AMR Surveillance, and Data Utilization for Healthcare and Public Health Decisions

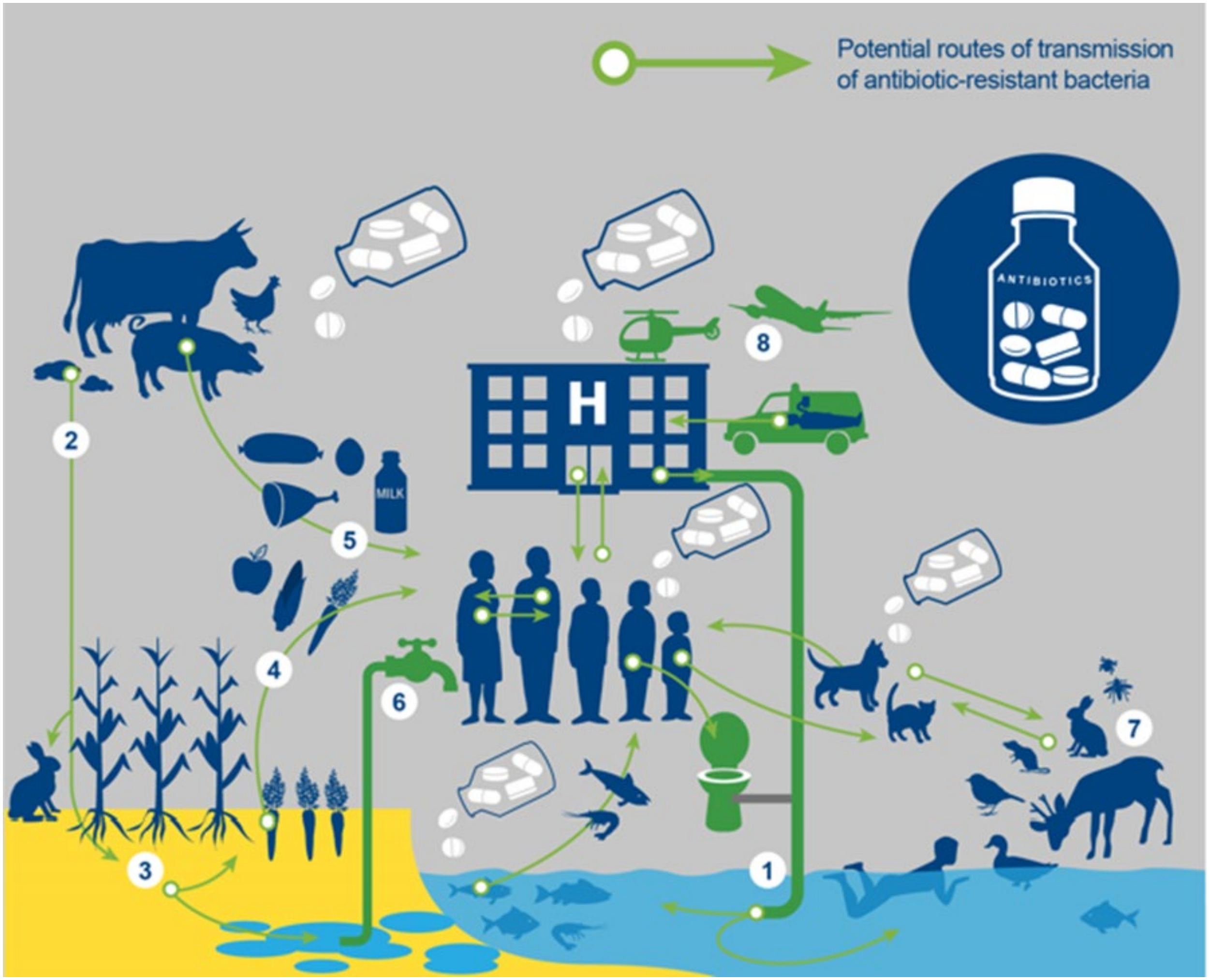
Dr. Lillian Musila
Research Director, MicroHub Kericho
WRAIR-A, KENYA

ASLM AMR Community of Practice (CoP) Webinar Series
August 2025

WRAIR
Walter Reed Army Institute of Research
Defense Health • Global Health

Disclaimer

Antibiotics - One Health



QUADRIPARTITE

1. Food and Agriculture Organization (FAO)
2. United Nations Environment Programme (UNEP)
3. World Health Organization (WHO)
4. World Organisation for Animal Health (WOAH)

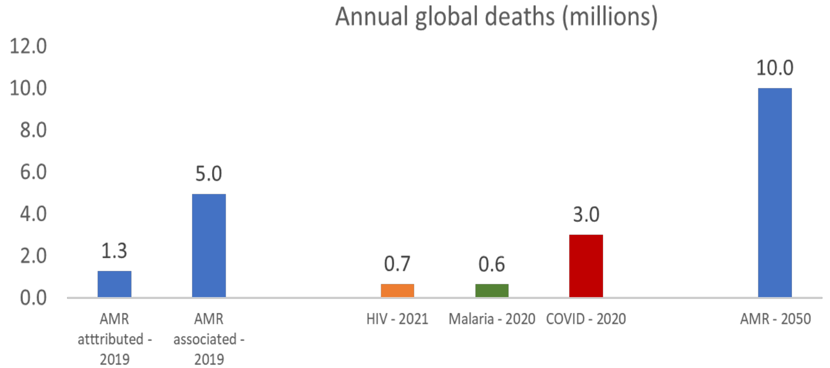
‘ ….Working to preserve antimicrobial efficacy and ensure **sustainable and equitable access** to antimicrobials for responsible and prudent use in human, animal and plant health…..”

Global burden of AMR

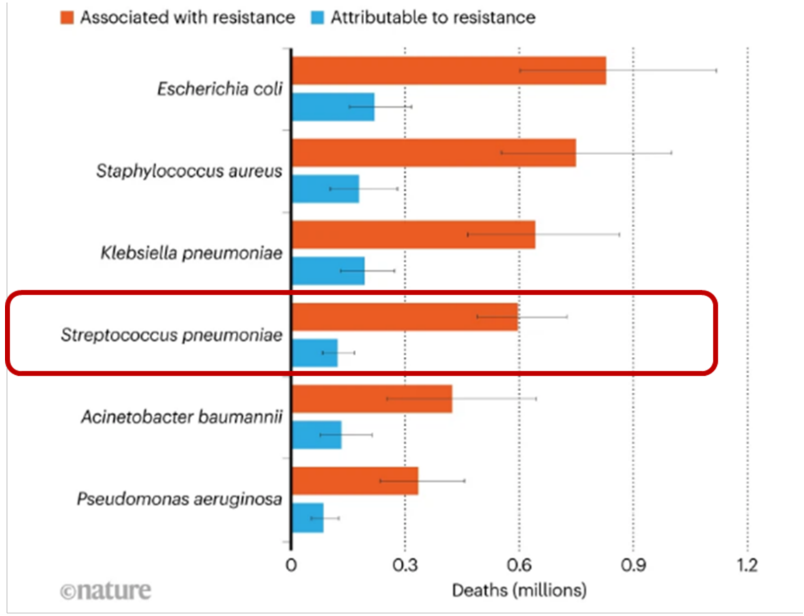
World Health Organization - "one of the biggest threats to global health, food security and development today"

- **Murray et al Lancet, 2022**: Causes more deaths than **HIV-AIDS** and Malaria combined
  - **1.27 million** direct deaths in 2019, **5 million** associated with AMR
- 10 million deaths by 2050

- 6 organisms responsible for **80%** of the 1.27 million deaths
- Highest attributable deaths in **Sub Saharan Africa**
- **S. pneumoniae -** Vaccine preventable, highest killer in SSA



World Health Organization (WHO), Murray et al 2021, O'Neil review , 2019



(Murray et al, Lancet 2021)

Data sets for Lancet 2022. **

- 23 pathogens and 88 pathogen–drug combinations in 204 countries and territories in 2019.
- Systematic literature reviews
- Hospital systems, surveillance systems, and other sources 471 million individual records or isolates and 7585 study-location-years.
- Predictive statistical modelling

*****Least data from S. Saharan Africa***

Questions AMR surveillance can address

"You can't manage what you don't measure" - Peter Drucker

Clinical

- What bacteria are causing infections and what are their drug-resistance patterns (baseline/health priorities)?
- Are the current antibiotics recommended for treatment of key pathogens effective and are we using our antibiotics responsibly?
- Can we detect and manage outbreaks in hospitals?
- Are our IPC measures effective?

Genetic

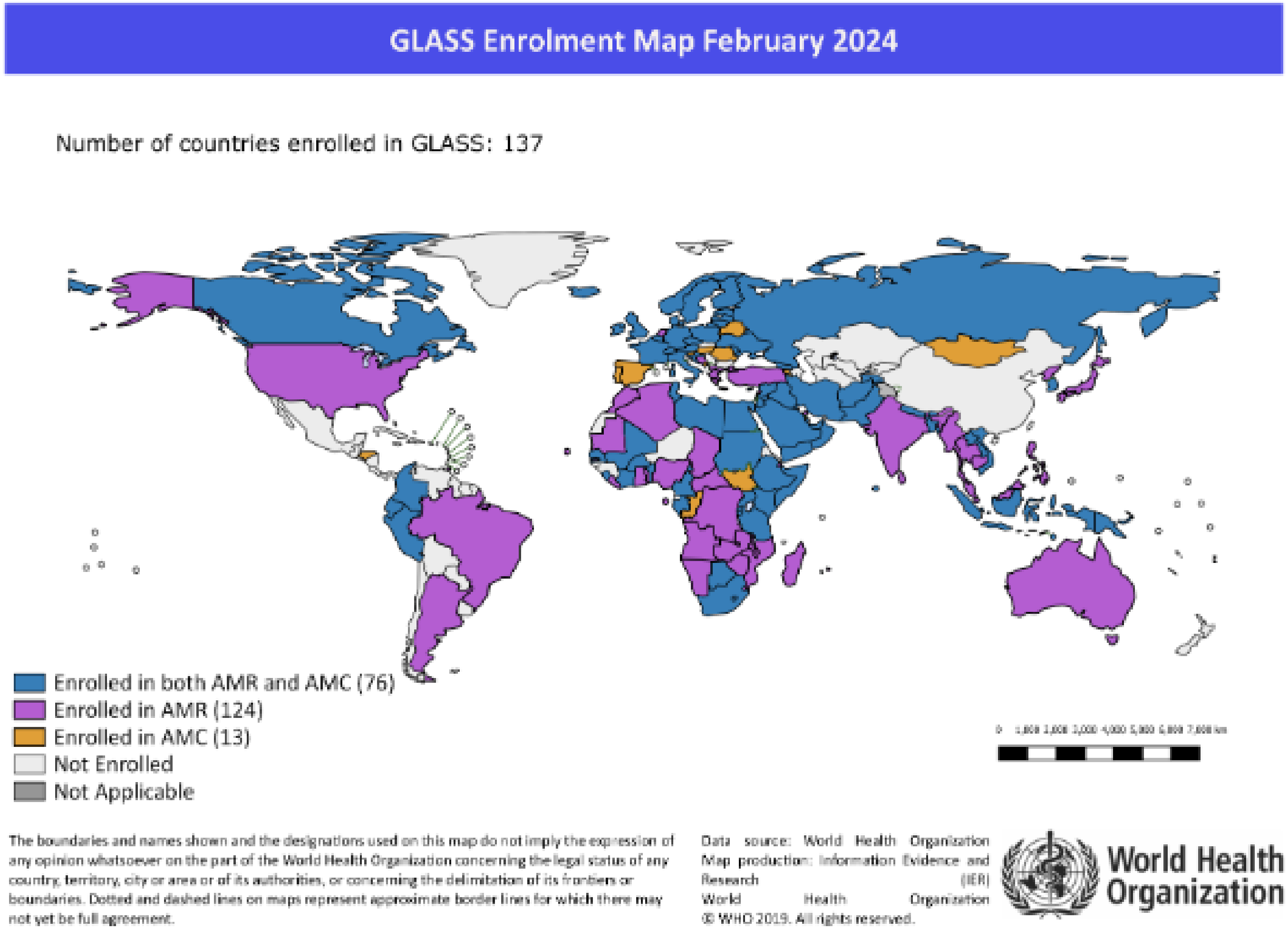
- What are the strains and drug resistance profiles of the bacteria causing infections?
- Can we identify emerging strains, resistance patterns/genes.
- Are vaccines effective against our endemic strains

One Health

- What is the main driver of human infections?
- What role does the environment and animals play in AMR?
- Can we identify the risks and drivers of AMR
- Do MDR bacterial strains move from animals to humans to the environment?


https://www.ripleys.com/weird-news/or-not-ostriches/

WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS)



Data source: World Health Organization
Map production: Information Evidence and Research (IER)
World Health Organization

NATIONAL ACTION PLANS

- accurate and reliable information
- lack of formal framework for data collection and sharing between laboratories
- **limited number of enrolment by LICs and LMICs**
- Only 11% of countries have funding to implement NAP
  - limited financial or human resources
  - insufficient capacity
  - varying levels of political support. (Lancet 2024)

Kenya AMR policy and surveillance documents


REPUBLIC OF KENYA

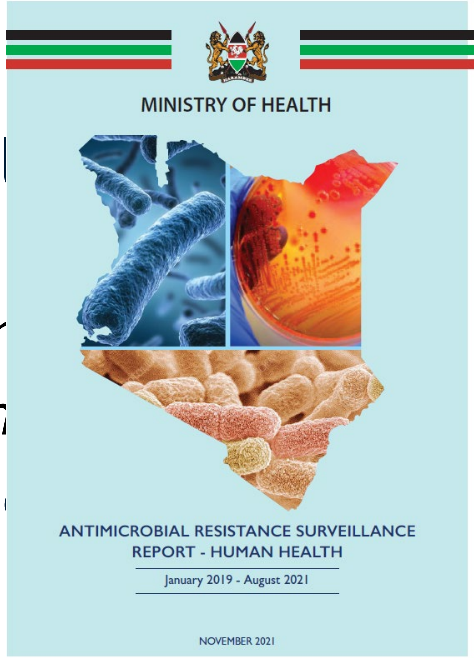
NATIONAL ACTION PLAN ON PREVENTION AND CONTAINMENT OF ANTIMICROBIAL RESISTANCE

2017 -2022

JUNE 2017


Ministry of Health

National Antimicrobial Resistance Surveillance


MINISTRY OF HEALTH

ANTIMICROBIAL RESISTANCE SURVEILLANCE REPORT - HUMAN HEALTH

January 2019 - August 2021

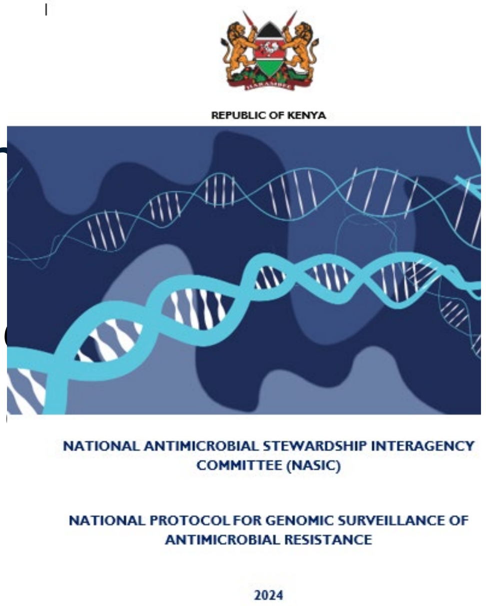
NOVEMBER 2021


REPUBLIC OF KENYA

NATIONAL ACTION PLAN ON PREVENTION AND CONTAINMENT OF

ANTIMICROBIAL RESISTANCE

2023-2027


REPUBLIC OF KENYA

NATIONAL ANTIMICROBIAL STEWARDSHIP INTERAGENCY COMMITTEE (NASIC)

NATIONAL PROTOCOL FOR GENOMIC SURVEILLANCE OF ANTIMICROBIAL RESISTANCE

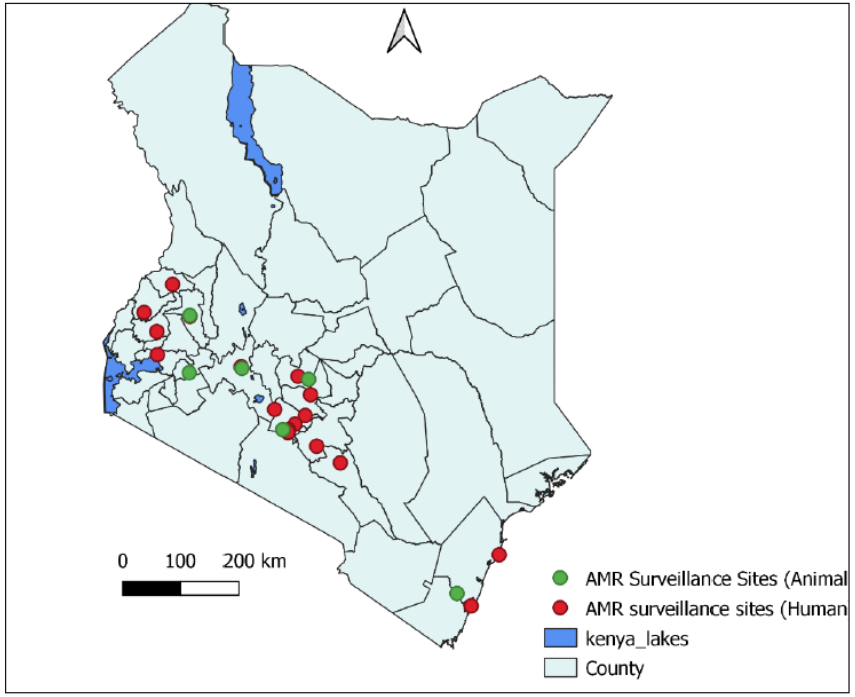
2024

National One Health surveillance sites – Kenya

AMR National Reference Centres

National Public Health Labs & Central Veterinary Lab as reference centres

Sentinel sites overlapping Animal (6), Human health 17



Staphylococcus aureus - antibiogram

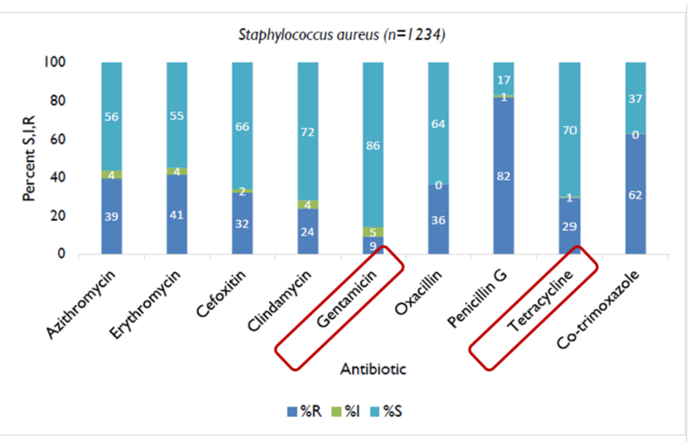


Figure 7. Antimicrobial susceptibility pattern for Staphylococcus aureus (human health)

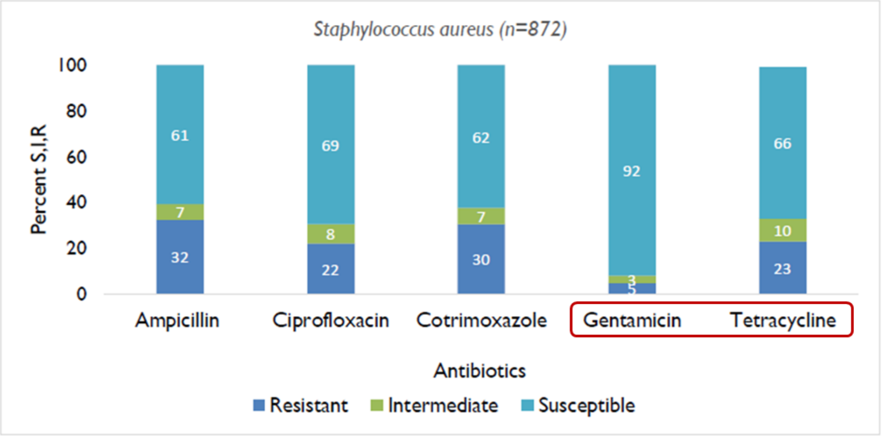


Figure 8. Antimicrobial susceptibility pattern for Staphylococcus aureus isolated from animal health clinical specimens

Integrated information management system for AMR in Human Health & Animal Health

AMR Surveillance

AMR SITES

MFLCODE	NAME
14947	KITALE DISTRICT HOSPITAL
11555	MALINDI DISTRICT HOSPITAL
12438	MACHAKOS LEVEL 5 HOSPITAL

AMR Tasks List

- AMR Weekly Data
- Antibiogram General Report
- Antibiogram Report By Sample Type
- AMR Reports

AMR Surveillance Search:

Site	AMR#	DatePosted	Gender	Age	Specimen	Diagnosis	Method	Organism	Type	
Malindi District Hospital(11555)		02/26/2019 12:00:00 AM	F	17 YEARS	PUS		MIC_SENSITIVITY	Pseudomonas aeruginosa	GRAM_NEG	
Malindi District Hospital(11555)		02/26/2019 12:00:00 AM	F	0 YEARS	BLOOD		DDA_SENSITIVITY	Acinetobacter baumannii	GRAM_NEG	
Kitale District Hospital(14947)		03/07/2019 12:00:00 AM	M	36	STOOL	ACUTE DIARRHOEAL ILLNESS	DDA_SENSITIVITY	Escherichia coli	PARASITE	Cefta
Kitale District Hospital(14947)		03/07/2019 12:00:00 AM	M	14	STOOL	GASTROENTERITIS	DDA_SENSITIVITY	Escherichia coli	PARASITE	Ceft
Kitale District Hospital(14947)		03/07/2019 12:00:00 AM	F	21			DDA_SENSITIVITY	Staphylococcus aureus	GRAM_POS	
Kitale District Hospital(14947)		03/07/2019 12:00:00 AM	F	27	HVS		DDA_SENSITIVITY	Escherichia coli	PARASITE	
Kitale District Hospital(14947)		03/07/2019 12:00:00 AM	M	23	SWAB	surgical site infection	DDA_SENSITIVITY	Staphylococcus aureus	GRAM_POS	
Kitale District Hospital(14947)		03/07/2019 12:00:00 AM	F	43	SPUTUM	bronciectasis	DDA_SENSITIVITY	Klebsiella pneumoniae	GRAM_NEG	Ampicil

Showing 1 to 1,121 of 1,121 entries

Welcome Dr. Romona Ndanyi : Superuser

Diagnostic Services and Efficacy Trials - Administration/OiC

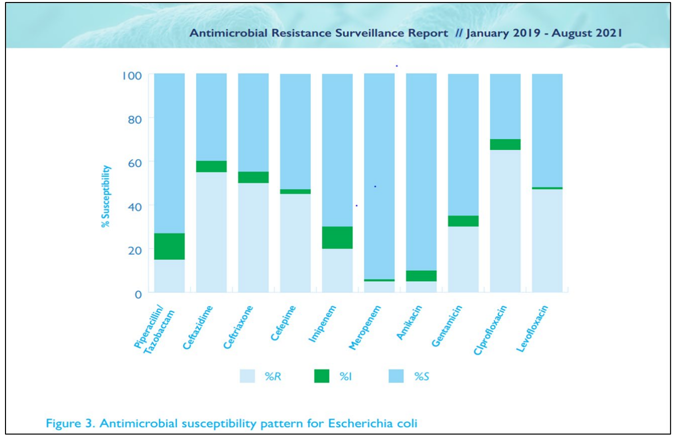
Version 2.1.0

Report

Date Received: from 04-08-2020 to 04-08-2021
Laboratory: Central Veterinary Laboratories
Testing Lab: CVL Central Veterinary Laboratories
Section: Bacteriology
Sampling purpose: ANTI-MICROBIAL SUSCEPTIBILITY TEST ☑ Purpose in report
Sampling plan: 2019 4 AMR SURVEILLANCE PILOT STUDY ☑ Plan in report

Central Data Warehouse

Human Health Reports

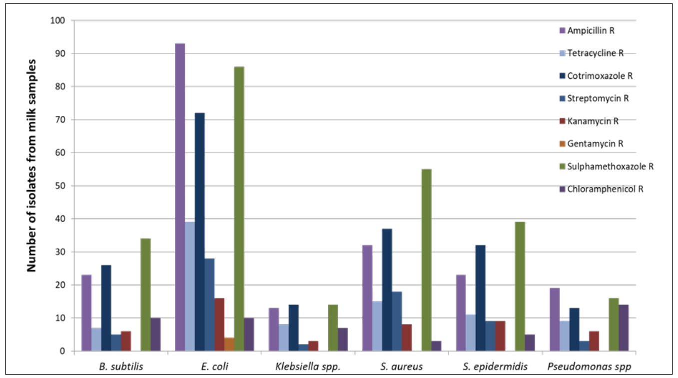


Antimicrobial Resistance Surveillance Report // January 2019 - August 2021

Figure 3. Antimicrobial susceptibility pattern for Escherichia coli

AMR dashboards

Animal Health Reports



KEMRI/WRAIR-Africa surveillance strategy

Active surveillance in **10 counties** across Kenya

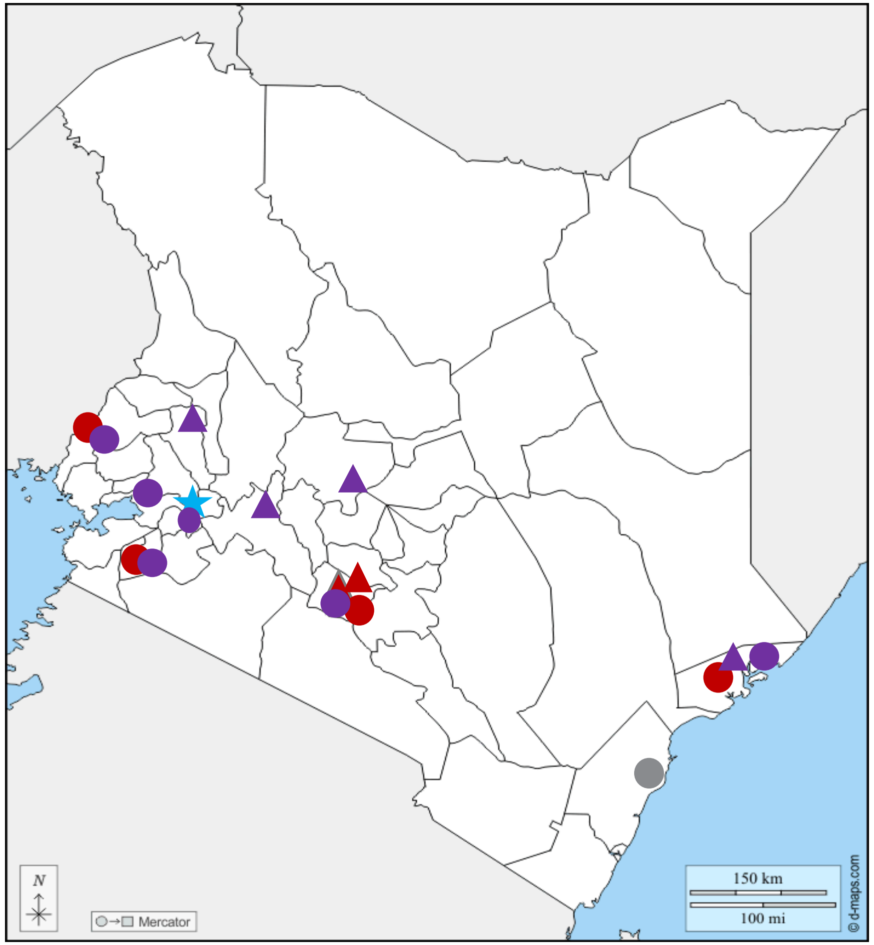
Public, private (L4/L5) health facility

Central lab in Kericho, Kenya

ESKAPE-E pathogens, Candida spp (10 years)

Enteric pathogens (15 years)

Phenotypic, molecular and genomic surveillance (ID, AST, ARG, STs, virulence)



● Enteric sites ▲Military sites ● AMR ★ Laboratory

Methods for identification, AST, typing, virulence and resistance gene detection of bacterial pathogens

Identification

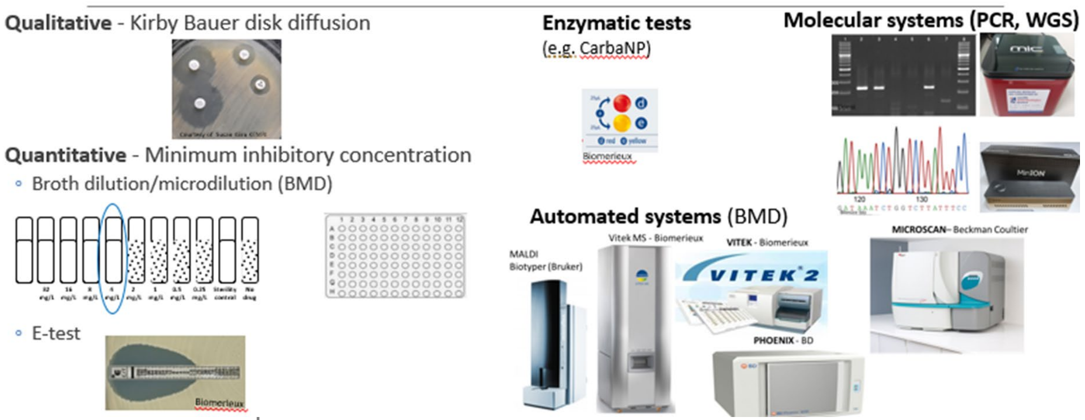
- Culture
- Microscopy and staining
- Biochemical
  - Manual
  - Automated
- Proteomics (MALDI-ToF)

Genomic characterization

- PCR/ Whole genome sequencing
  - Species/strain specific detection
  - 16srRNA
- Metagenomics

Typing

- Molecular (typing)
- Serology
  - Salmonella
- Virulence factors
  - E.coli ETEC



PCR

Thermocycler

Gel electrophoresis

Ibright imager

Mic qPCR

Next generation sequencing and bioinformatics

Kingfisher Automated DNA extraction robot

Tapestation Agilent 4200 (Fragment analysis

Nanopore minion mk1b/mk1c

Illumina Nextseq 1000

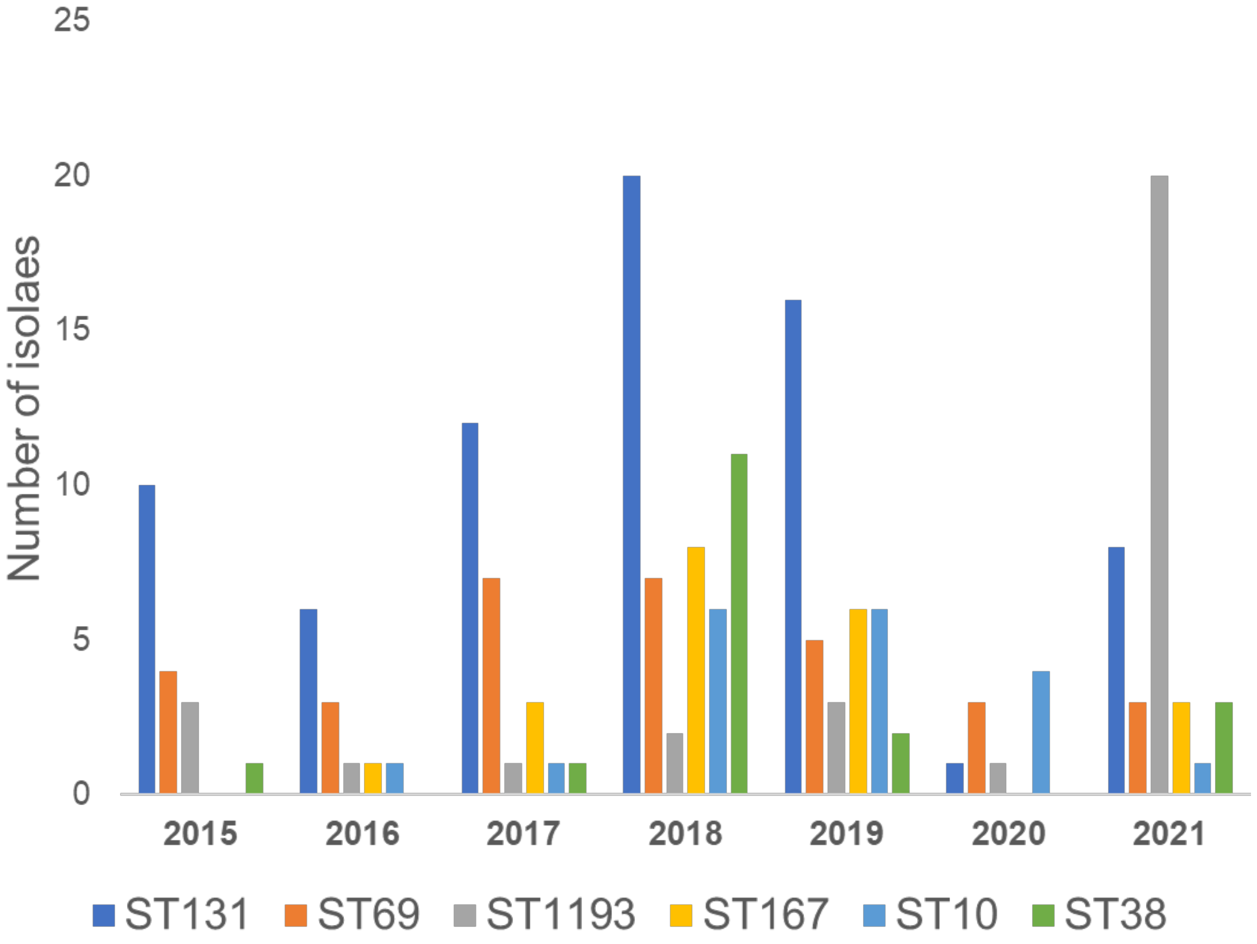
Surveillance strategies and methodologies for AMR surveillance and how the data can drive decision-making

Use cases for

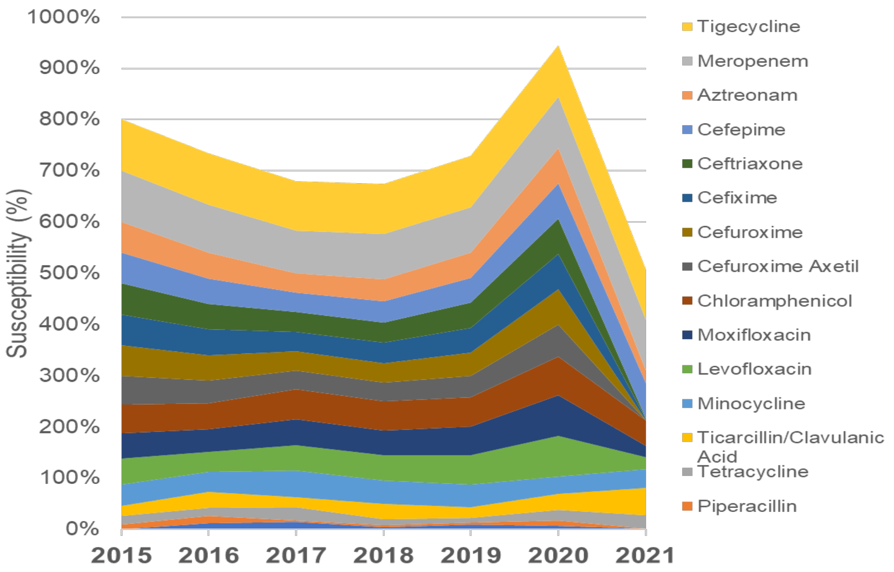
1. Track epidemiology and evolution of bacterial strain types and resistant strains.
2. Resistance gene detection, location and spread
3. Outbreak detection and response
4. AMR sources and transmission cycles
5. Artificial intelligence and AMR

Use Case 1: Track epidemiology and evolution of bacterial strain types and resistant strains

Temporal changes in *E.coli* strain types 2015 - 2021



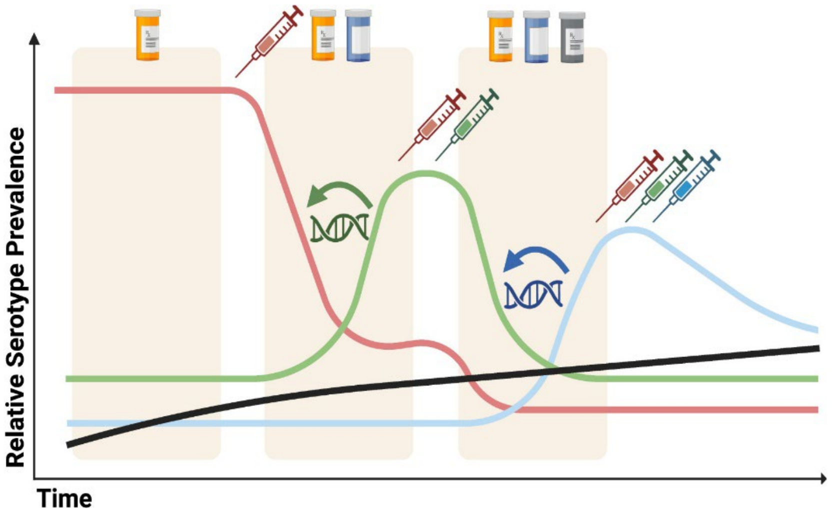
Strain type	# of isolates (n=378)	Risk status	Global/regional/local strain
ST 131	19.3% (n=73)	High risk	Most dominant global strain
ST 69	8.5% (n=32)	Pandemic high risk	Global
ST 1193	8.2% (n=31)	High risk	Second dominant global
ST 167	5.6% (n=21)	High risk	Emerging Global
ST 10	5.0% (n=19)	High risk	Global
ST 38	4.8% (n=18)	High risk	Global
Others	48.7% (n=184)	N/A	N/A



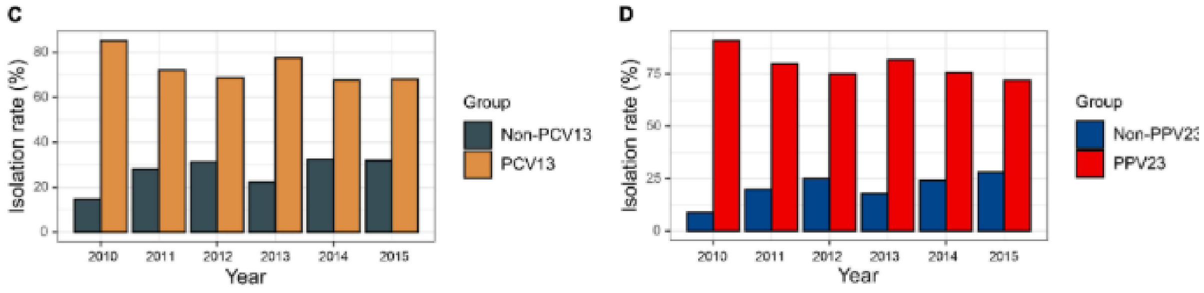
Vaccines and serotype replacement in Streptococcus pneumoniae

- Pneumococcal vaccines have been successful but led to the increase in non-vaccine serotypes (NVTs), partially offsetting the total disease reduction
- **Serotype replacement**, is due to the greater serotype diversity in developing countries The NVTs
  - result in increased transmission and disease
  - Reduces the effectiveness of the currently available PCVs.
  - Are highly invasive in nature and have high levels of resistance to antibiotic

- Surveillance key to identify new emerging serotypes and gain insights into the evolving epidemiology of *S. pneumonia*



Cell Chemical Biology, Volume 31, Issue 2, 15 February 2024, Pages 185-186

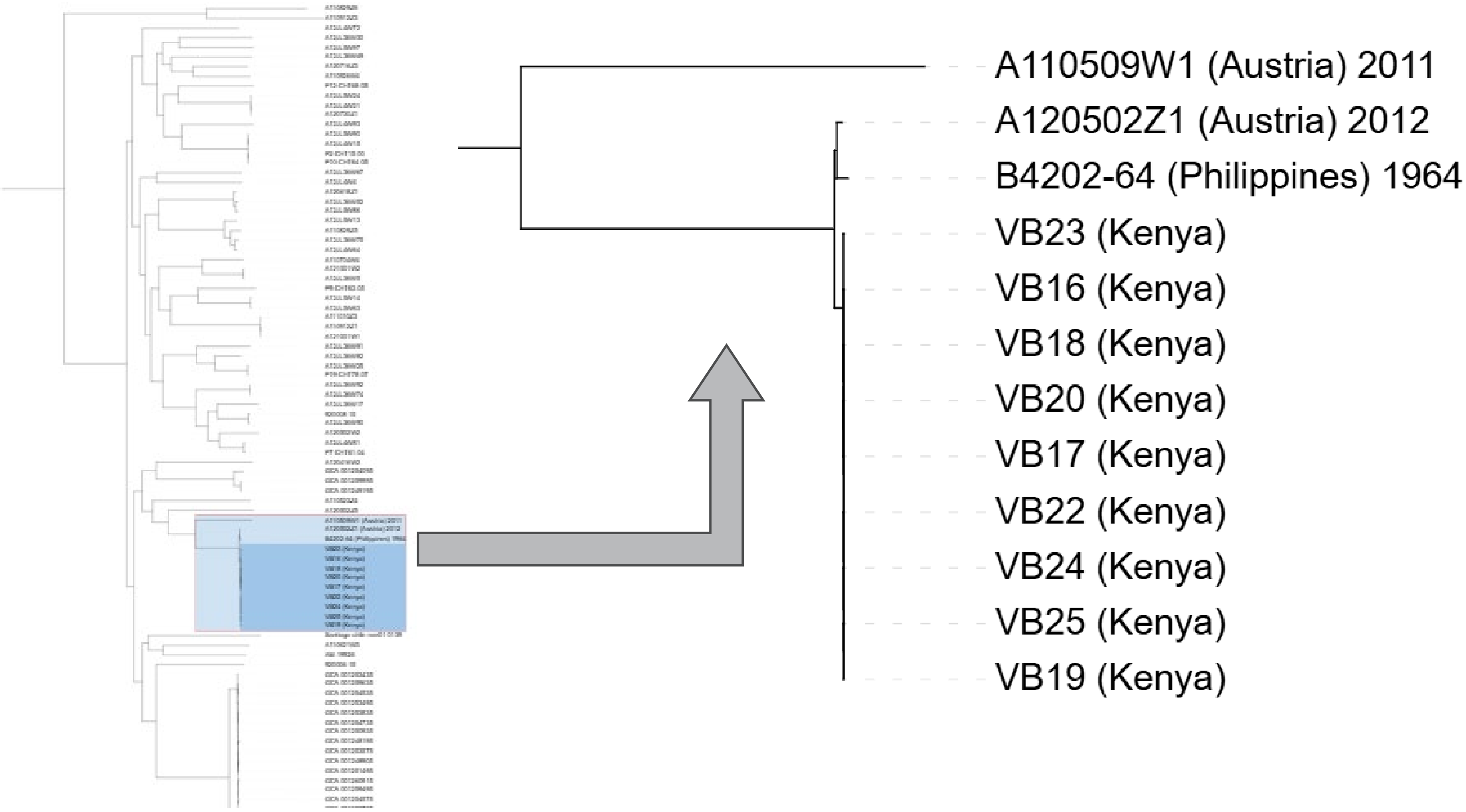


Group	2010	2011	2012	2013	2014	2015	*P* value
Non-PCV13	14.7	28	31.3	22.3	32.43	32	0.2053
PCV13	85.3	72	68.8	77.7	67.57	68	

Group	2010	2011	2012	2013	2014	2015	*P* value
Non-PPV23	8.8	20	25	18.1	24.3	28	0.1114
PPV23	91.2	80	75	81.9	75.7	72	

Front. Microbiol., 13 January 2022 Sec. Antimicrobials, Resistance and Chemotherapy Volume 12 - 2021 |https://doi.org/10.3389/fmicb.2021.798750

Origins of *V. cholerae* ST-8 emergent strains in *W. Kenya* linked to Austria

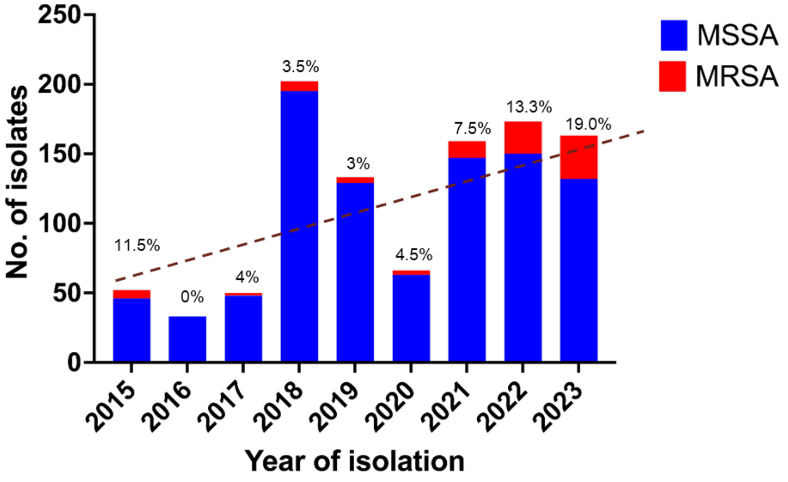


- Outbreak isolates in 2019
- During an international training exercise
- Carry carbapenem (*varG*) and colistin (*almE, almF, almG*) resistance genes

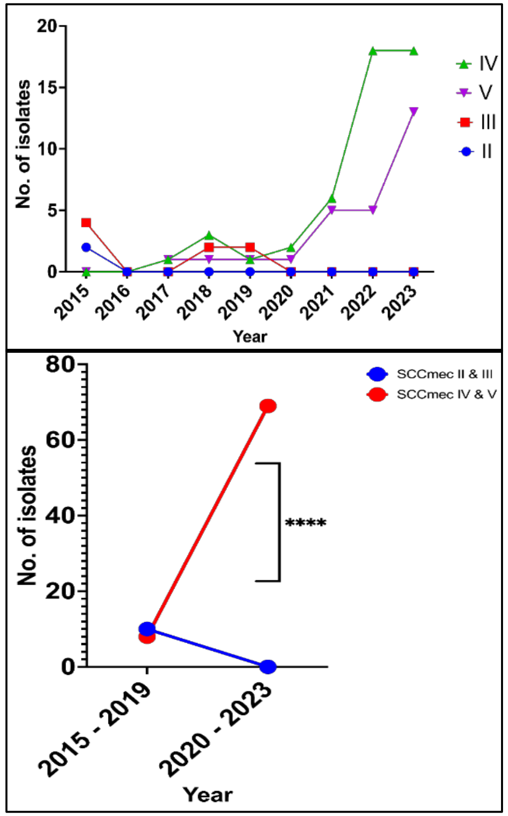
Use case 2: Resistance gene detection, location and spread

Trends: MRSA Temporal shifts from hospital to community-associated high-risk strains

MRSA rates show general increase over the years

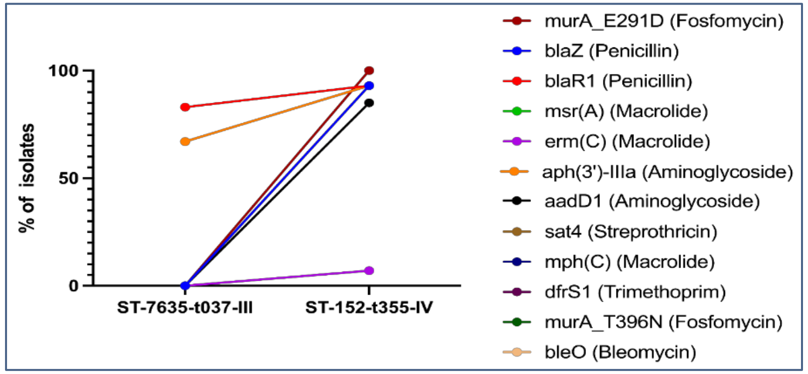


Temporal shifts in SCC*mec* types

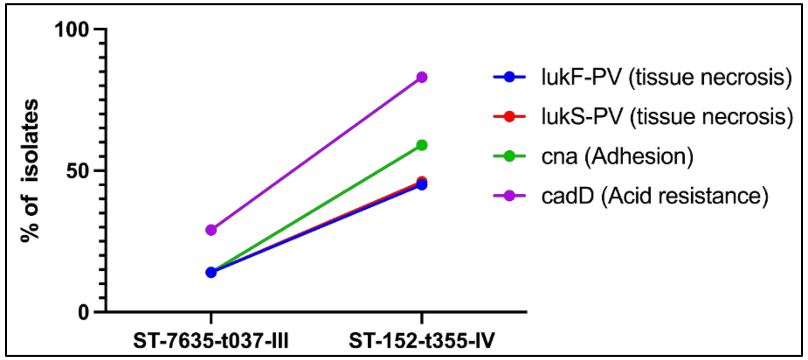


HA-ST-7635-t037-SCCmec III → CA-ST-152-t355-SCCmec IV

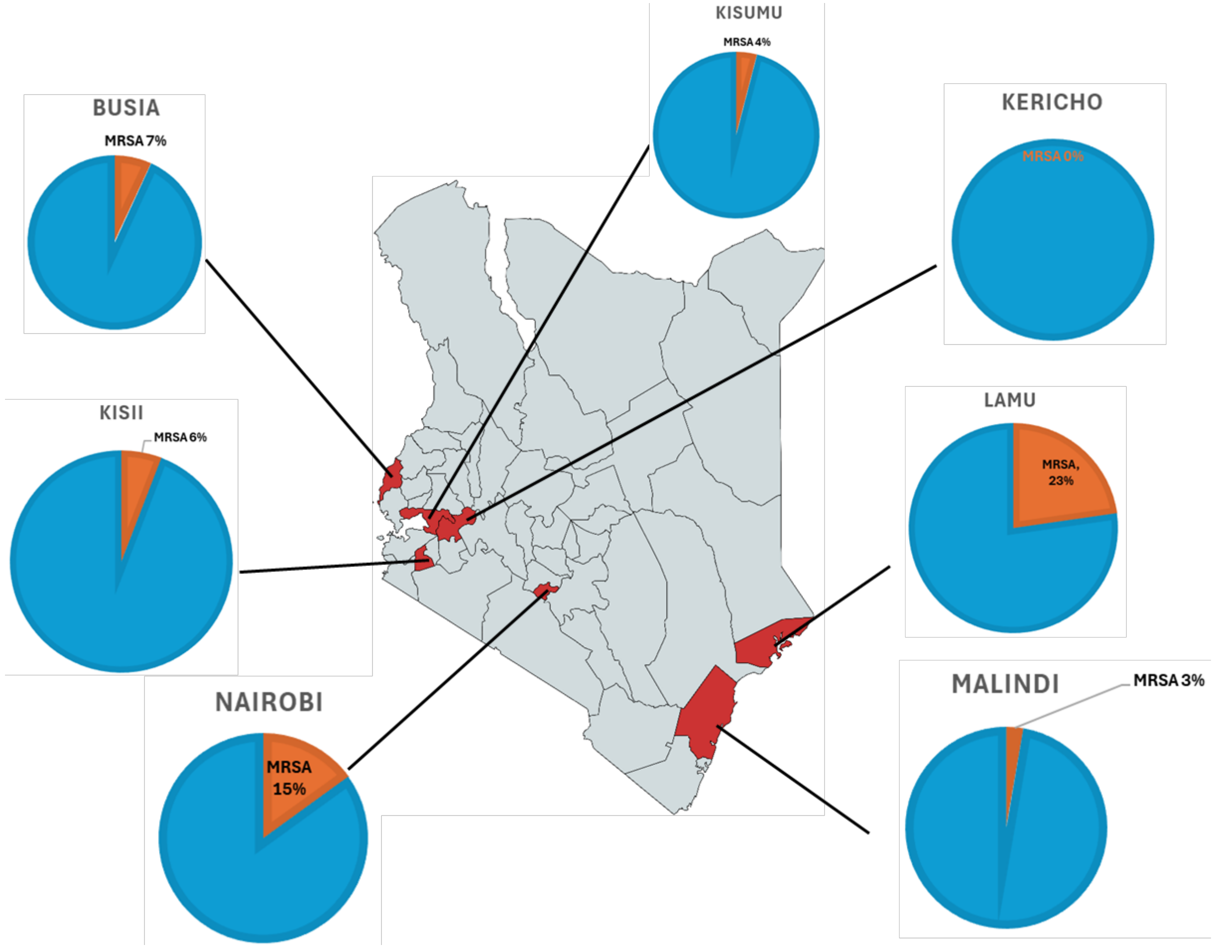
ARGs increase due to population shift



Virulence increase due to population shift



MRSA Hotspots in Kenya

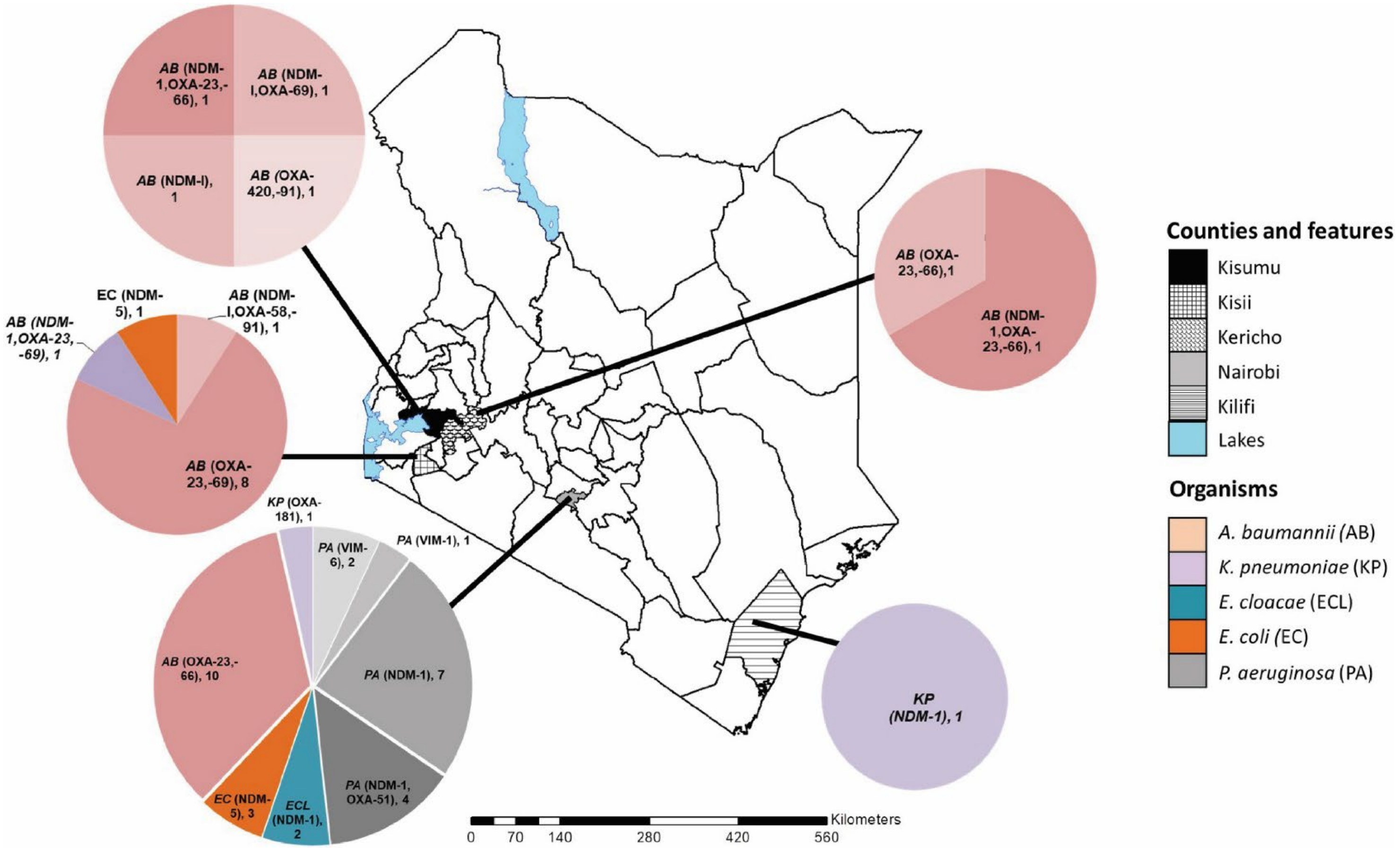


- Methicillin-resistant *Staphylococcus aureus* (MRSA) are resistant to B-lactams antibiotics used to treat ordinary staph infections.

- High proportion: Nairobi and coastal regions

- Low proportion in Western Kenya

The geographical distribution of the carbapenem non-susceptible gram-negative bacteria and carbapenemase genes in five Kenyan counties



Emerging threats: Novel genotypes and first reports

Novel strain types

- *E. faecalis* (ST-1907 & ST-1908)
- *E. faecium* (ST-2672)
- *S. aureus* (ST-9818 & ST-9819)

Novel SCC*mec* type in MRSA

- IS-1272-mecA-ccr5 = SCC*mec* type XVI

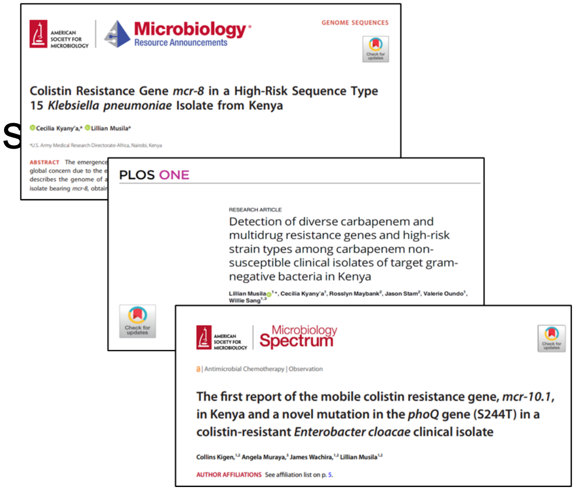
Novel S244T gene mutation in phoQ conferring colistin resistance

- New mutations causing resistnce

Putative novel *mcr* gene

- *mcr-3* like gene (1600bp) in a colistin resistant *A. hydrophila*

- *mcr-8.1* (Colistin resistance)
- *mcr-10.1* (Colistin resistance)
- *bla*$_{\text{NDM-5}}$ (Carbapenem resistance)
- *bla*$_{\text{NDM-6}}$ (Carbapenem resistance)
- **Cefiderocol** resistance genes (ftsI_N337NYRIN)
  - 5th line cephalosporin – not introduced yet.


AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Colistin Resistance Gene *mcr-8* in a High-Risk Sequence Type 15 *Klebsiella pneumoniae* Isolate from Kenya

Cecilia Kyany'a,[a] Lillian Musila[a]

[a]U.S. Army Medical Research Directorate-Africa, Nairobi, Kenya

ABSTRACT The emergence
global concern due to the
describes the genome of
isolate bearing *mcr-8*, obtai

PLOS ONE

RESEARCH ARTICLE

Detection of diverse carbapenem and multidrug resistance genes and high-risk strain types among carbapenem non-susceptible clinical isolates of target gram-negative bacteria in Kenya

Lillian Musila[1*], Cecilia Kyany'a[1], Rosslyn Maybank[2], Jason Stam[2], Valerie Oundo[1], Willie Sang[1,3]

AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Spectrum

| Antimicrobial Chemotherapy | Observation

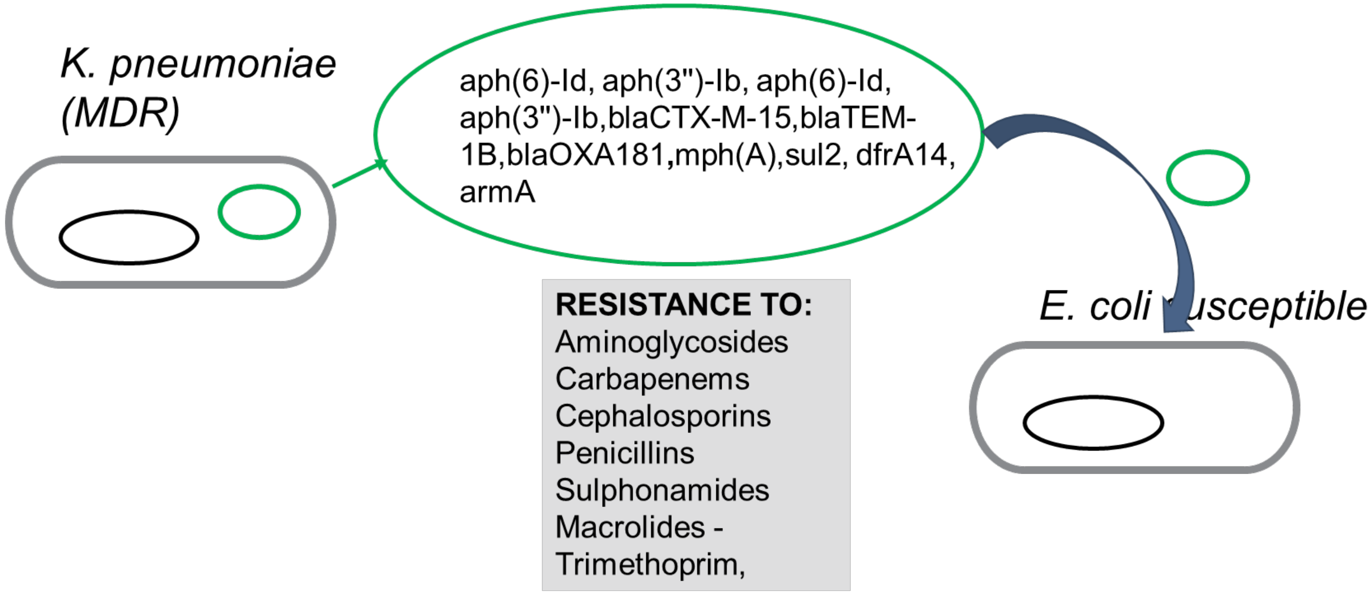
The first report of the mobile colistin resistance gene, *mcr-10.1*, in Kenya and a novel mutation in the *phoQ* gene (S244T) in a colistin-resistant *Enterobacter cloacae* clinical isolate

Collins Kigen,[1,2] Angela Muraya,[3] James Wachira,[1,2] Lillian Musila[1,2]

AUTHOR AFFILIATIONS See affiliation list on p. 5.

How is resistance spreading? Mobile antimicrobial resistance genes

- Conjugative plasmids play a key role in the dissemination of antimicrobial resistance (AMR) genes across bacterial pathogens.
- Plasmids encoding antibiotic resistance tend to be **mobile** and have **broader host** ranges than the others. Coluzzi et al Molecular Biology and Evolution, Volume 42, Issue 3, March 2025 msaf060, https://doi.org/10.1093/molbev/msaf060
- AMR is facilitated by the abundance of transposable elements and integrons in AMR plasmids



K. pneumoniae *(MDR)*

aph(6)-Id, aph(3")-Ib, aph(6)-Id, aph(3")-Ib,blaCTX-M-15,blaTEM-1B,blaOXA181,mph(A),sul2, dfrA14, armA

RESISTANCE TO:
Aminoglycosides
Carbapenems
Cephalosporins
Penicillins
Sulphonamides
Macrolides -
Trimethoprim,

E. coli susceptible

*“The ability of AMR plasmids to transfer independently presents a serious challenge for epidemiologists attempting to monitor the prevalence and spread of AMR using genomics approaches, because the **patterns of transmission of AMR plasmids, and AMR genes, might be distinct from those of the host bacteria**”* JPIAMR

Plasmid – replicon surveillance

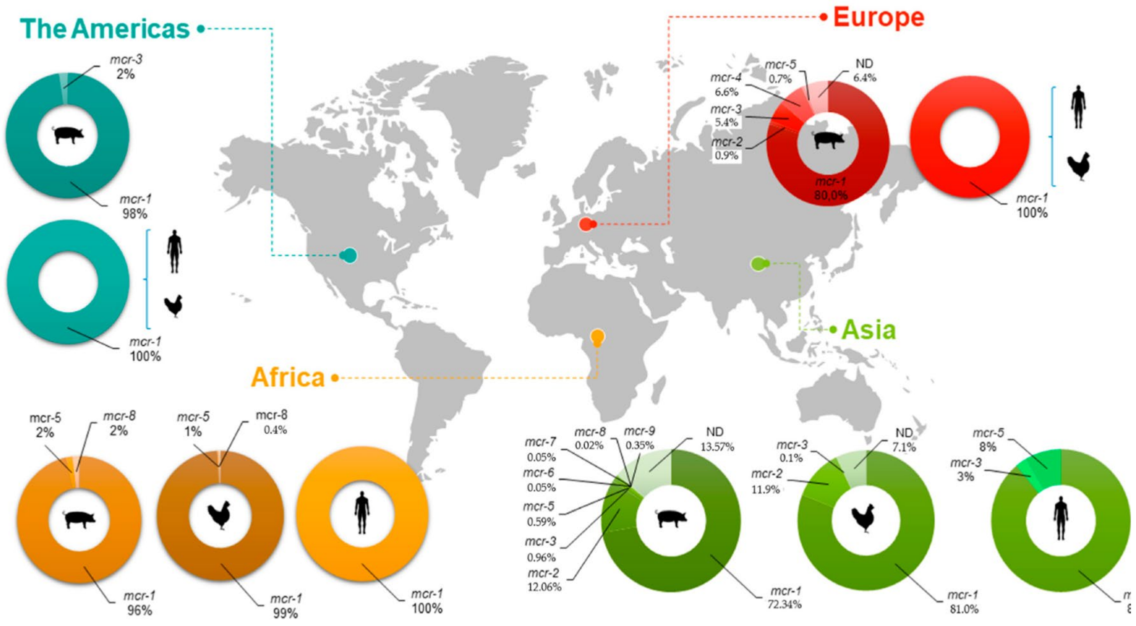
Highly MDR isolates

Species	Total
Pseudomonas aeruginosa	6
Acinetobacter baumannii	9
Escherichia coli	5
Klebsiella pneumoniae	4
Enterobacter spp	4

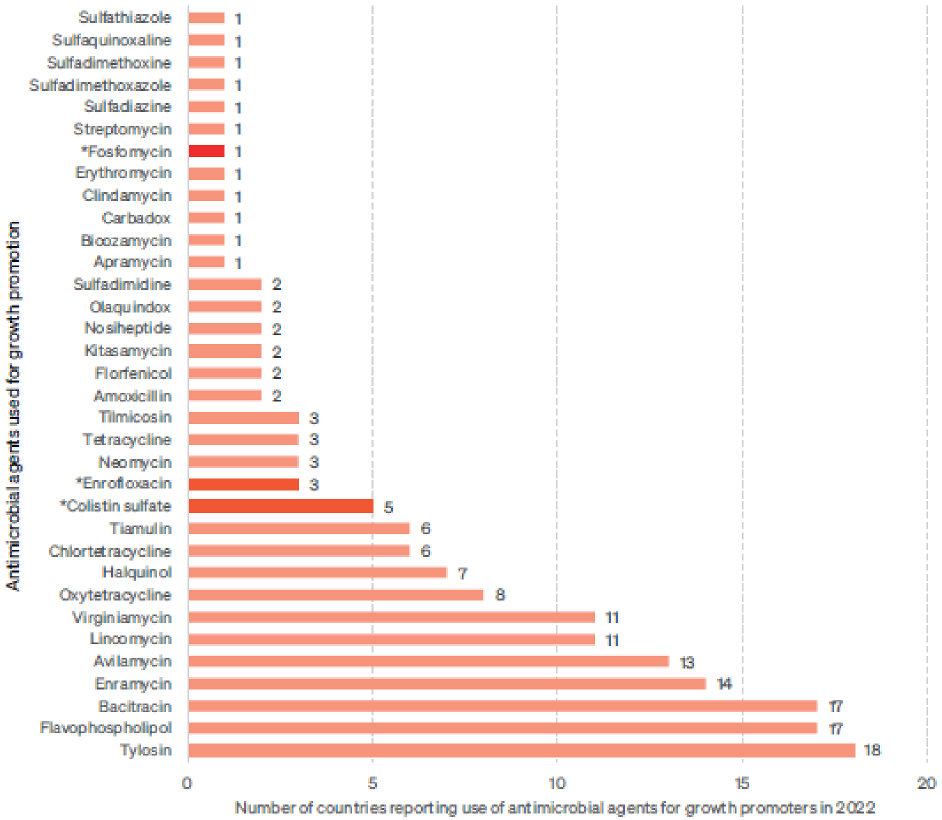
Species	# plasmids	Replicon type
E. coli	4	IncA/C2_1, IncFIB(AP001918)_1, IncFIA_1, IncFII(pRSB107)_1_pRSB107,Col156_1, IncI1_1_Alpha, ColRNAI_1, ColRNAI_1, ColRNAI_1
E. coli	4	ColRNAI_1, Col8282_1, IncFII(pRSB107)_1_pRSB107, IncFIB(AP001918)1, Col156_1, IncFIA_1, IncFII(pCoo)_1_pCoo
E. coli	1	IncFIA_1, IncFII(pRSB107)_1_pRSB107, IncFIB(AP001918)_1
E. coli	3	IncFIB(AP001918)_1, IncFIA_1, IncFII(pRSB107)_1_pRSB107, IncI2_1, IncFII_1
K. pneumoniae	4	IncFIB(Mar)_1_pNDM-Mar, IncHI1B_1_pNDM-MAR, IncFIB(pQil)_1_pQil IncFII(pAMA1167-NDM-5),1_pAMA1167-NDM-5, IncFIA, ColKP3, ColKP3_1
K. pneumoniae	1	IncFIB(pKPHS1)_1_pKPHS1, IncR_1, IncFIA(HI1)_1_HI1
K. pneumoniae	3	IncFIB(K)_1_Kpn3,IncFII_1_pKP91, ColpVC_1, Col(BS512)_1,ColKP3_1,Col440I_1
K. pneumoniae	3	ColKP3_1, Col440I_1, IncFII_1_pKP91, IncFIB(K)_1_Kpn3
E. cloacae	2	IncHI2_1, RepA_1_pKPC-CAV1321, IncHI2A_1,
E. cloacae	1	IncR_1, IncFIA(HI1)_1_HI1,
E. cloacae	2	Col440II_1, ColRNAI_1,ncHI2_1, RepA_1_pKPC-CAV1321, IncHI2A_1
P. aeruginosa	1	Untyped replicons
A. baumannii	4	Untyped replicons
A. baumannii	4	Untyped replicons
A. baumannii	4	Untyped replicons
A. baumannii	2	Untyped replicons
A. baumannii	2	Untyped replicons
A. baumannii	1	Untyped replicons

Plasmid replicons were screened with Plasmidfinder, and AbritAMR was used to examine AMR genes in the plasmids. Mobile elements were screened using the MGEfinder tool.

Worldwide Prevalence of *mcr*-mediated Colistin-Resistance *Escherichia coli* in Isolates of Clinical Samples, Healthy Humans, and Livestock

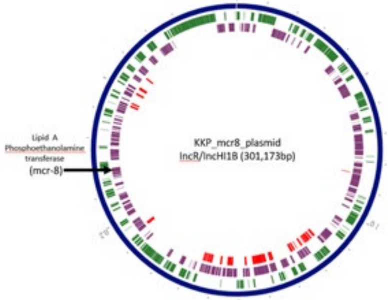


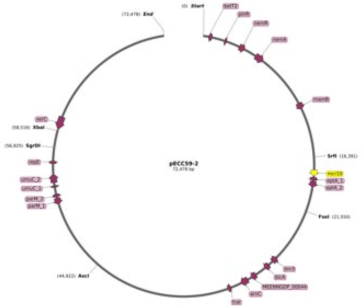
Pathogens 2022, 11(6), 659; https://doi.org/10.3390/pathogens11060659



* The classes in the WHO Medically Important Antimicrobial List should be the highest priority for Members when phasing out the use of antimicrobial agents as growth promoters.

WHOA Annual Report on Antimicrobial Agents Intended for Use in Animals 8th Report

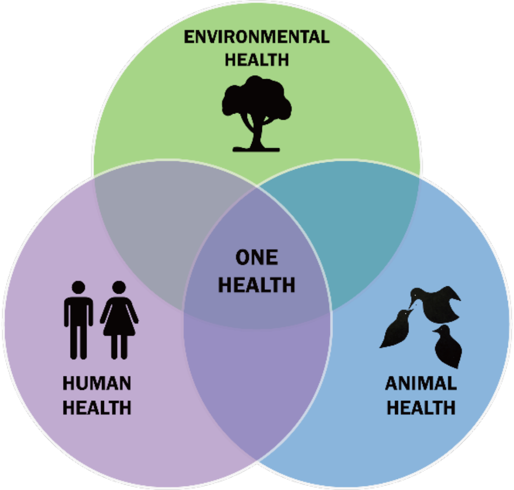


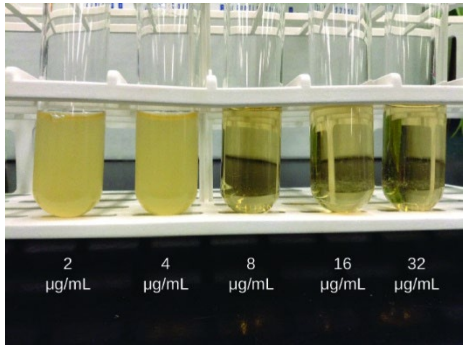


One health surveillance for colistin resistance

1. WRAIR-Africa (KE, UG, TZ)
2. University of Nairobi (UoN) Veterinary college

Escherichia coli, Enterobacter spp., P.aeruginosa and *Klebsiella pneumoniae*



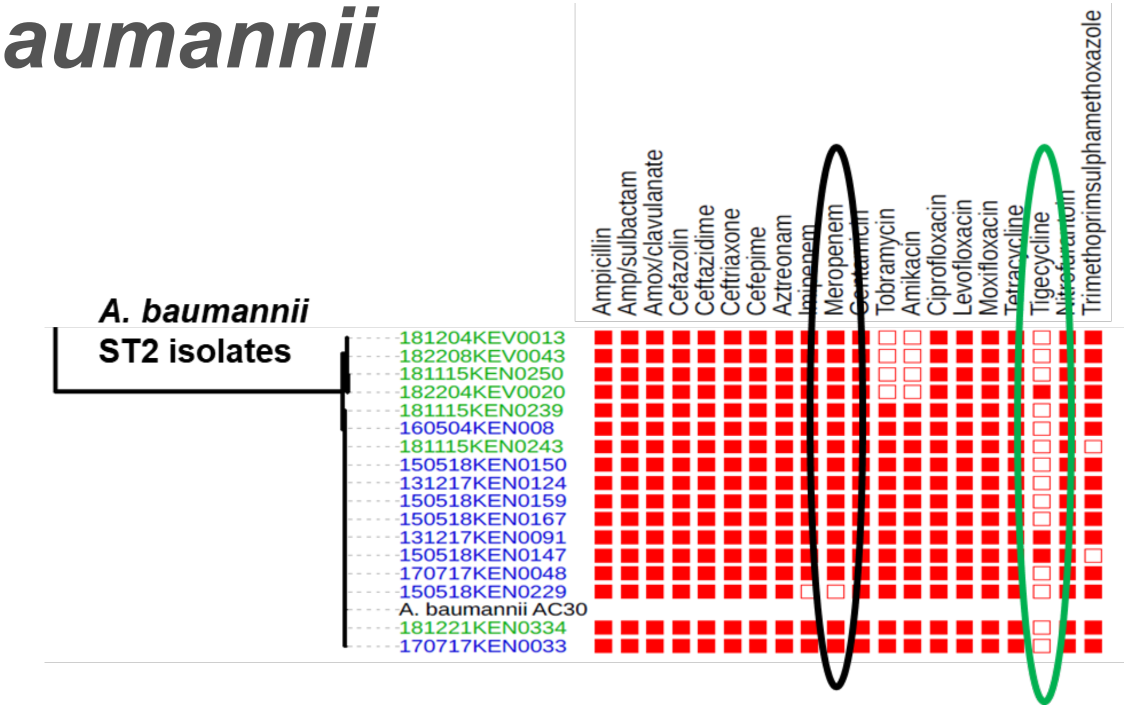


1. *mcr genes*
2. *Chromosomal mutations*
   a) *lpxCAD,*
   b) *pmrAB,*
   c) *phoPQ,*
   d) *mgrB*
   e) *crrB* genes

Use case 3: Outbreak detection

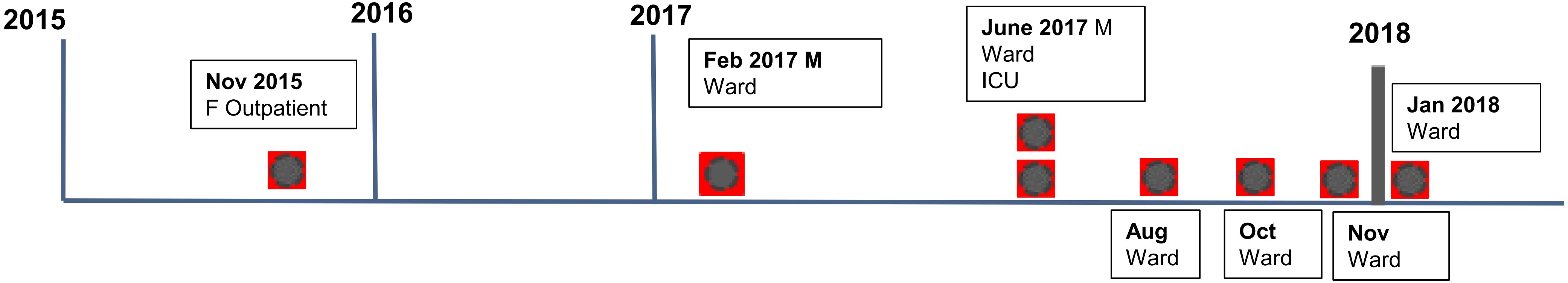
Unchecked outbreak of MDR *Acinetobacter baumannii*

- ST2 - MDR *A. baumannii* outbreak with protracted local transmission
- Carbapenem resistant
- Susceptible only to tigecycline



A. baumannii ST2 isolates

	Ampicillin	Amp/sulbactam	Amox/clavulanate	Cefazolin	Ceftazidime	Ceftriaxone	Cefepime	Aztreonam	Imipenem	Meropenem	Gentamicin	Tobramycin	Amikacin	Ciprofloxacin	Levofloxacin	Moxifloxacin	Tetracycline	Tigecycline	Nitrofurantoin	Trimethoprimsulphamethoxazole
181204KEV0013	■	■	■	■	■	■	■	■	■	■	■	□	□	■	■	■	■	□	■	■
182208KEV0043	■	■	■	■	■	■	■	■	■	■	■	□	□	■	■	■	■	□	■	■
181115KEN0250	■	■	■	■	■	■	■	■	■	■	■	□	□	■	■	■	■	□	■	■
182204KEV0020	■	■	■	■	■	■	■	■	■	■	■	□	□	■	■	■	■	■	■	■
181115KEN0239	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■
160504KEN008	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■
181115KEN0243	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	□
150518KEN0150	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■
131217KEN0124	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■
150518KEN0159	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■
150518KEN0167	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■
131217KEN0091	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
150518KEN0147	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□
170717KEN0048	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■
150518KEN0229	■	■	■	■	■	■	■	■	□	□	■	■	■	■	■	■	■	□	■	■
A. baumannii AC30																				
181221KEN0334	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■
170717KEN0033	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	□	■	■



Nov 2015
F Outpatient

Feb 2017 M
Ward

June 2017 M
Ward
ICU

Aug
Ward

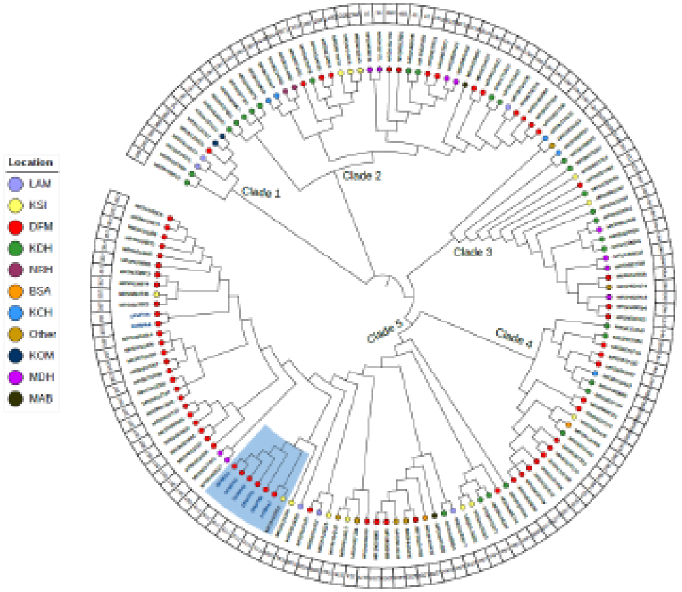
Oct
Ward

Nov
Ward

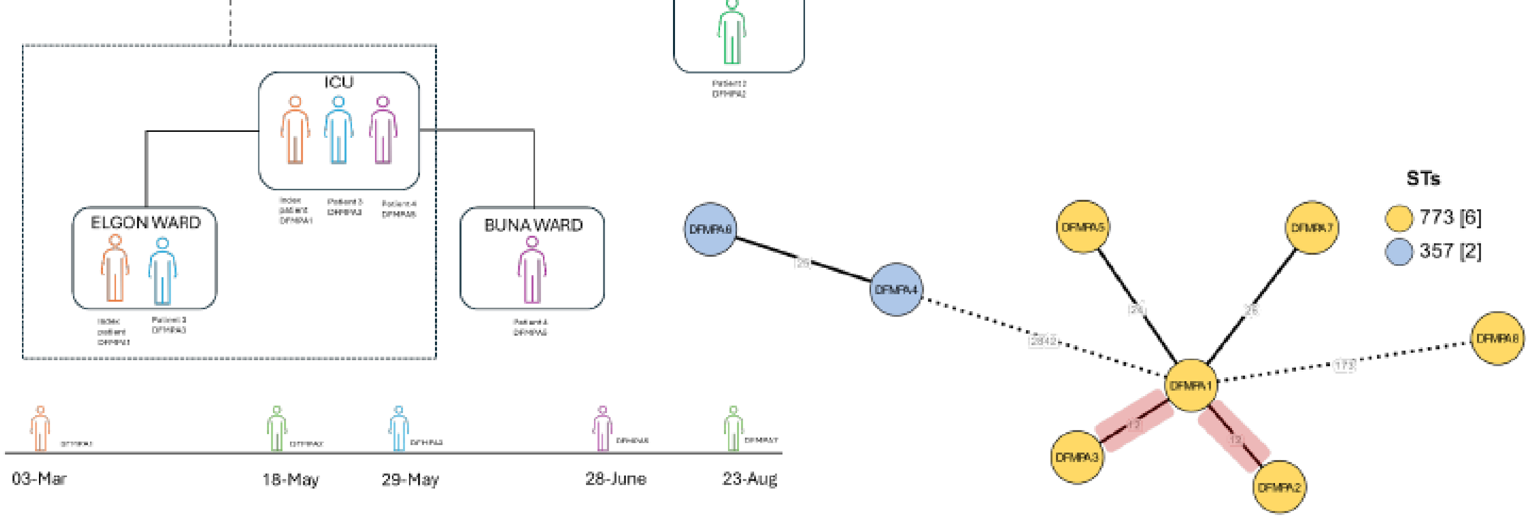
Jan 2018
Ward

Outbreak of a pan-drug resistant *Pseudomonas aeruginosa* at a hospital between March and October 2024 is associated with Emerging high-risk ST-773

- Resistant to all tested antibiotics, including last-resort options colistin (harboring the *pmrBV15I* mutation) and meropenem (carrying the *NDM-1* gene).
- Emerging high-risk **ST-773** strain associated with HAI, MDR, medical tourism from asia



Common source – index patient



Still ongoing - >20 cases

Minimum spanning tree -ChewBacca

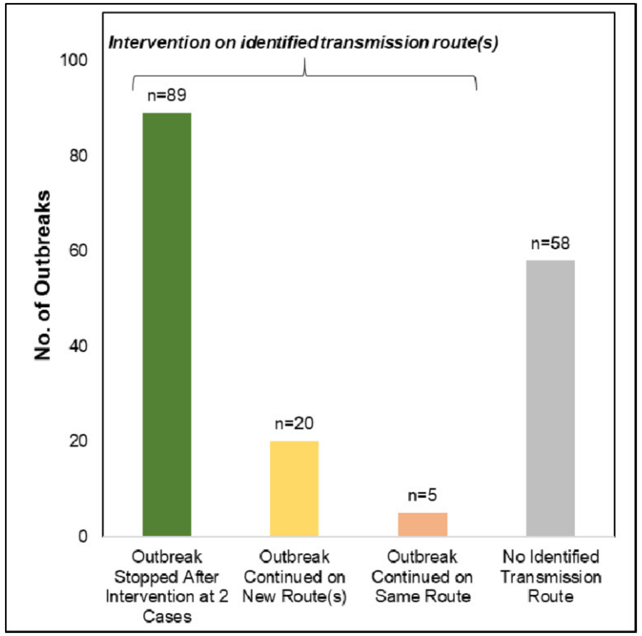
Impact of real-time WGS on outbreak detection and arrest

University of Pittsburgh Medical Center (UPMC)-affiliate hospital

Clinical Infectious Diseases, 2025;, ciaf216, https://doi.org/10.1093/cid/ciaf216

Strategy

- Routine weekly prospective WGS surveillance of patient isolates – 2 years
- When two or more patients with closely related bacterial isolates identified, the IP&C team was alerted immediately
  - notification and education of staff
  - enhanced cleaning efforts
  - hand-hygiene and personal protective equipment compliance
  - enhanced microbiologic surveillance to identify the source



Outcome

- prevented 62 outbreaks and five deaths
- saved ~ $700,000—a more than 3-fold return on investment.
- prevent infections, improve outcomes, and strengthen patient safety.

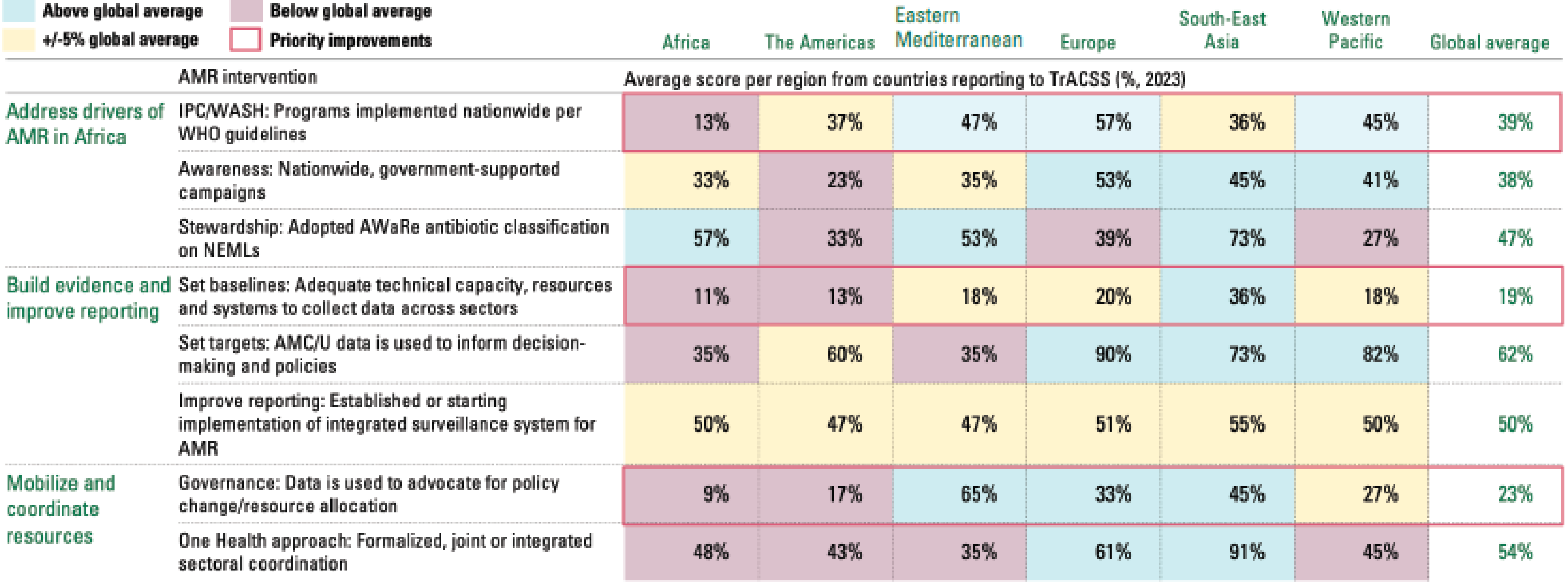
"Implementation of real-time WGS surveillance can have substantial clinical impact and cost-savings,“ **IF**

- genomic surveillance occurs routinely in real time not reactive
- detected outbreaks are accompanied by real-time **infection prevention and control interventions**

Sequencing alone will not do much

African Union AMR Landmark Report: Voicing African Priorities on the Active Pandemic," launched by the Africa CDC

Africa falls behind on key AMR interventions of IPC/WASH, setting baselines and targets, and using data to inform policies



Above global average | Below global average
+/-5% global average | Priority improvements

	AMR intervention	Africa	The Americas	Eastern Mediterranean	Europe	South-East Asia	Western Pacific	Global average
		Average score per region from countries reporting to TrACSS (%, 2023)						
Address drivers of AMR in Africa	IPC/WASH: Programs implemented nationwide per WHO guidelines	13%	37%	47%	57%	36%	45%	39%
	Awareness: Nationwide, government-supported campaigns	33%	23%	35%	53%	45%	41%	38%
	Stewardship: Adopted AWaRe antibiotic classification on NEMLs	57%	33%	53%	39%	73%	27%	47%
Build evidence and improve reporting	Set baselines: Adequate technical capacity, resources and systems to collect data across sectors	11%	13%	18%	20%	36%	18%	19%
	Set targets: AMC/U data is used to inform decision-making and policies	35%	60%	35%	90%	73%	82%	62%
	Improve reporting: Established or starting implementation of integrated surveillance system for AMR	50%	47%	47%	51%	55%	50%	50%
Mobilize and coordinate resources	Governance: Data is used to advocate for policy change/resource allocation	9%	17%	65%	33%	45%	27%	23%
	One Health approach: Formalized, joint or integrated sectoral coordination	48%	43%	35%	61%	91%	45%	54%

Use case 4: AMR sources and transmission cycles

Where is the highest risk for acquiring a community MDR infection?


Pond 5


The Water Project


https://kenya.hsmagazine.digital/


Freshbox.co.ke

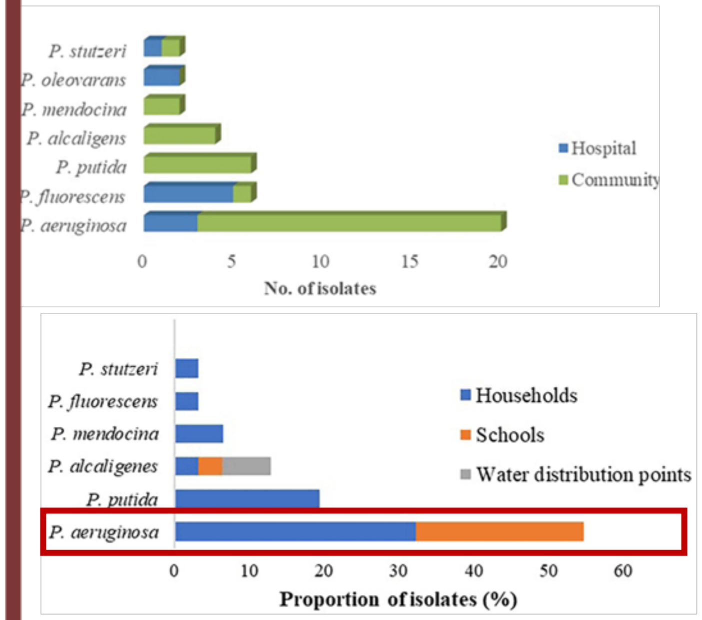
Complex problem – what’s the right question or approach to accurately measure human/animal/environmental aspects of AMR ?

“…….solving a complex problem uncovers hidden assumptions and ever more knowledge, trade-offs that we didn't anticipate …Erik Naggum”

Community water - *Pseudomonas aeruginosa reservoir*

- **~90%** of *P. aeruginosa* isolates from patients in Kisumu County hospital are community acquired (CAI)
  - 38% of which are MDR.
  - Resistance to carbapenems and colistin
- Characteristic green pigment
- Associated with moist surfaces and water pipes
- Forms biofilms that protect against environmental stresses, antibiotics and disinfectants present in water pipes, wells, medical implants, air conditioning

P. aeruginosa community reservoirs



Environmental reservoirs of multidrug-resistant pseudomonads in a geographical location in Kenya with high community-acquired infections

May 2024 · F1000Research · 13:474

Water tanks. taps, old piping systems

Location Sampled	Sample source	*PA* prevalence (%)
Households (40)	Taps	5 (9%)
	Sinks	6 (32%)
	Storage containers	0 (0%)
	Tank	0 (0%)
	Borehole	0 (0%)
SCH (10)	Tanks	6 (25%)
	Taps	1 (4.8%)
	Borehole	1 (50%)
Water points (8)	Tap outlet	0 (0%)
	Vendor containers	0 (0%)

Sub-location	*PA* prevalence (%)
Kaloleni	2
Milimani	34
Manyatta A	0
Manyatta B	12
Nyalenda A	0
Nyalenda B	0
Hospital	6
TOTAL	7

Manyatta


Lake region bulletin

Hospital tanks

https://www.projectwaterfall.org/clean-water-for-schools

Water Vendors

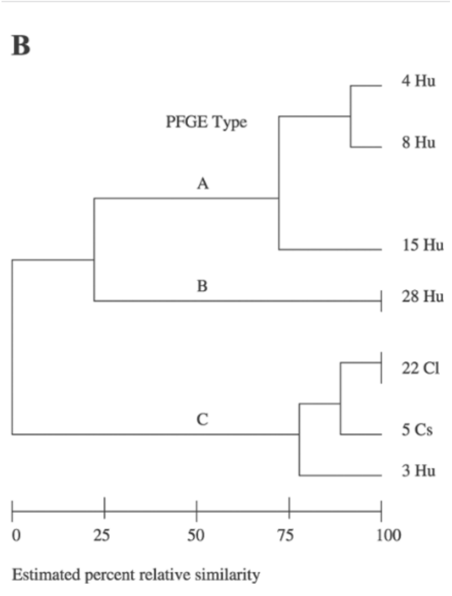

ResearchGate

Limited relationships between strains in humans, animals and the environment - *Salmonella* spp.

> FEMS Immunol Med Microbiol. 2002 Jul 12;33(3):165-71. doi: 10.1111/j.1574-695X.2002.tb00587.x.

Lack of clonal relationship between non-typhi Salmonella strain types from humans and those isolated from animals living in close contact

Samuel Kariuki [1], Gunturu Revathi, Francis Gakuya, Victor Yamo, Jane Muyodi, C Anthony Hart



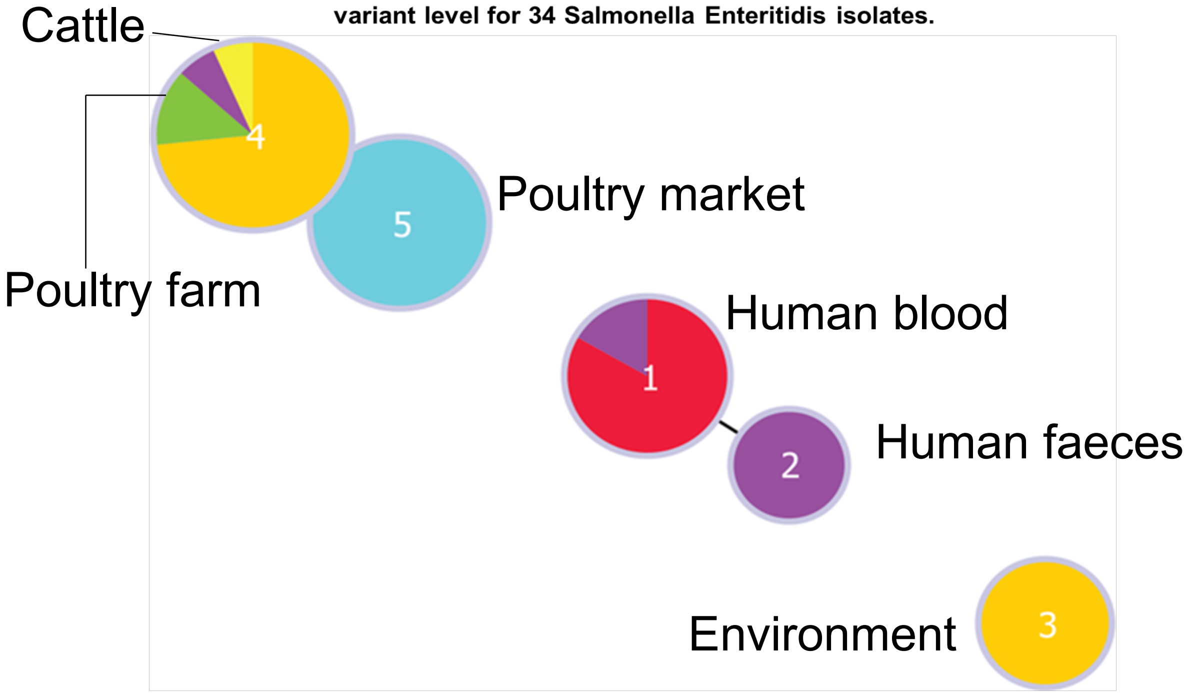
Animals and the environment (water, soil, sewer, and food) may not constitute an important reservoir for Non-typhoidal

Potential Sources and Transmission of *Salmonella* and Antimicrobial Resistance in Kampala, Uganda

Josephine A. Afema, Denis K. Byarugaba, Devendra H. Shah, Esther Atukwase, Maria Nambi, William M. Sischo

Published: March 21, 2016 • https://doi.org/10.1371/journal.pone.0152130

Fig 3. Clusters of MLVA genotypes produced by goeBURST algorithm at the single locus variant level for 34 Salmonella Enteritidis isolates.



Afema JA, Byarugaba DK, Shah DH, Atukwase E, Nambi M, et al. (2016) Potential Sources and Transmission of Salmonella and Antimicrobial Resistance in Kampala, Uganda. PLOS ONE 11(3): e0152130. https://doi.org/10.1371/journal.pone.0152130 https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0152130

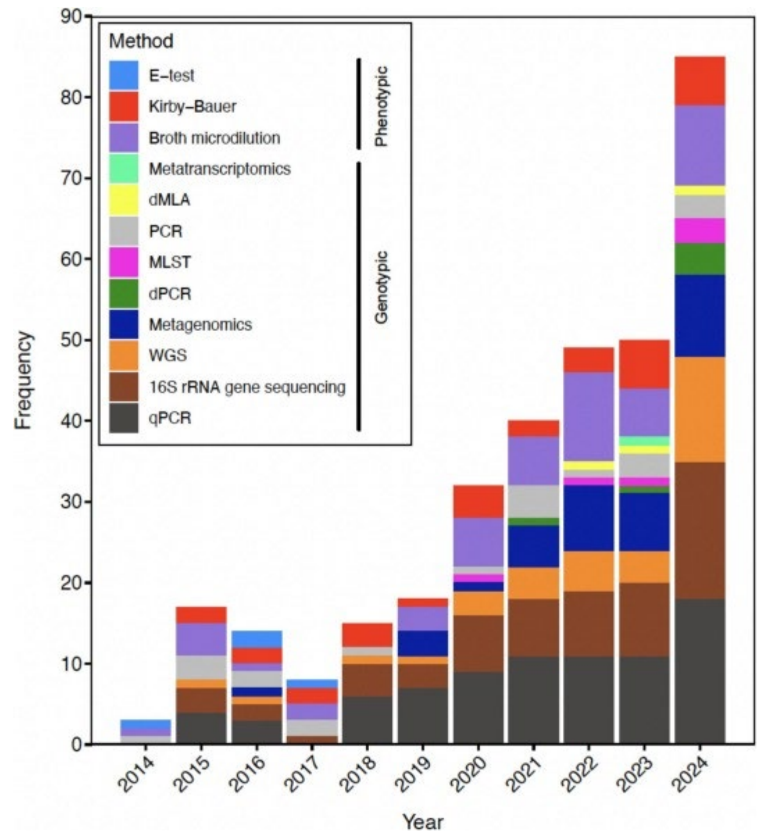
Waste water surveillance

- A method for early detection of diseases shed in faeces such as, shigella, polio, cholera and SARS-CoV-2
- analyses of wastewater for markers of pathogens
- community scale information
- simultaneously sample wastewater and both healthcare- and community-associated populations
- Tracks resistance trends across different populations and region

Sewage surveillance of antibiotic resistance holds both opportunities and challenges

D. G. Joakim Larsson ✉, Carl-Fredrik Flach & Ramanan Laxminarayan

Nature Reviews Microbiology **21**, 213–214 (2023) | Cite this article



Opportunities

- complement clinical surveillance by early detection of novel ARGs
  - tracking time/space variation essential for detecting outbreaks
  - Community level monitoring
- evaluating efficacy of evidence-based interventions
- identifying high-risk populations for targeted monitoring
- providing early warning of the emergence and spread of antibiotic-resistant bacteria (ARBs)
- inform protective public health measures

Challenges

- quantitation of ARBs and ARGs with current methods is **too variable** to reliably track space/time variation

Mitigation

- composite sampling of wastewater influent i.e. a mixture of individual samples collected over a specific period of time e.g. hourly for a day
- longitudinal sampling >12 months
- **time-/location-matched sampling of wastewater and human compartments**

ELSEVIER

Environment International
Volume 162, April 2022, 107171

Systematic review of wastewater surveillance of antimicrobial resistance in human populations

K.K. Chau [a] ✉, L. Barker [a] ✉, E.P. Budgell [a] ✉, K.D. Vihta [a] ✉, N. Sims [b] ✉, B. Kasprzyk-Hordern [b] ✉, E. Harriss [c] ✉, D.W. Crook [a, d] ✉, D.S. Read [e] ✉, A.S. Walker [a, f] ✉, N. Stoesser [a, d] ✉

Show more

+ Add to Mendeley   Share   Cite

Wastewater surveillance for AMR

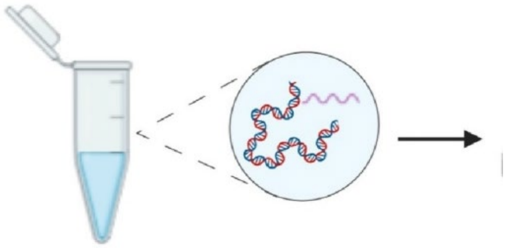
Gap: Wastewater surveillance has emerged as a method of disease surveillance, offering an initial alert system for both known and novel health risks however, the clinical utility remains poorly understood especially concerning clinical evidence of pathogen and resistance transmission.

Study Aims: Evaluate clinical significance of wastewater, animal, and environment surveillance as indicators of human infection risk and determine microbial and AMR gene reservoirs.

Surveillance Targets: Enteric bacteria and skin/soft tissue pathogens.

Study population: humans, animals including livestock, dogs, horses, poultry, the sewerage system, water sources, and the water storage tanks **within a closed community**

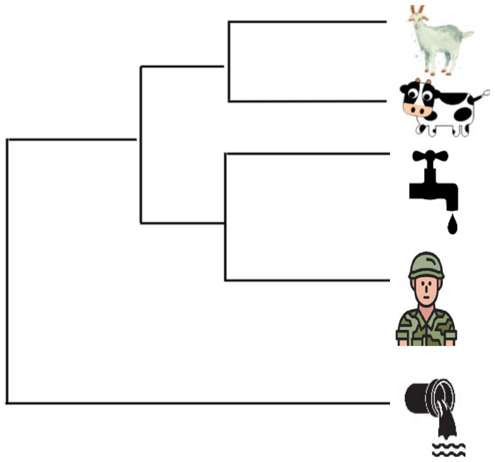
Step 1: DNA extraction



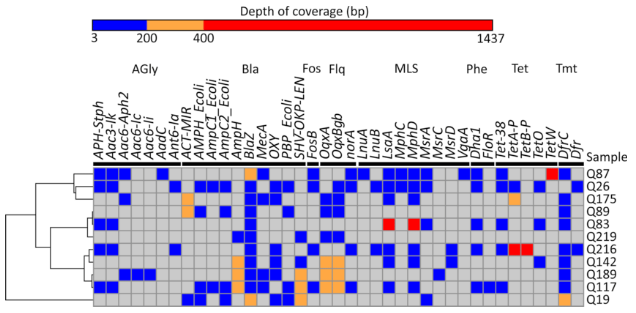
Step 2: Next-generation sequencing

Metagenomics of wastewater sample to infer pathogen dynamics

Step 3: Analysis



Step 4: AMR gene carriage



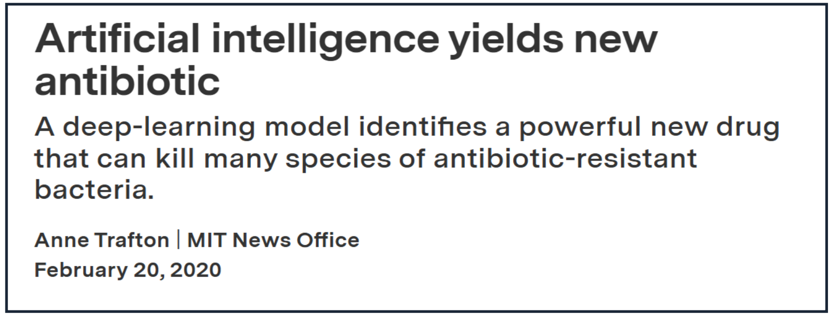
Use case 5: AI and AMR

AI and AMR

Approved antibacterial agents
2017 - 2023

Of the **128 distinct programmes** in the clinical antibacterial pipeline aimed at treating bacterial priority pathogens, **only 16** have received market approval.

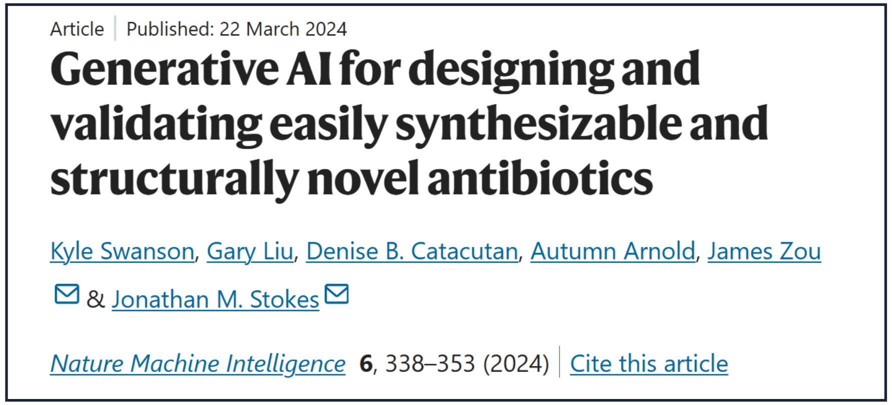
2023 Antibacterial agents in clinical and preclinical development: an overview and analysis. Geneva: World Health Organization; 2024.



Artificial intelligence yields new antibiotic

A deep-learning model identifies a powerful new drug that can kill many species of antibiotic-resistant bacteria.

Anne Trafton | **MIT News Office**
February 20, 2020



Article | Published: 22 March 2024

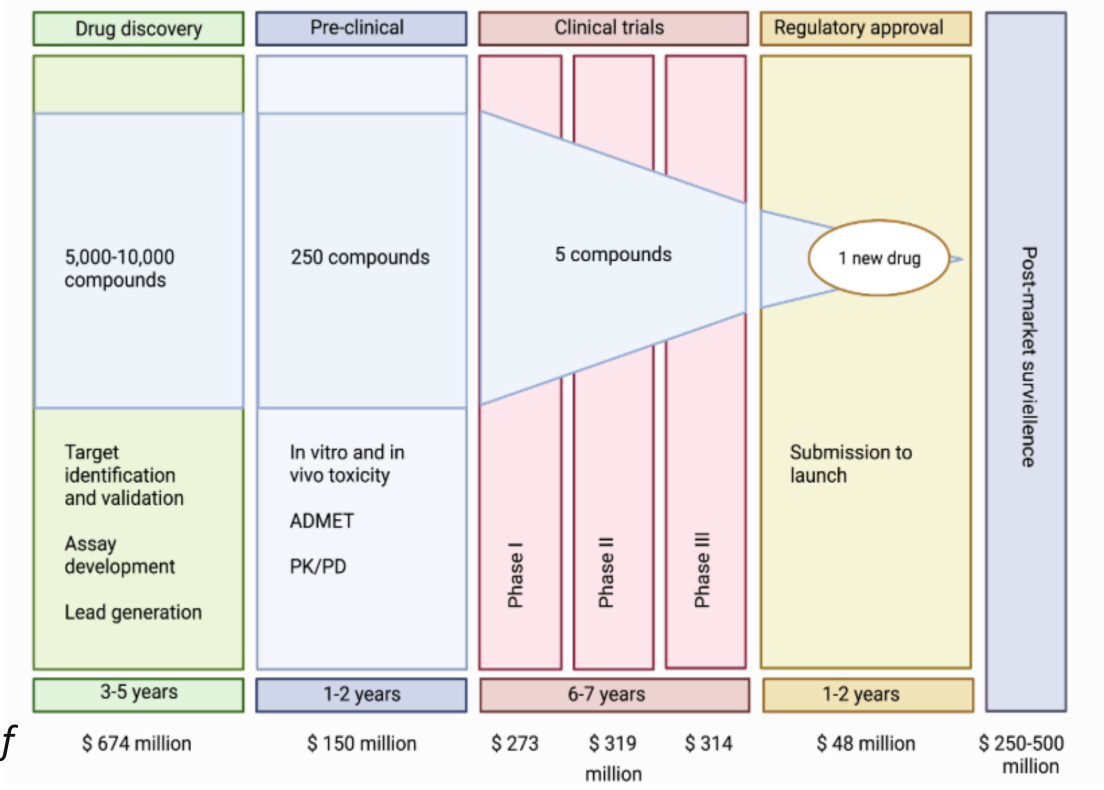
Generative AI for designing and validating easily synthesizable and structurally novel antibiotics

Kyle Swanson, Gary Liu, Denise B. Catacutan, Autumn Arnold, James Zou ✉ & Jonathan M. Stokes ✉

Nature Machine Intelligence **6**, 338–353 (2024) | Cite this article

- **Prediction** – The model screens huge virtual libraries of molecules, learning patterns in existing chemical structures, and molecular interactions and identifies novel compounds with antimicrobial potential.

- **Generative design** –*create entirely new* chemical structures predicted to have strong antibacterial activity.



https://www.uniboglobalhealth.com/module%202#fig-clinicaltrials

> *"So instead of having to wait five, six years to come up with one candidate, now, on the computer, we can, in just a few hours, come up with hundreds of thousands of candidates."*

AI – any big data

Drug compound libraries

Bacterial protein structures

Metagenomics

Farm production data

Natonal surveillance data

Antibiotic levels in rivers

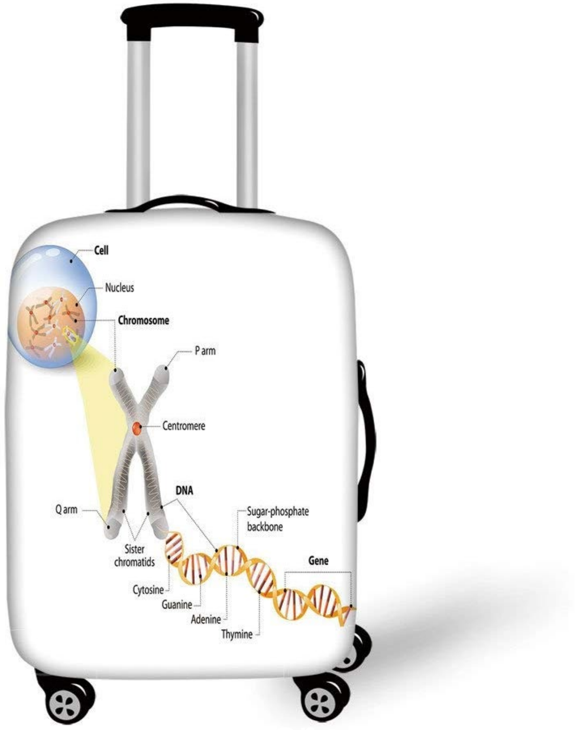
Prescription or antibiotic purchase data

Wastewater

Google symptoms searches

Summary

- Appropriate global approaches across sectors to combat AMR
- Hospital environments key contributor to spread of MDR infections
- IPC – how do we change behaviour e.g. hand hygiene
- To eliminate reservoirs that enhance transfer of resistance genes
- Bacterial strains may be restricted to their environments but genetic elements are not
- Mobile AMR genes are the greatest transmission risk
- How do we leverage AI to mine all the big surveillance data?



Acknowledgement

Funding: GEIS, AFHSD

Partners and collaborating institutes: MoH /KDF, private hospitals

MicroHub Kericho members

CCR and CMR, KEMRI

WRAIR
Walter Reed Army Institute of Research
AFRICA

KENYA MEDICAL RESEARCH INSTITUTE
KEMRI

HJFMRI