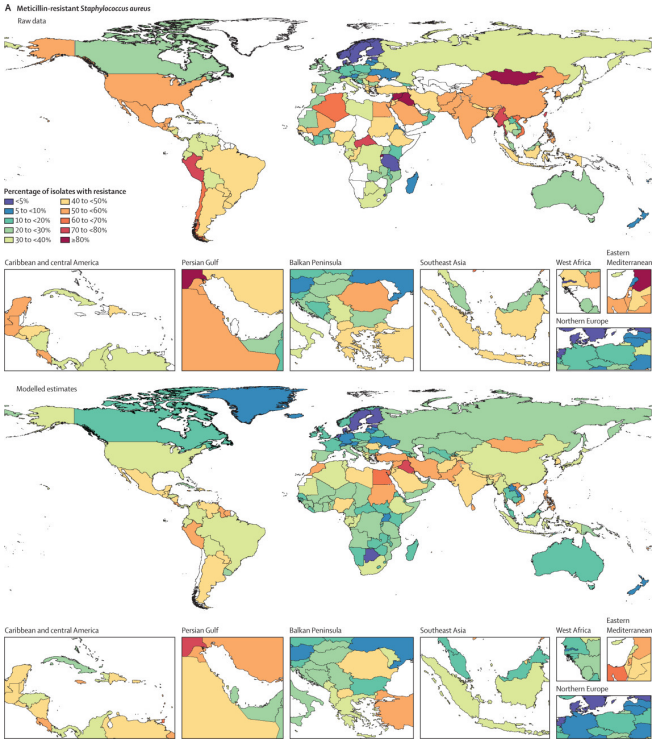


…is “complicated”

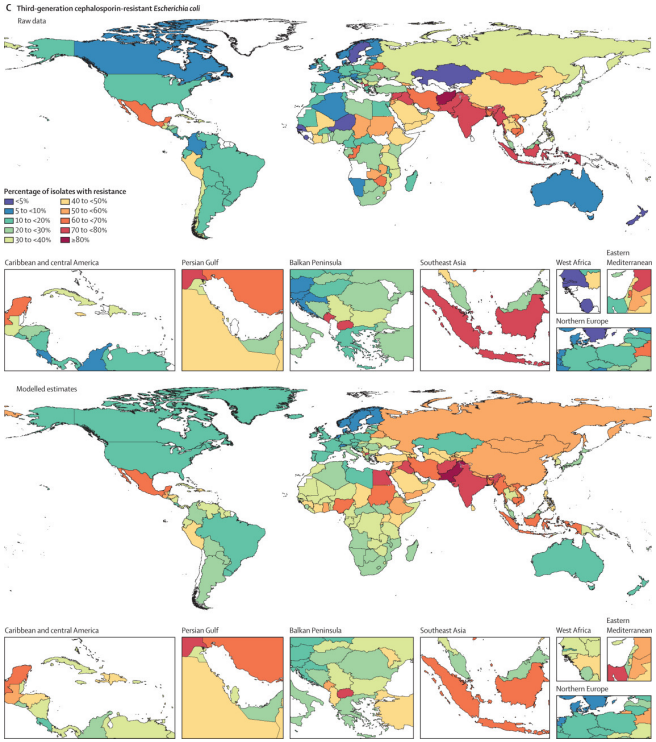
https://doi.org/10.1016/S0140-6736(21)02724-0

The maps

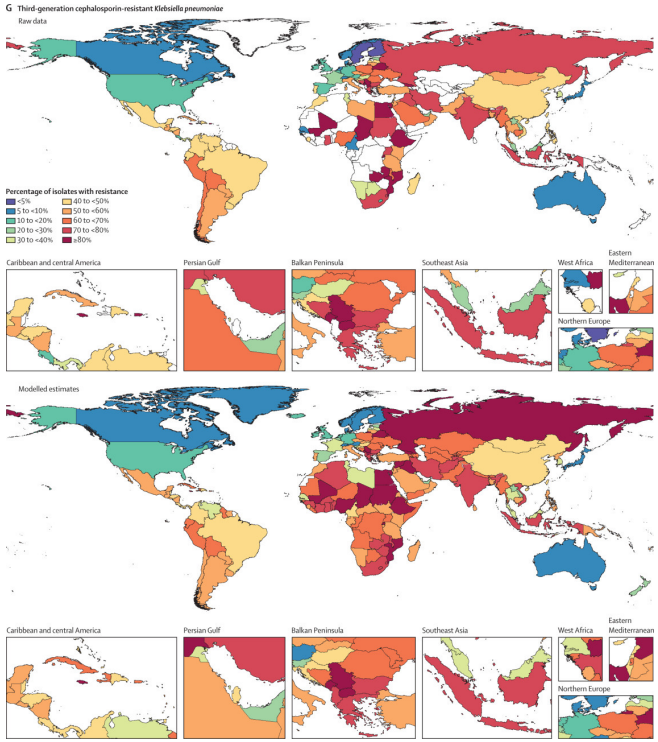
Methicillin R
S. aureus



3rd gen cephalosporin R
E. coli



3rd gen cephalosporin R
K. pneumoniae



Key messages

- Huge burden of AMR
  - O'Neill report figures appear to be an underestimate

- Under-recognised mortality in Africa and in children

Limitations

Not much data from LMICs

This study has several limitations, the most important being the sparsity of data from many LMICs on the distribution of pathogens by infectious syndrome, the prevalence of resistance for key pathogen–drug combinations, and the number of deaths involving infection; and the severe scarcity of data linking laboratory results to outcomes such as death.

CAI versus HAI

In future iterations of the project, we hope to improve on the identification of community-acquired and hospital-acquired infections.

AMR data not standardised

Additionally, no universal laboratory standard exists to demarcate resistance versus susceptibility, and we often had to defer to laboratory interpretation to classify the isolates in our data, resulting in heterogeneous classification. Whenever possible, we classified resistance using the most recent CLSI guidelines based on the minimum inhibitory concentrations provided in the data; however, CLSI breakpoints have changed over time, and many datasets did not provide sufficient detail to allow for retrospective reanalysis of the data.[67]

A vague mention that some of the lab data may not have been great quality

There are many well described barriers to good-quality clinical bacteriology in LMICs, and proper quality assurance and quality-control measures are crucial for quality care and accurate laboratory-based surveillance.[66]

Dame Sally Davies take

The study also demonstrates data disparities and the lack of infrastructure and capacity for surveillance that we need to detect and respond to pandemics.

https://www.flemingfund.org/

AMR surveillance in SE Asia

J Antimicrob Chemother
doi:10.1093/jac/dkx260

Journal of Antimicrobial Chemotherapy

A current perspective on antimicrobial resistance in Southeast Asia

Raphaël M. Zellweger[1], Juan Carrique-Mas[1,2], Direk Limmathurotsakul[2,3], Nicholas P. J. Day[2,3], Guy E. Thwaites[1,2] and Stephen Baker[1,2,4]* on behalf of the Southeast Asia Antimicrobial Resistance Network†

- SE Asia is a global hub for AMR and contributes to its global spread
- High prevalence of infectious diseases but often poor diagnostic capacity
- Rapid increases in food production systems
- Broad access to antimicrobials of varying quality with limited regulation

Yam et al. Antimicrobial Resistance and Infection Control (2019) 8:202
https://doi.org/10.1186/s13756-019-0654-8

Antimicrobial Resistance and Infection Control

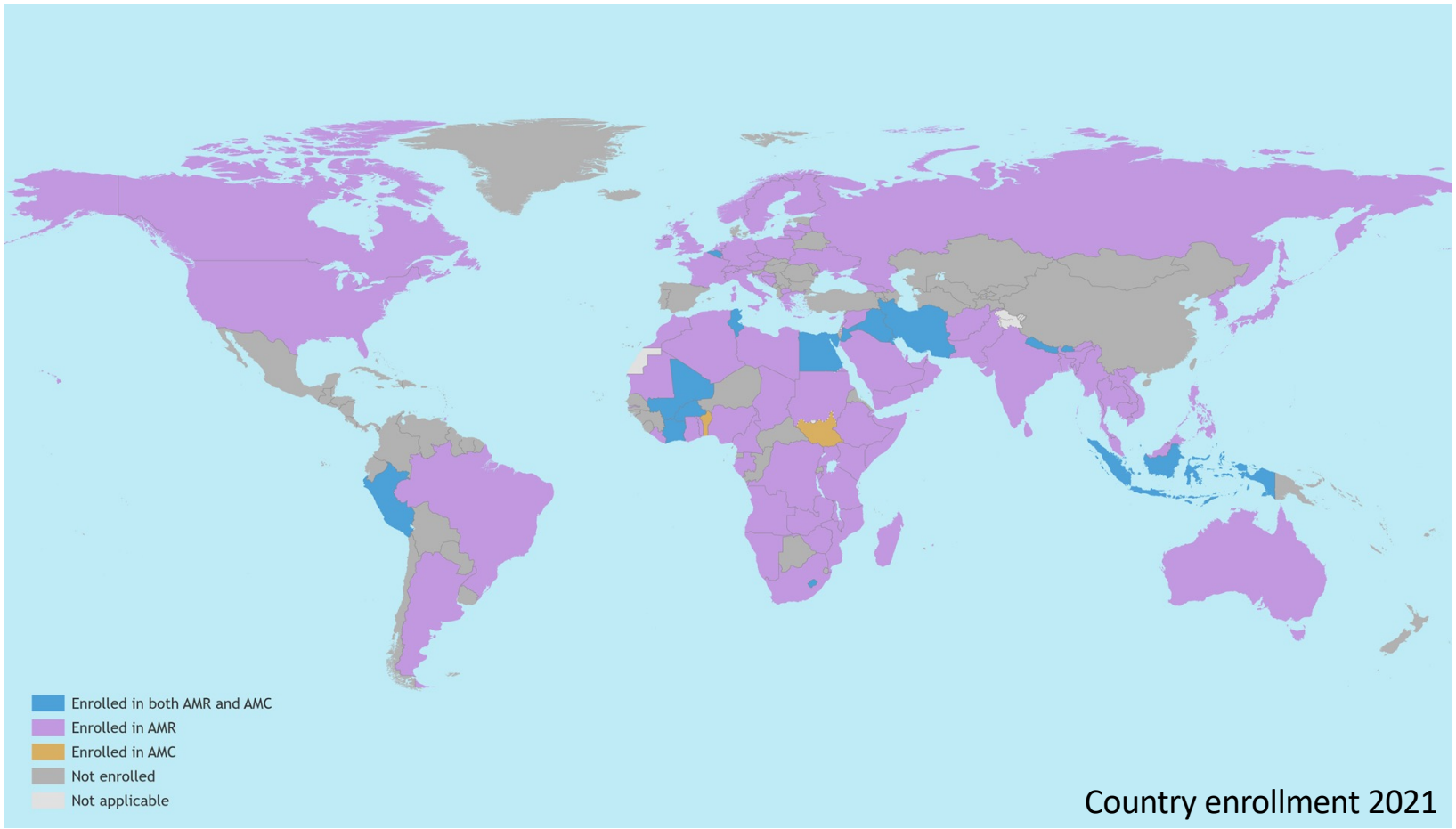
MEETING REPORT Open Access

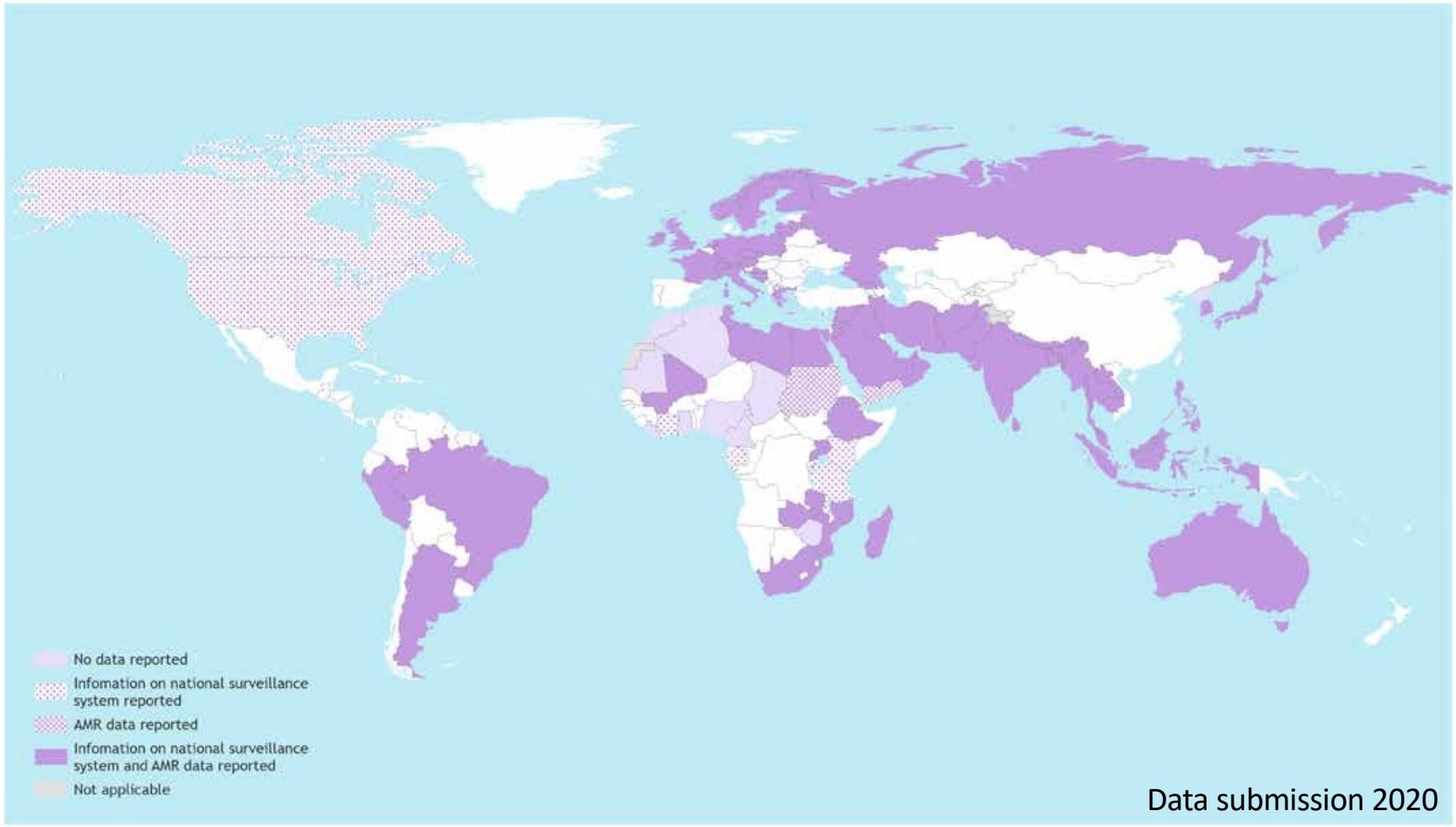
Antimicrobial Resistance in the Asia Pacific region: a meeting report

Esabelle Lo Yan Yam[1*], Li Yang Hsu[2], Eric Peng-Huat Yap[1], Tsin Wen Yeo[1], Vernon Lee[2,3], Joergen Schlundt[4], May O. Lwin[5], Direk Limmathurotsakul[6,7], Mark Jit[8,9,10], Peter Dedon[11,12], Paul Turner[13,14] and Annelies Wilder-Smith[1,15,16*]

- Enhanced surveillance and research to provide improved evidence-based strategies and policies are needed
- A regionally coordinated effort that is target-driven, sustainable and builds on a framework facilitating communication and governance will strengthen the fight against AMR in the Asia Pacific region

SE Asia from a GLASS perspective





The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: WHO, Global Antimicrobial Resistance and Use Surveillance System (GLASS)
Map Production: WHO GIS Centre for Health, DNA/DDI

World Health Organization

Thailand

Population 69,625,581 (2019)

Select Country: Thailand

Data submission

specimen	Pathogen name	Number of tested patient	AST results	Age	Gender	Infection origin
BLOOD	Acinetobacter spp.	●	●	●	●	●
	E. coli	●	●	●	●	●
	K. pneumoniae	●	●	●	●	●
	S. aureus	●	●	●	●	●
	S. pneumoniae	●	●	●	●	●
	Salmonella spp.	●	●	●	●	●
GENITAL	N. gonorrhoeae	●	●	●	●	●
STOOL	Salmonella spp.	●	●	●	●	●
	Shigella spp.	●	●	●	●	●
URINE	E. coli	●	●	●	●	●
	K. pneumoniae	●	●	●	●	●

70-100% data reported ●
<70% data reported ●
No data reported ●

Data Overview

Number of tested patients

Specimen t..	Community origin	Hospital origin	Unknown origin
BLOOD	47887	12269	313
GENITAL	2688	201	18
STOOL	3626	1534	25
URINE	25528	11432	162

N.R. : Not Reported

Number of infected patients

Specimen type	Pathogen name	Community origin	Hospital origin	Unknown origin
BLOOD	Acinetobacter spp.	176	39	1
	E. coli	754	357	10
	K. pneumoniae	2,100	339	14
	S. aureus	256	444	2
	S. pneumoniae	170	7	3
	Salmonella spp.	570	215	6
GENITAL	N. gonorrhoeae	79		
STOOL	Salmonella spp.	732	102	11
	Shigella spp.	11	1	
URINE	E. coli	1,297	792	15
	K. pneumoniae	5,207	1,674	26

Malaysia

Population 31,949,789 (2019)

Select Country: Malaysia

Data submission

specimen	Pathogen name	Number of tested patient	AST results	Age	Gender	Infection origin
BLOOD	Acinetobacter spp.	●	●	●	●	●
	E. coli	●	●	●	●	●
	K. pneumoniae	●	●	●	●	●
	S. aureus	●	●	●	●	●
	S. pneumoniae	●	●	●	●	●
	Salmonella spp.	●	●	●	●	●
GENITAL	N. gonorrhoeae	●	●	●	●	●
STOOL	Salmonella spp.	●	●	●	●	●
	Shigella spp.	●	●	●	●	●
URINE	E. coli	●	●	●	●	●
	K. pneumoniae	●	●	●	●	●

70-100% data reported ●
<70% data reported ●
No data reported ●

Data Overview

Number of tested patients

Specimen t..	Community origin	Hospital origin	Unknown origin
BLOOD	13171	3653	53807
GENITAL	N.R	N.R	N.R
STOOL	N.R	N.R	N.R
URINE	N.R	N.R	N.R

N.R. : Not Reported

Number of infected patients

Specimen type	Pathogen name	Community origin	Hospital origin	Unknown origin
BLOOD	Acinetobacter spp.	1,058	506	4,107
	E. coli	243	25	431
	K. pneumoniae	1,810	812	6,253
	S. aureus	200	303	1,498
	S. pneumoniae	253	51	775
	Salmonella spp.	1,753	369	4,747
GENITAL	N. gonorrhoeae	76		92
STOOL	Salmonella spp.	336	104	1,715
	Shigella spp.	2	4	4
URINE	E. coli	1,191	230	4,011
	K. pneumoniae	3,965	475	9,440

No data for VN

https://www.who.int/data/gho/data/themes/topics/global-antimicrobial-resistance-surveillance-system-glass/glass-country-profiles

Barriers to better surveillance

(and barriers to better use of surveillance data)

Bias and incompleteness of data

Collection of samples for microbiologic testing is not part of a standard diagnostic work-up for many clinical syndromes

Microbiologists often do not receive any clinical information important for interpreting laboratory results and surveillance data, *e.g.* whether an infection is community- or hospital-acquired

All of these biases favour an overrepresentation of results from DRI among surveillance data

Patients have access to over-the-counter antibiotics in the community and are often already taking these when admitted to hospital

Samples are often collected only in more severe cases or in case of treatment failure

Clinician utilisation of the microbiology laboratory is often sub-optimal in Cambodia

Om et al. Antimicrobial Resistance and Infection Control (2016) 5:58
DOI 10.1186/s13756-016-0159-7

Antimicrobial Resistance and Infection Control

RESEARCH Open Access

"If it's a broad spectrum, it can shoot better": inappropriate antibiotic prescribing in Cambodia

Chhorvoin Om[1], Frances Daily[2], Erika Vlieghe[3], James C. McLaughlin[2] and Mary-Louise McLaws[1*]

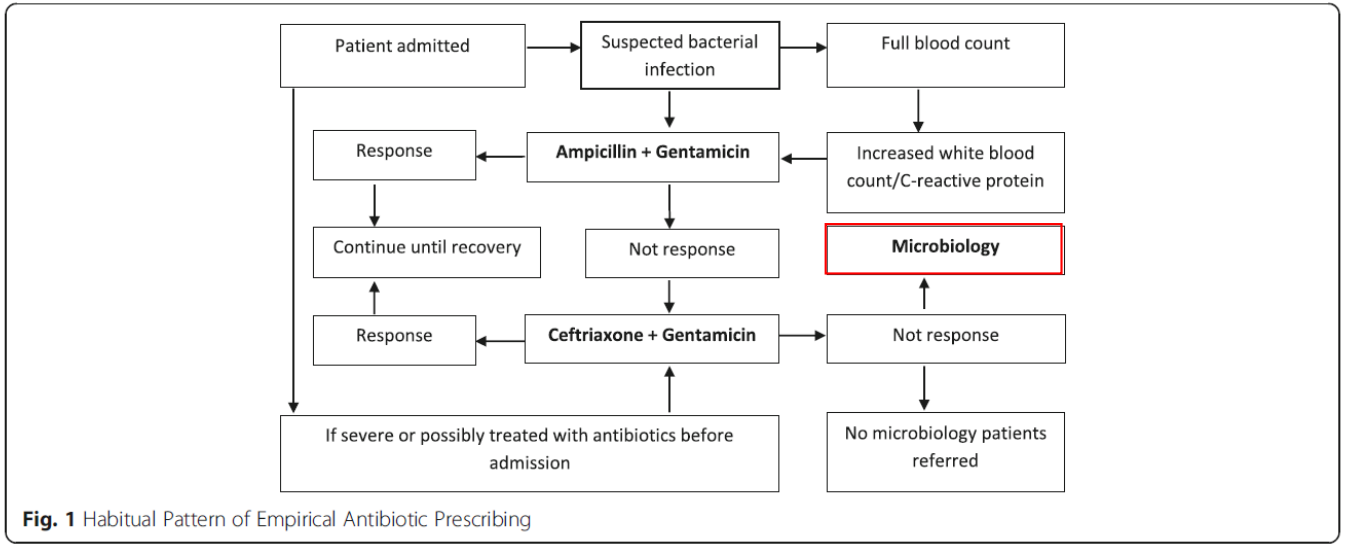


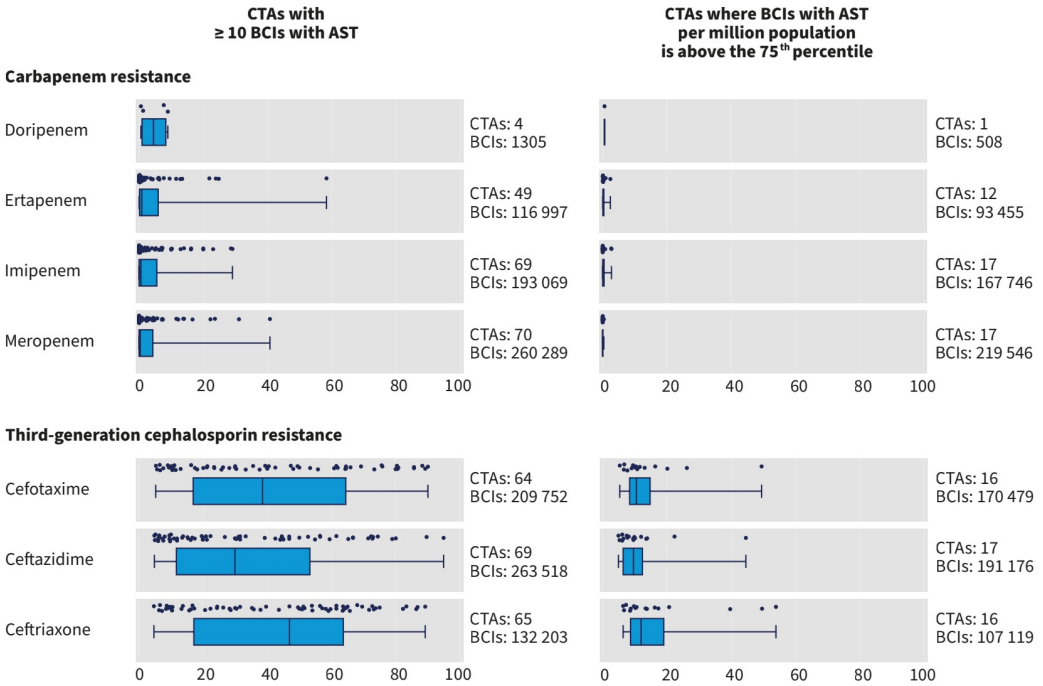
Fig. 1 Habitual Pattern of Empirical Antibiotic Prescribing

Specimens are often submitted for culture only after non-response to first and second-line antibiotics

Antimicrob Resist Infect Control. 2016;5:58

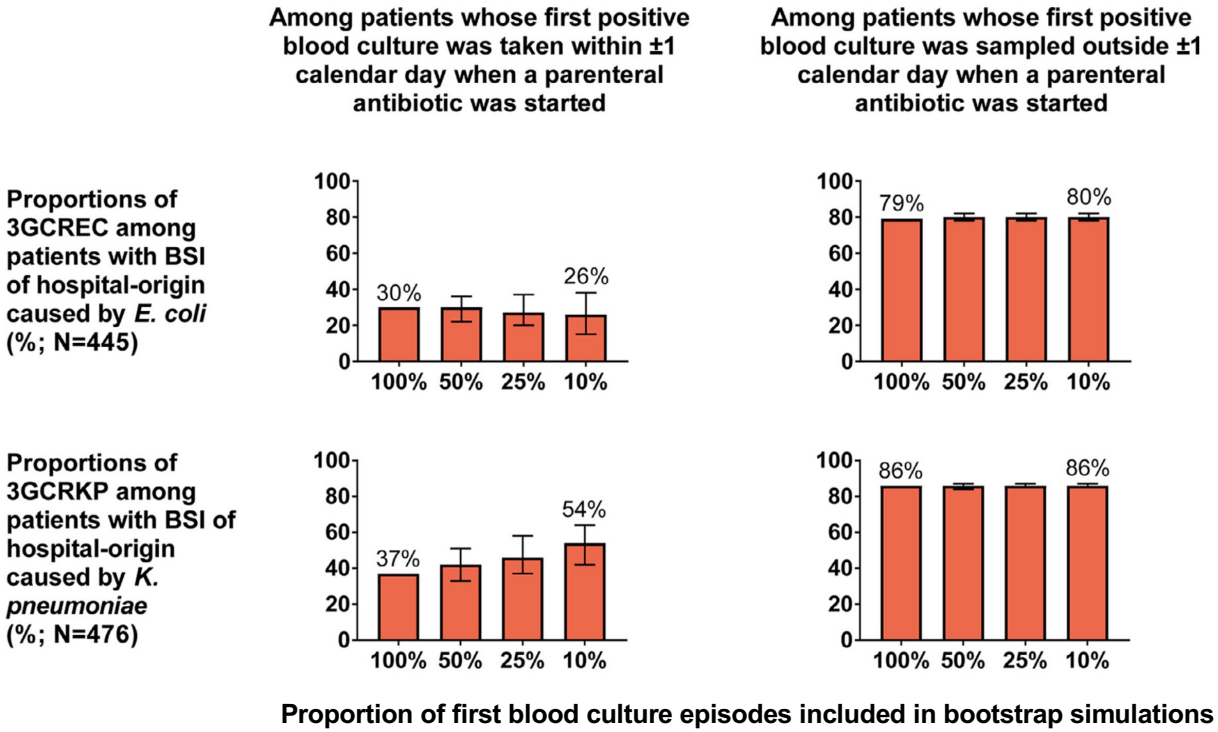
WHO GLASS report demonstrates the impact of low blood culture rates

Fig. 3.7b. Percentage resistance to antimicrobials under surveillance in *E. coli* in all CTAs reporting ≥10 *E. coli* bloodstream infections with AST results compared to CTAs where the reported number per million population was above the 75th percentile in 2020



GLASS report 2022

Modelling highlights the impact of exposure to antibiotics prior to blood culture



Bootstrap simulations based on data from a referral large hospital in NE Thailand

J Infect. 2021;82(3):355-362

Little / No clinical context

Need to recall why are we really doing AMR surveillance?

Laboratory data quality

AMR lab data quality…

Table 7 Percentage sensitivity patterns of most prevalent pathogens to selected antimicrobials

	Region	Africa		South-East Asia			
Organism	Antimicrobial	Adejuyigbe *et al* (20)	Muhe *et al* (27)	Mathur *et al* (37)	Panigrahi *et al* (39)	Darmstadt *et al* (35)	Tallur *et al* (41)
Escherichia coli	Amoxycillin (AMX)	60.0	–	–	–	–	–
	Ampicillin (AMP)	40.0	100.0	–	–	100.0	29.0
	Cefotaxime (CTX)	–	–	–	–	–	100.0
	Ceftazidime (CAZ)	–	100.0	–	–	100.0	–
	Ceftriaxone (CRO)	–	–	–	–	100.0	100.0
	Ciprofloxacin (CIP)	–	–	–	–	100.0	–
	Gentamicin (GEN)	80.0	100.0	–	–	100.0	71.0
	Imipenem (IMP)					100.0	–
Staphylococcus aureus	Amoxycillin (AMX)	73.0	–	–	–	–	–
							21.0
							–
							–
							–
	Ciprofloxacin (CIP)	–	–	–	–	80.0	–
	Gentamicin (GEN)	85.8	–	–	–	90.0	29.0
	Imipenem (IMP)	–	–	–	–	90.0	–
Klebsiella species*	Amoxycillin (AMX)	0.0	–	–	–	–	–
	Ampicillin (AMP)	–	–	10.0	–	0.0	25.5
	Cefotaxime (CTX)	–	–	–	–	–	76.5
	Ceftazidime (CAZ)	–	–	–	22.0	33.3	–
	Ceftriaxone (CRO)	–	–	71.4	–	33.3	81.0
	Ciprofloxacin (CIP)	–	–	64.8	11.0	66.7	–
	Gentamicin (GEN)	100.0	–	42.8	–	66.7	59.5
	Imipenem (IMP)	–		100.0	–	100.0	–

*Averages were taken when more than one variant's sensitivity patterns were reported.

…there are issues to be aware of

J Glob Health. 2011;1(2):154-70

Staphylococcus aureus

Staphylococcus aureus	Amoxycillin (AMX)	73.0	–	–	–	–	–
	Ampicillin (AMP)	–	–	–	–	0.0	21.0
	Cefotaxime (CTX)	–	–	–	–	–	–
	Ceftazidime (CAZ)	–	–	–	–	66.7	–
	Ceftriaxone (CRO)	–	–	–	–	90.0	–
	Ciprofloxacin (CIP)	–	–	–	–	80.0	–
	Gentamicin (GEN)	85.8	–	–	–	90.0	29.0
	Imipenem (IMP)	–	–	–	–	90.0	–

How much MRSA: no cefoxitin / oxacillin results?

- Could just guess from the imipenem or ceftriaxone data?
- But how were these results generated?

Ceftazidime for *S. aureus:* might be ok 2/3 of the time…really?

EUCAST EUROPEAN COMMITTEE ON ANTIMICROBIAL SUSCEPTIBILITY TESTING
European Society of Clinical Microbiology and Infectious Diseases

Are these isolated issues or part of a larger quality management problem?

Improving future surveillance in LMICs

Key surveillance approaches

- Isolate-based
  - Information only on species of interest
  - e.g. 43% of *E. coli* from blood culture specimens were ciprofloxacin resistant
- Specimen-based
  - Adds a level of laboratory data: specimen denominator and may be limited contextual data (patient age, hospitalisation status)
  - e.g. 10% of blood cultures grew a WHO priority pathogen, and of those…
- Case-based
  - Adds clinical data: patients meeting a case definition
  - e.g. 8% of patients with suspected sepsis had a positive blood culture, and of those…

Easiest / Cheap

Least informative

WHO GLASS

Hardest / Expensive

Most informative

Strengths and weaknesses of these approaches

	Strength	Weakness
Strategies for identifying antimicrobial resistant (AMR) infections / drug resistant infections (DRI)		

Specimen-based ("routine microbiology data")	• Relatively easy to implement and sustain, even in LMICs where resources are limited
	• Can generate data summaries, so a good start
	  • % of samples positive
	  • % isolates resistant
	  • Possible to stratify by age, CAI / HAI, etc if some clinical data provided to laboratories
	• Outbreak detection possible
		• Prone to bias based on laboratory utilisation and pre-culture antibiotic treatment
		• Comparability over space and time often limited in LMIC settings
		• May not provide clinically useable data summaries (e.g. for treatment guideline development)

Case-based ("patients meeting a syndrome case definition")	• More robust to variations in microbiology utilisation
	• Capable of addressing several surveillance objectives
	  • Treatment guideline development
	  • Assessment of interventions and changes over time
	  • Defining health impacts of AMR
		• Labour-intensive
		• Expensive
		• Difficult to sustain, especially in LMICs with limited resources
		• Needs investment in training, guidelines, and diagnostic capacity, especially in LMICs

From: Clin Microbiol Infect. 2021;27(10):1391-1399

Strengths and weaknesses of these approaches

	Strength	Weakness
Sampling strategies		
DRI: consecutive sample	• Easy to perform	• Risk of bias due to clinical sampling behavior
DRI: lot quality assurance sampling (LQAS)	• Requires small sample size for useable estimates to inform empiric treatment guidelines	• Definition of thresholds defining the “low” and “high” prevalence of resistance are challenging, especially where limited treatment options exist
Comparator cohort: exposure density sampling	• Ensures a more accurate estimation of health burdens due to DRI	• Would need training and detailed protocol, which may be more challenging in LMIC settings

From: Clin Microbiol Infect. 2021;27(10):1391-1399

Strengths and weaknesses of these approaches

	Strength	Weakness
Strategies for reporting antimicrobial susceptibility testing (AST) data		
Report susceptibility to individual antimicrobials	• Easy to generate summary statistics (e.g. using WHONET)	• Limited capability for translation to clinical practice
Weighted-incidence syndromic combination antibiogram (WISCA)	• Statistics generated can be translated to clinical practice (i.e. empiric treatment guidelines)	• May be difficult to generate in settings where there is a lack of analytic expertise, given the absence of open-access applications to process the data

From: Clin Microbiol Infect. 2021;27(10):1391-1399

What tools are needed

- Money
- Good microbiology
  - Several excellent capacity building initiatives on-going
  - Important to connect labs to clinical services
- Human resources
  - Clinical staff require support to use microbiology effectively
  - In the absence of fully electronic patient, pharmacy, and lab information systems surveillance takes time and requires effort
- Case definitions
  - That are simple and do not require serial bloods / radiology
- IT infrastructure

Clinical bacteriology in low-resource settings: today's solutions

Sien Ombelet, Jean-Baptiste Ronat*, Timothy Walsh, Cedric P Yansouni, Janneke Cox, Erika Vlieghe, Delphine Martiny, Makeda Semret, Olivier Vandenberg, Jan Jacobs, on behalf of the Bacteriology in Low Resource Settings working group†*

Lancet Infect Dis. 2018;18(8):e248-e58.

LMIC laboratory development

Practice

BMJ Global Health

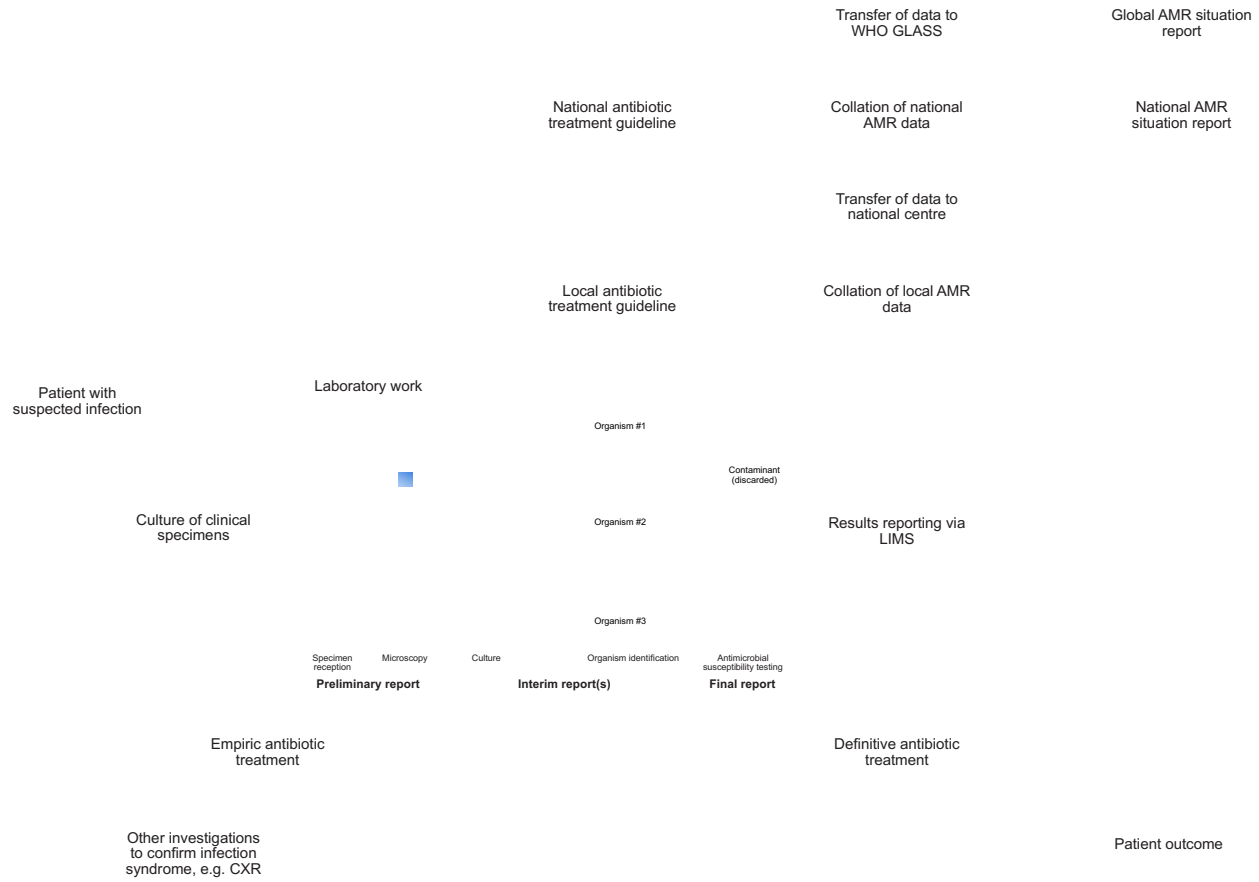
Leapfrogging laboratories: the promise and pitfalls of high-tech solutions for antimicrobial resistance surveillance in low-income settings

Iruka N Okeke ,[1] Nicholas Feasey,[2] Julian Parkhill,[3] Paul Turner ,[4] Direk Limmathurotsakul ,[5] Pantelis Georgiou,[6] Alison Holmes,[7] Sharon J Peacock[8]

"Traditional methods for AMR surveillance can be challenging to establish and truly representative, high-quality surveillance may be easier to achieve by combining those approaches with new innovations or exploring entirely novel paths to usable resistance information"

BMJ Glob Health. 2020;5(12):e003622

Better AMR surveillance IT tools



Lancet Infect Dis. 2021;21(6):e170-e174

Using information technology to improve surveillance of antimicrobial resistance in South East Asia

Sirenda Vong and colleagues argue that investing in information technology surveillance systems to detect trends is an essential first step in tackling antimicrobial resistance in South East Asian countries

- Lack of IT infrastructure is often cited as a barrier to comprehensive AMR surveillance and antibiotic usage stewardship programmes in LMICs
- Few open access software options that might support an IT infrastructure for AMR surveillance are available

BMJ. 2017;358:j3781

Better AMR data analysis tools

The microbiology laboratory database software.

AMR (for R) | Home | How to | Manual | Authors | Changelog

AMR (for R)

Note: the rules of 'EUCAST Clinical Breakpoints v11.0 (2021)' are now implemented.

What is AMR (for R)?

(To find out how to conduct AMR data analysis, please continue reading here to get started.)

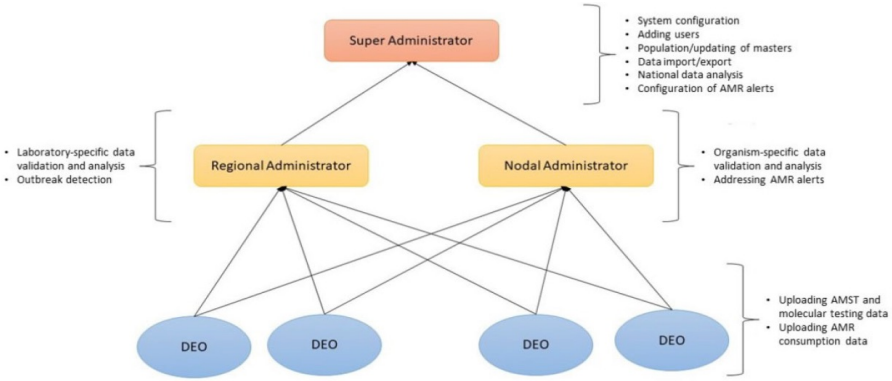
AMR is a free, open-source and independent R package to simplify the analysis and prediction of Antimicrobial Resistance (AMR) and to work with microbial and antimicrobial data and properties, by using evidence-based methods. **Our aim is to provide a standard** for clean and reproducible AMR data analysis, that can therefore empower epidemiological analyses to continuously enable surveillance and treatment evaluation in any setting.

JAC Antimicrob Resist
doi:10.1093/jacamr/dlab023

JAC-Antimicrobial Resistance

ICMR's Antimicrobial Resistance Surveillance system (*i*-AMRSS): a promising tool for global antimicrobial resistance surveillance

Jasmine Kaur[1,2,3]†, Ajay Singh Dhama[1]†, Harish Buttolia[1]†, Jasleen Kaur[1], Kamini Walia[4], Vinod Ohri[4], Vinit Kumar[1], Andrew M. Lynn[2], Alok Srivastava[3,5] and Harpreet Singh[1]*

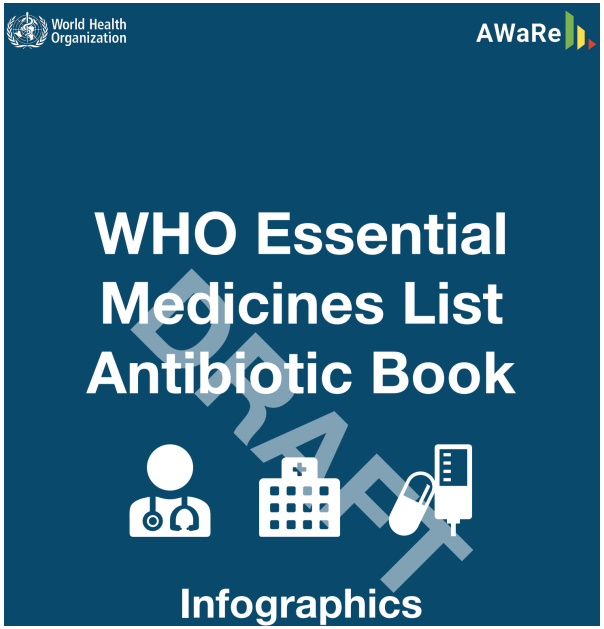


Clinical data analysis?

- Guideline development
- Outcomes / Risk factors

Treatment guideline development

- Complicated
  - Multiple possible pathogens
    - need **lab data**
  - Syndrome specific considerations
    - need **clinical data**
  - Wide variations in AST prevalence
    - need **local data**



Wellcome Open Research
Wellcome Open Research 2018, 3:131 Last updated: 08 NOV 2018

Check for updates

RESEARCH ARTICLE

Using machine learning to guide targeted and locally-tailored empiric antibiotic prescribing in a children's hospital in Cambodia [version 1; referees: 1 approved]

Mathupanee Oonsivilai [1], Yin Mo[1,2], Nantasit Luangasanatip[1], Yoel Lubell [1], Thyl Miliya[3], Pisey Tan[3], Lorn Loeuk[3], Paul Turner [3,4], Ben S. Cooper[1,4]

EXPERT REVIEW OF ANTI-INFECTIVE THERAPY
https://doi.org/10.1080/14787210.2021.1967145
Taylor & Francis
Taylor & Francis Group

ORIGINAL RESEARCH

Check for updates

Improving empiric antibiotic prescribing in pediatric bloodstream infections: a potential application of weighted-incidence syndromic combination antibiograms (WISCA)

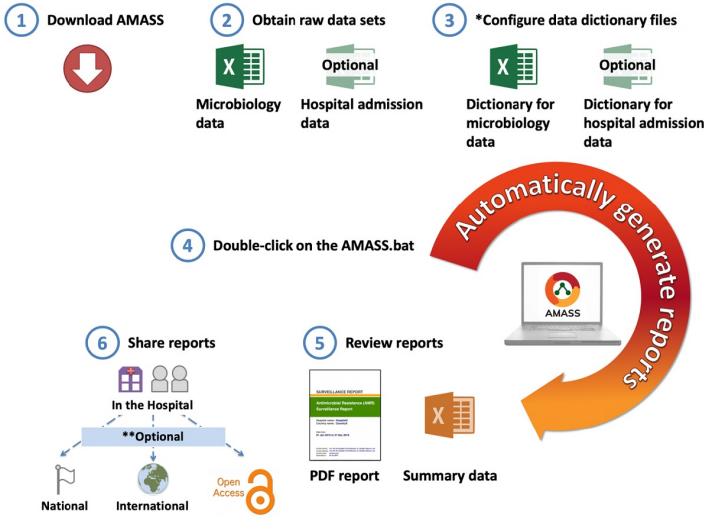
Aislinn Cook, Mike Sharland, Yasmine Yau, PediBSI Group*, and Julia Bielicki

Paediatric Infectious Diseases Research Group, Institute for Infection and Immunity, St George's, University of London, London, United Kingdom

Joining up clinical and lab data…
and putting in the hands of local clinicians

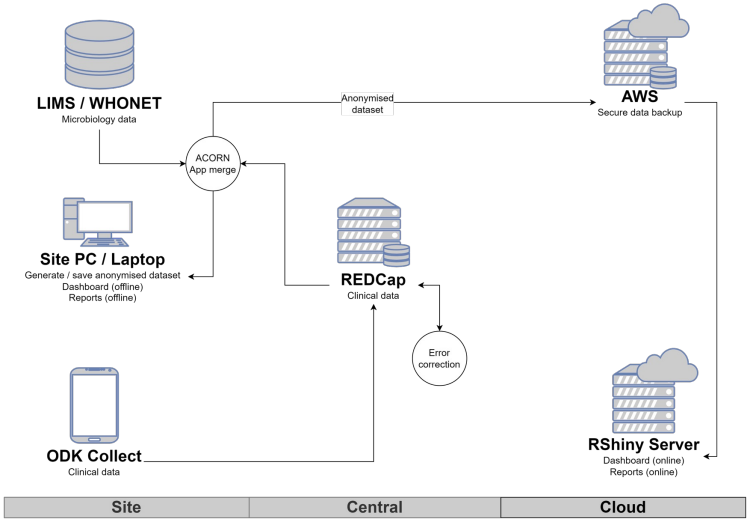
AMASS

- Automated reports using existing hospital data



ACORN

- Prospective pragmatic clinical surveillance



J Med Internet Res. 2020;22(10):e19762.

www.acornamr.net

MICRO

Microbiology Investigation Criteria for Reporting Objectively:
A framework for the reporting and interpretation of clinical microbiology data

BMC Medicine. 2019;17(1): 70

Tackling antimicrobial resistance (AMR) is a Global Health priority

Poor quality data hampers efforts to understand the burden of AMR

Use the MICRO framework to enhance the quality and scientific reporting of clinical microbiology data:

- Increase data utility and comparability
- Improve AMR surveillance
- Facilitate meta-analyses
- Inform policy and interventions from local to global levels

UNIVERSITY OF OXFORD

To sum up…

- Generation and interpretation of AMR burden data is complicated
- There are still large data (+ data quality) and knowledge gaps
- Data management is a major road block to progress
  - Urgently need better LIMS and IT infrastructure to support this
  - User friendly analysis tools would unlock local data use
- Not enough attention is being paid to local use of data
- More focus on the local situation will improve uptake and usefulness of global surveillance

Thanks for listening: any questions?

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https://www.ndm.ox.ac.uk/team/paul-turner

www.webbertraining.com/schedulep1.php

February 27, 2024	*(European Teleclass)* **A DRIVE TO SURVIVE: COVID-19 IMPLICATIONS FOR SYSTEMIC RESILIENCE ON ETHICS, DATA SCIENCE AND RISK-MANAGEMENT** Speaker: **Prof. Andro Košec**, University of Zagreb, Croatia
February 29, 2024	**INFECTION PREVENTION THROUGH THE LENS OF IMPLEMENTATION SCIENCE** Speaker: **Dr. Mireille Dekke**, Amsterdam University Medical Center, Netherlands
March 5, 2024	*(FREE Teleclass ... Denver Russell Memorial Teleclass Lecture)* **WATER AS A RISK OF HEALTHCARE-ASSOCIATED INFECTION** Speaker: **Prof. Jon Otter**, Imperial College London
March 7, 2024	*(FREE Teleclass)* **INFECTION PREVENTION AND CONTROL CERTIFICATION: OBTAINING YOUR ENTRY LEVEL IPC CERTIFICATION THROUGH CBIC** Speaker: **Jessica Dangles**, Certification Board of Infection Prevention and Control
March 14, 2024	**COVID-19 PREPAREDNESS – WHAT WENT WRONG? WHAT ARE THE NEXT STEPS? THE POINT OF VIEW OF A BIOMEDICAL ENGINEER**

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