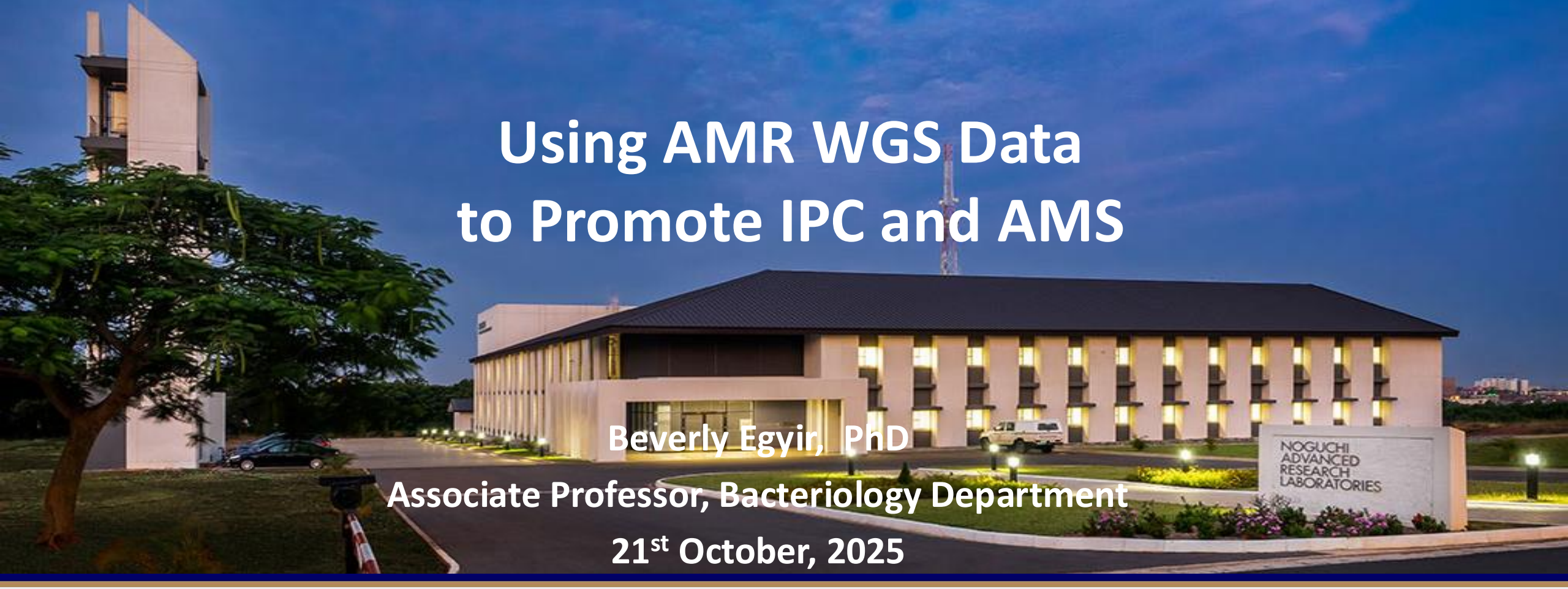

Using AMR WGS Data to Promote IPC and AMS

Beverly Egyir, PhD

Associate Professor, Bacteriology Department

21st October, 2025

UNIVERSITY OF GHANA

INTEGRI PROCEDAMUS

NMIMR

NOGUCHI

Memorial Institute for Medical Research

University of Ghana

Outline

- ❑AMR menace
- ❑NMIMR SeqAfrica activities
- ❑Case studies: AMR WGS data to support IPC and AMS
- ❑Lessons learned
- ❑Questions

Menace: Antimicrobial Resistance

- ❑ **AMR** is still a critical global health challenge
- ❑ Recent WHO report-1 in 6 infections worldwide- now resistant to antibiotics.
- ❑ Heaviest in the LMICs

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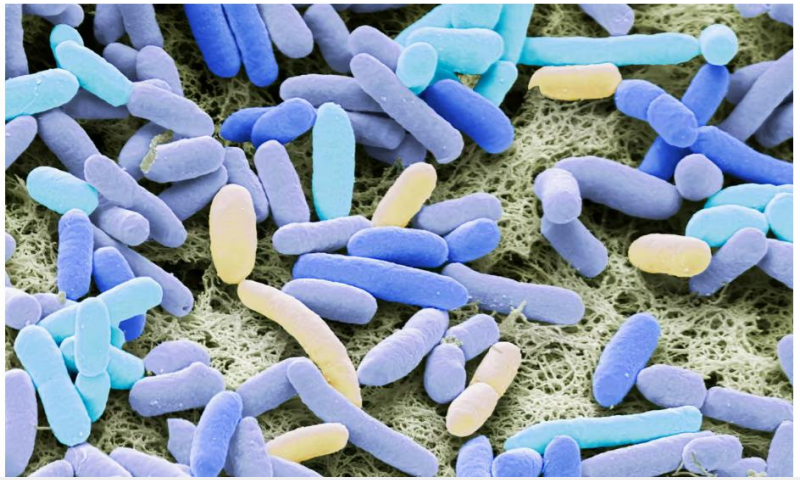
The Guardian Int

World Health Organization

Sharp global rise in antibiotic-resistant infections in hospitals, WHO finds

Experts describe findings as deeply concerning and predict 70% increase in related deaths by 2050



Ian Sample
Science editor

Mon 13 Oct 2025 08.00 BST

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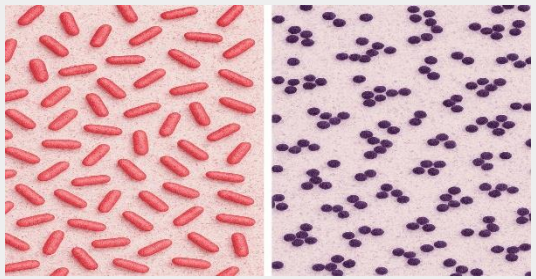

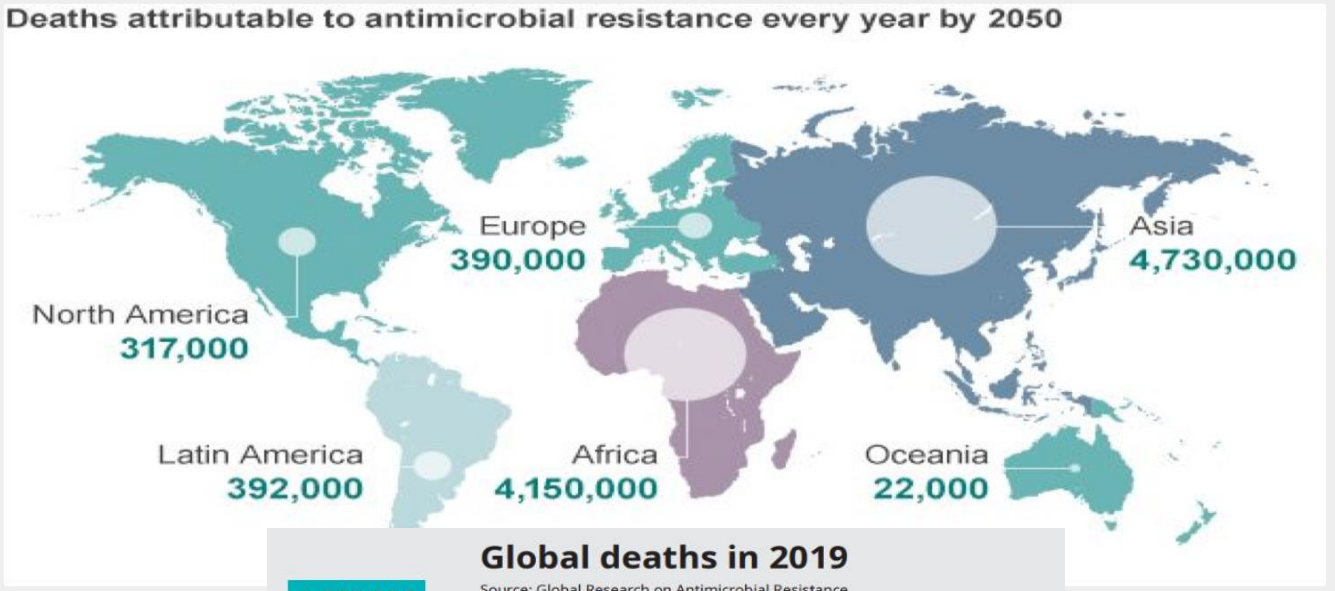

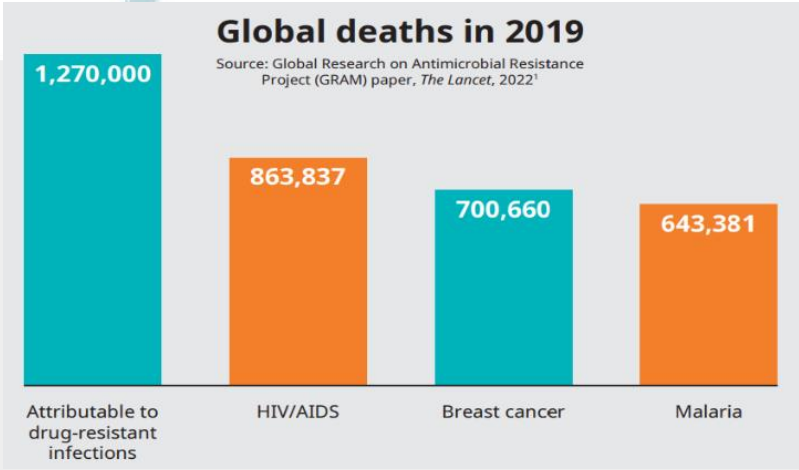

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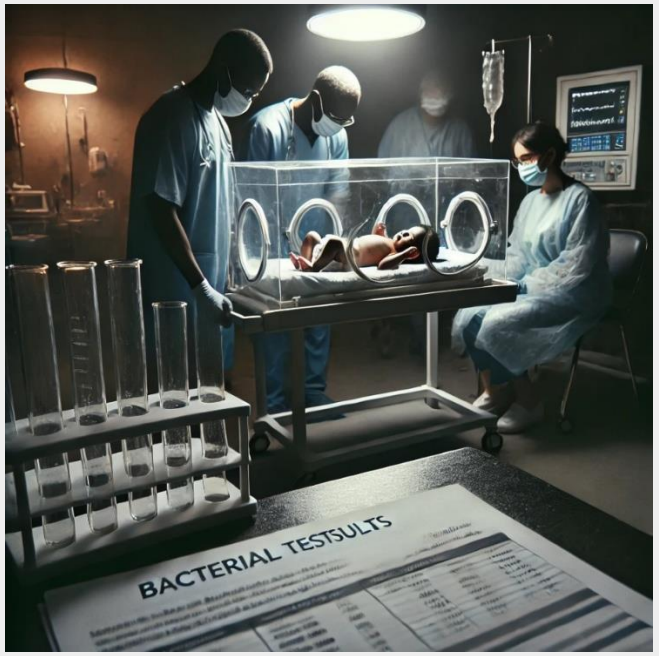
Menace of Antimicrobial Resistance



- A case in a hospital in Ghana

- *Klebsiella pneumoniae/Blood sample- 23 day old-NICU*
- *Ampicillin and gentamicin were administered*
- Resistant to all **(13)** antimicrobials tested including: *Gentamicin, ciprofloxacin and meropenem.*

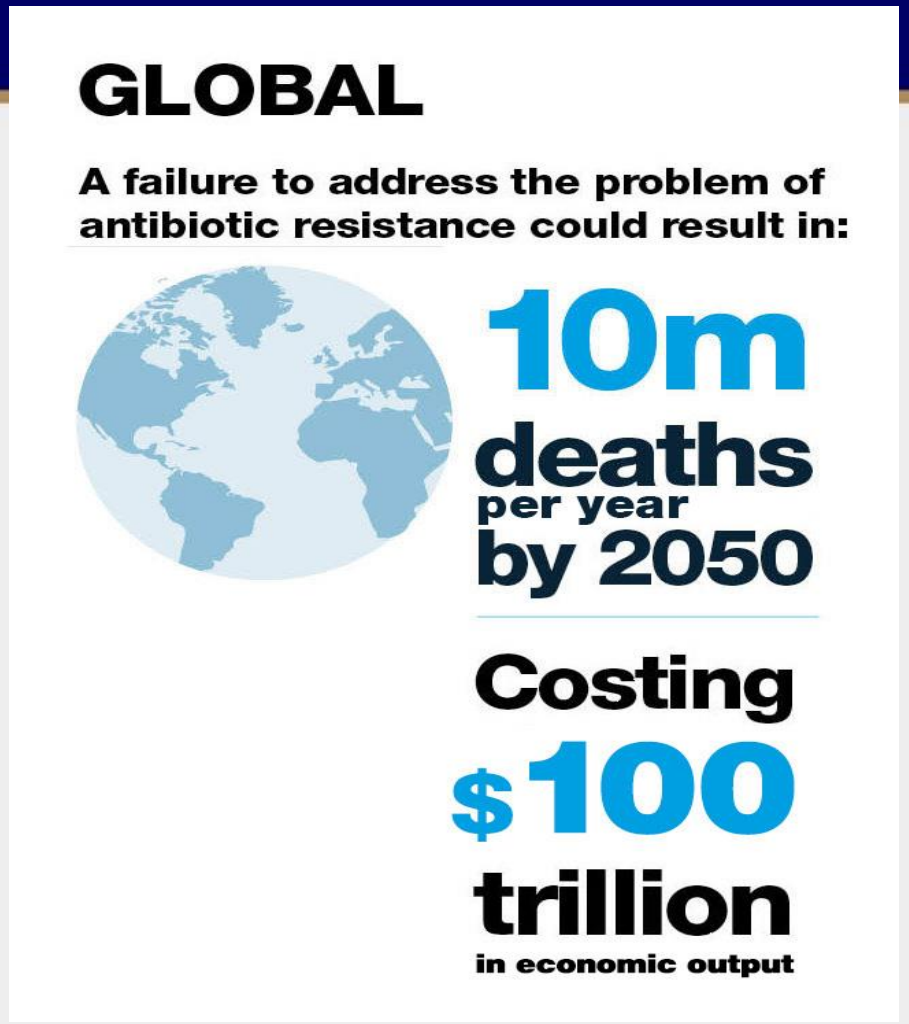
ST	Resistance genes/Implication
ST15	✓ Ext. resistant *K. pneumonaie* ✓ carbapenemase genes (***blaNDM-1,blaOXA-232***) ✓ ESBL, broad aminoglycoside and fluoroquinolone resistance markers (***blaCTX-15, aac(3)-lla,aac(6')-lb-cr,aadA2,aph(3")-lb, aph(6)-ld,armA, qnrB***) ✓ High risk clone- nosocomial transmission and poor clinical outcomes ✓ public health threat that calls for **IPC** and **AMS** intervention

Menace of Antimicrobial Resistance

❑A case in a hospital in Ghana

- A blood sample was taken for testing from a *day-old baby*
- *Flucloxacillin and cefotaxime* were administered
- Test results revealed ESBL-producing *Klebsiella pneumonaie*
- Baby passed away

Actions include….

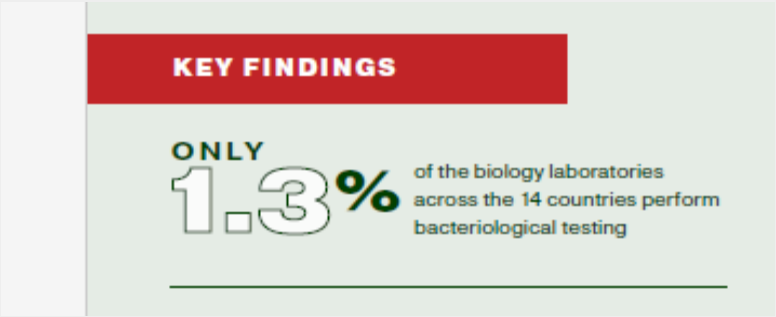


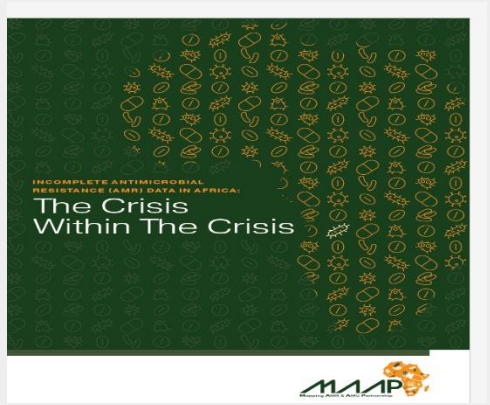
- **Infection prevention and control -**done to stop infections from spreading *e.g. proper hand hygiene, isolating infectious patients etc*
- **Antibiotic stewardship-** done to ensure responsible use of antibiotics *eg. using the right antibiotic or using it when its is only needed*
- **Capacity building** (laboratory infrastructure and personnel)
- **Sustainable investment** in countering antimicrobial resistance
- **Surveillance……**

Surveillance

- One of the biggest challenges in addressing AMR in Africa is the lack of data.

- **MAAP REPORT:**

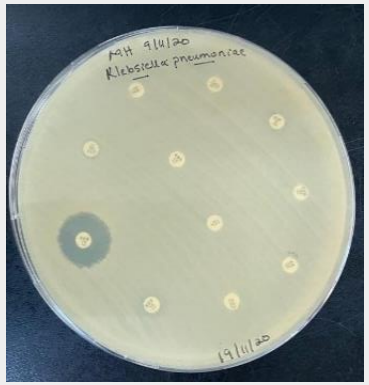




- Policy frameworks are in place, but real-time data to drive IPC and AMS is missing
- Very few labs in Africa can perform bacteriological testing.
- Data on AMR is still limited
- Genomic data to understand the mechanisms of resistance is also scarce
- Surveillance data is key to inform treatment decisions, antibiotic stewardship programs and Infection prevention and control efforts.

Whole Genome Sequencing (WGS): Importance

- **Phenotypic AST** : shows what is resistant, but *not* **how** or **where** it's spreading



- **WGS:** high resolution to see beyond the **petri dish**: ***to detect outbreaks, trace resistance, and guide stewardship.***

To determine virulence mechanisms

Development of point-of-care tests for AMR-novel diagnostics

Support vaccine development

To determine pathogen evolution

Identification of new targets for antimicrobials and vaccines

SeqAfrica Consortium

❑**July, 2020-**Noguchi Memorial Institute for Medical Research **joined the SeqAfrica** consortium

❑Sequencing bacteria isolates from humans, animals and environment (in *West Africa*)-to understand the pathogens better

❑ Training of lab staff/students-sequencing and sequence analysis

Rene

Pernille

Christa

Iruka

Beverly

Anthony

Marco

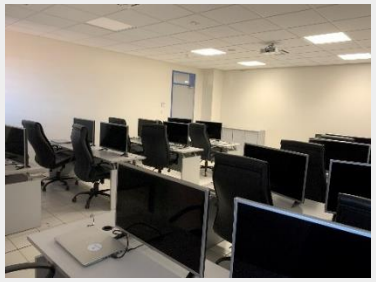
Yakhya

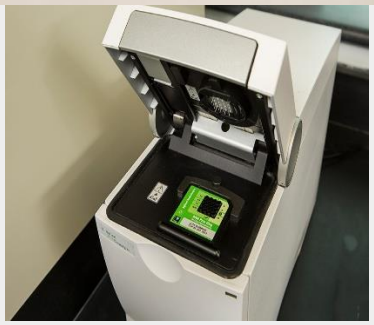
Noguchi Memorial Institute for Medical Research

- ✓ Animal Experimentation
- ✓ Bacteriology
- ✓ Virology
- ✓ Parasitology
- ✓ Epidemiology
- ✓ Immunology
- ✓ Nutrition
- ✓ Clinical pathology
- ✓ Electron Microscopy

- Conduct **research** into diseases of public health importance
- Provide **Training** opportunities for students (UG/PG)
- Provide **cutting edge** laboratory diagnostic and surveillance services (MoH and GHS and others)

Work Areas





Hamilton for library preps

Workflow and Methodology- At NMIMR

Isolates submitted

Growth on appropriate media
Blood, Mannitol salt, McConkey Agar

Identification
MALDI-TOF-MS

Antimicrobial Susceptibility Testing
BD Phoenix, Disk Diffusion (CLSI Guidelines)

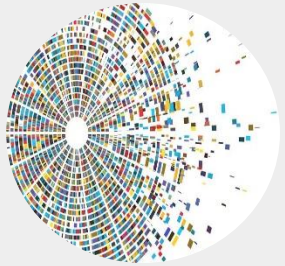
Extraction and Purification of Genomic DNA
Qiagen DNA Extraction Kits

DNA Library Preparation
Illumina library prep / Rapid Barcoding kit

Sequencing DNA libraries
Illumina NextSeq / GridIon

QC, De novo Assembly

Analysis of DNA Sequencing reads
Illumina: Trimmomatic, fastqc, multiqc, unicycler/skesa.
Nanopore: Fastp, porechop, fastqc, flye, Medaka.

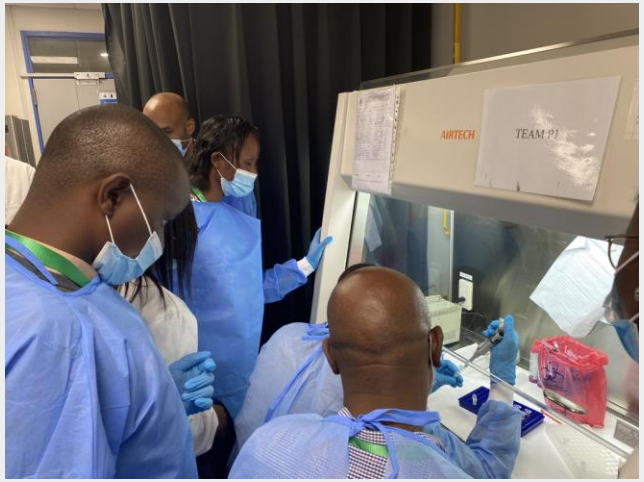


Resistance genes
Virulence genes
Serotypes
Plasmids
MLST
CGE, Pathogenwatch, CARD, VFDB

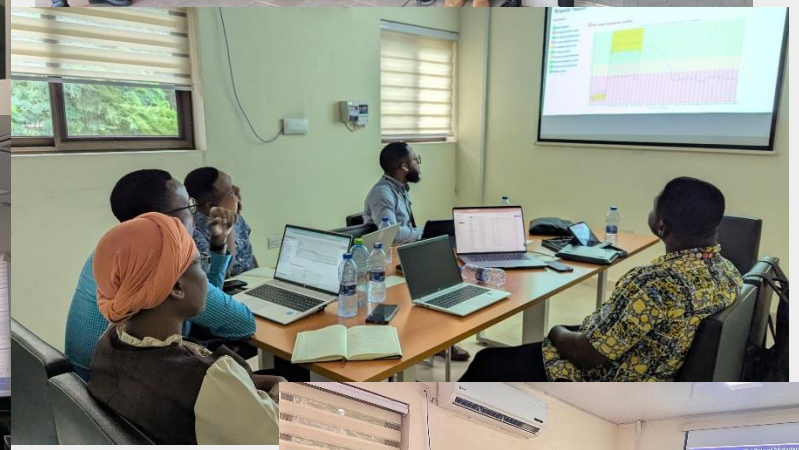
Training of Scientists from 11 African countries (WGS/Analysis-Hands on- Wet and Dry Lab)

Workforce expansion

Several Workshops



Hosting/Training of Fleming Fellows….



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Bacterial genomes sequenced…4,300

Owners	Country	Organism	Source	Total
FF-Fellows	Ghana and Nigeria	ESBL positive *E. coli Salmonella, Shigella*	Humans and animals	**351**
Small projects (*individual/students*)	Benin, Ethiopia, Ghana, Namibia, Niger, Nigeria, Zambia	*E. coli, Salmonella spp, S. aureus, Klebsiella spp, Enterococcus spp, Acinetobcater spp, Aeromonas spp, Candida spp, Streptococcus spp.*	Humans, animals and aquaculture	**1,966**
Ten African Countries (FAO-SeqAfrica Trainees)	Benin, Cameroon, Eswatini, Ghana, Kenya, Malawi, Nigeria, Sudan Zambia, Zimbabwe	ESBL *E.coli*	Animals, Environment and Humans	**188**
Country Grant	Ghana	*K. pneumoniae, S. aureus, E. coli, A baumannii, S pneumo, Burkholderia spp, P aeruginosa*	Humans	**225**
Tricycle	Ghana	ESBL-positive *E. coli*	Animals, environment and humans	**201**
National Pilot	Ghana	*Klebsiella spp, E. coli, S. aureus, Acinetobacter spp, P. aeruginosa, Vibrio cholerae, others*	Humans, (from 12 Hospitals across Ghana)	**1,369**

National Pilot -AMR Surveillance Workflow

- Sentinel sites/ Network of labs (ID and AST)
- transport isolates to sequencing facility

1. Tamale Teaching Hosp.
2. St Patrick's Hosp.
3. Eastern Regional Hosp.
4. Effie Nkwanta Regional Hosp.
5. St Martins de Porres (Eikwe)
6. UG-Legon Hosp.
7. Lekma Hosp.
8. KBTH –Hosp.
9. 37 Military Hosp.
10. Bolga Hosp.
11. Ho Teaching Hosp
12. Margaret Marquat Hosp.

Sequencing facility

Bacteria Isolates

- ✓ Bacteria Identification
- ✓ AST
- ✓ WGS
- ✓ Sequence analysis
- ✓ Storage of Isolates and Data

AMR DATA

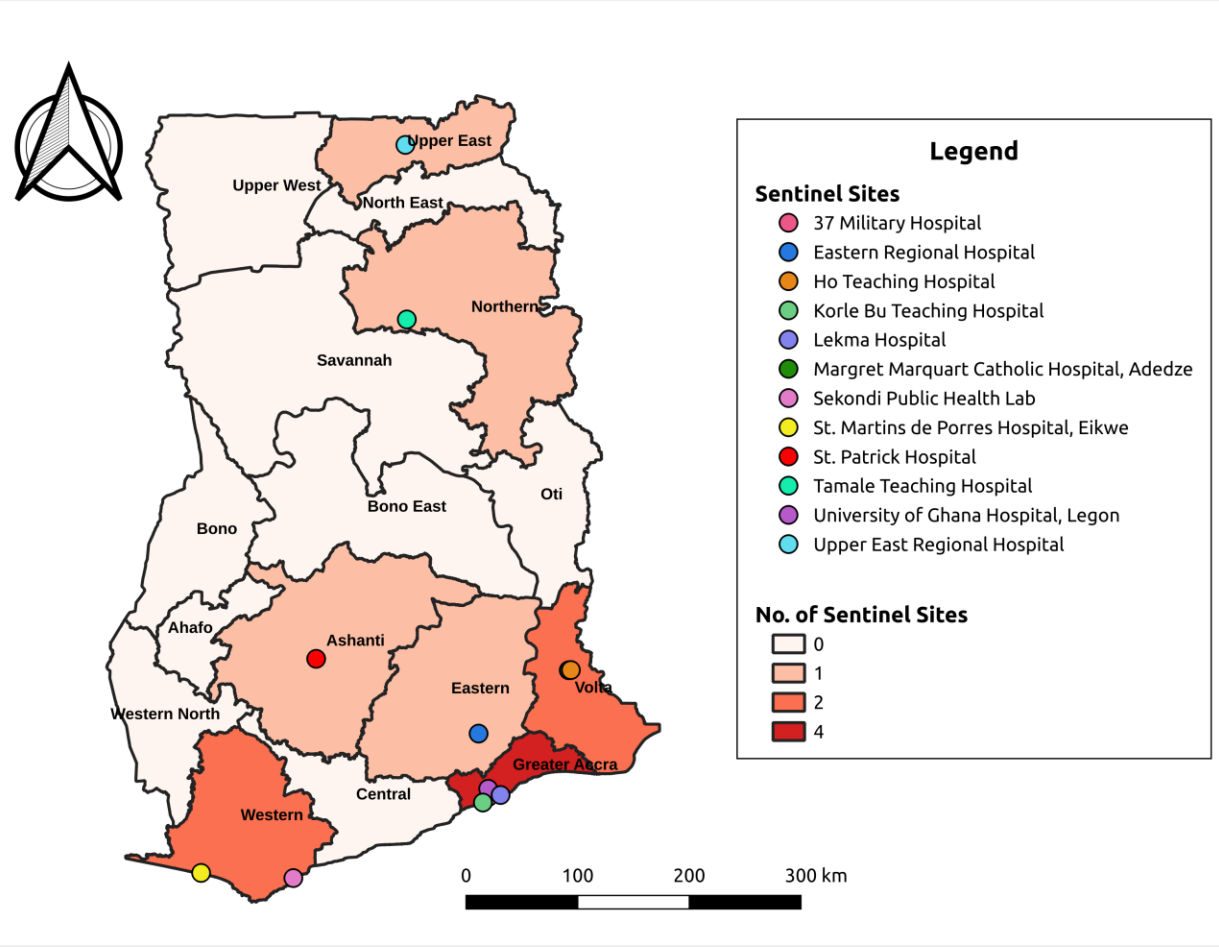
Share data with:

- ✓ Sentinel sites: hospitals/communities
- ✓ National AMR Platform
- ✓ Others

- Policy briefs
- Peer reviewed articles

bloodstream infections, wound swabs, urine, etc

National Pilot: 12 Sentinel Sites in Ghana



Sentinel Site	No of Isolates Sequenced
St Patrick Hospital	251 (18.3%)
Eastern Regional Hos.	180 (13.1%)
37 Military Hospital	156 (11.4%)
Legon Hospital	148 (10.8%)
St Martin De Porres E.	126 (9.2%)
Ho Teaching Hospital	101 (7.4%)
Upper East Regional Hos.	98 (7.2%)
Sekondi Public Health Lab	89 (6.5%)
Korle-bu Teaching Hos.	81 (5.9%)
Tamale Teaching Hospital	55 (4.0%)
Lekma Hospital	44 (3.2%)
Margaret Marquat	40 (2.9%)

✓ **1,369** Genomes sequenced on Genomic Surveillance project from **12** sentinel sites

Overview: National Pilot Sequence types and Resistance genes

Organism	Characteristics	
	Common Sequence types	Resistance genes
Klebsiella pneumoniae	ST17, ST39, ST15	***Quinolone (****OqxA, OqxB, aac(6')-Ib-cr, qnrS1*) ***Fosfomycin*** *(fosA)* ***ESBL*** *(blaCTX-M-15)*
Staphylococcus aureus	ST152 , ST3249, ST5	***Methicillin*** (*mecA)* ***Tetracycline*** (*tetK*) **macrolide** (*ermC)*
Acinetobacter baumannii	ST164, ST744, ST1418	***tetracyclines*** [*tet(39), tet(B), tet(X3)*], ***aminoglycosides*** *[aac(3)-Ia, aac(3)-Iid, ant(2'')-Ia, ant(3'')-Ia, aph(3'')-Ib],* ***carbapenems*** *(blaNDM-1 and variants of blaOXA)*

K. pneumoniae:

- ***Isolates harboured*** carbapenem resistance genes (*bla*NDM-1, *bla*OXA-181, *bla*OXA-232)
- **Wound Isolate carried** colistin resistance gene (***mcr-10)***

WGS DATA, IPC and AMS

- Data is required to inform AMS and IPC efforts

- AMR data is only valuable when it leads to action

- And for the ***needed action to be taken, DATA*** *has to be* shared with the ***relevant*** stakeholders: for e.g. clinicians, pharmacists, and hospital administrators.

- WGS data can only be useful when it leaves the ***sequencers*** to the ***wards***

- **AMR DATA IN ACTION SAVES LIVES**

Case Study 1: Dissemination at Eastern Regional Hospital

- Secondary level referral facility
- Serve all districts in Eastern Region
- 462 bed capacity

Target audience:
IPC and AMS committee members, hospital administrators, clinicians, nurses, pharmacists, public health personnel among others

Message: Isolates, clinical sources AST, genomic content, public health impact, importance of genomic data

Dissemination: Eastern Regional Hospital

Data category	Data shared
Clinical Sources	*Wound, urine and blood*
Bacteria spp	*S. aureus, K. pneumoniae and E coli*
AST	• **40% cefoxitin** resistance among *S. aureus (MRSA)* • **71%** *K. pneumonaie* & **40%** *E. coli*- ***ESBLs*** • **40%- *quinolone*** *resistant Enterobacterales* • **7%- *meropenem*** *resistant Enterobacterales*
Genomic Data	• **42% *mecA* gene** among *S. aureus* (MRSA) • high risk-clones **ST 152 MRSA associated with outbreaks/necrotizing pneumonaie** • High risk clones of K. *pneumonaie* -**ST39, ST17** and **ST307** • **ESBL** gene $bla_{CTX\text{-}M\text{-}15}$ and **carbapenemase** gene $bla_{NDM\text{-}1}$ • Clustered genomes showing **SNP** differences of **<10** • Haemolysin genes: (*hlgA, hlgB, hla, hlb)/*Biofilm forming genes

Dissemination: Eastern Regional Hospital

Clinical Implication	What has changed/impact
• Isolates resistant to multiple antimicrobials- • **Finding ESBL, MRSA and Carbapenemase genes-means limited therapeutic options** • **High risk clones** associated with **severe infections and outbreaks** • **SNP difference of <10**, indicating possible outbreaks • Biofilm forming genes lead to **persistent infections**	• **Awareness** was created among all staff: prescribers, administrators, and lab staff • **Management** showed more commitment to tackle AMR • **The AMS committee** audits antibiotic prescriptions (*e.g. cut down unnecessary cephalosporin use)* • **Antibiogram f**or the hospital is being compiled by the lab (80% complete) • **IPC coordinator** organized training for all heads of units and wards • **Intense collaboration between** clinicians, lab staff and pharmacists • **Lab now screens for ESBL, MRSA** and other resistant phenotypes

Case Study 2: Disseminations at Effia Nkwanta Hospital

- **300 bed** capacity
- Secondary level facility
- Serves the Sekondi Takoradi Metropolis
- Receives referrals from **all parts of the country**

- **Audience**

Clinicians, pharmacists, nurses, lab scientists, and other stakeholders

- Highlighted the impact of AMR and the importance of sequencing isolates beyond routine AST.

Dissemination: Effia Nkwanta Regional Hospital

Data category	Data shared
Clinical Sources	Sputum, wound, and blood
Bacteria species	*S. aureus, K. pneumoniae* and *E. coli*
AST	• **8%** cefoxitin resistance • **50% ESBL** among Enterobacterales • **33-50%- quinolone** resistance among Enterobacterales
Genomic Data	• high risk-clones, *K. pneumonaie* -**ST39, ST17 , ST147,** and **ST307** • **ESBL** gene $\boldsymbol{bla_{CTX\text{-}M\text{-}15}}$ • A. baumannii isolates harboured carbapenemase genes (*blaOXA-121, blaOXA-91, blaOXA-51, blaNDM-1*) • Biofilm forming genes

Dissemination: Effia Nkwanta Regional Hospital

Clinical Implication	What has changed/impact
• Isolates resistant to multiple antimicrobials- • **ESBL, MRSA and Carbapenemase genes- means limited therapeutic options** • **High risk clones** associated with severe infections and outbreaks • **Biofilm forming genes** lead to persistent infections	• **Awareness** was created among all staff: prescribers, administrators, and lab staff • **Renewed commitment** among the hospital staff to tackle AMR • Generated research ideas for collaboration • **Lab screens for ESBL, MRSA** and other resistant phenotypes

Case Study 3: Disseminations at St Martins Depores Hospital

- **200** bed capacity
- **Serve** several districts in the Western region
- **Audience:** Clinicians, nurses, lab scientists, and other stakeholders
- Shared their site-specific data- AMR profiles, resistance and virulence genes, and clonal diversity of bacterial species
- highlighted the impact of AMR and the role of sequencing to complement AST

Dissemination: St Martins De-porris Hospital

Data category	Data shared
Clinical Sources	Wound and blood
Bacteria species	*S. aureus, K. pneumoniae and E coli*
AST	• **37%** cefoxitin resistance • **50%** *K. pneumonaie* **ESBLs** • **40%- quinolone** resistant Enterobacterales • **7%- meropenem** resistant Enterobacterales
Genomic Data	• **35%** ***mecA gene*** **(MRSA)** • Clustered genomes showing **SNP** differences of **<10** • high risk-clones **ST 152 MRSA,** *K. pneumoniae* clones **ST39,** and **ST307** • *Acinetobacter baumanii-* carbapenemase genes (*blaNDM-1* • Biofilm forming genes

Dissemination: St Martins De-porris Hospital

Clinical Implication	What has changed/impact
• Isolates resistant to multiple antimicrobials- • **ESBL, MRSA and Carbapenemase genes** • **limited therapeutic options** • **High risk clones** associated with **severe infections and outbreaks** • **SNP difference of <10**, indicating possible outbreaks • Biofilm forming genes lead to **persistent infections**	• **Awareness** was created among all staff: prescribers, administrators, and lab staff • An engaging discussion-led to an appointment of an **AMR Champion** to coordinate AMR activities within the • **Enhanced Surveillance-** swabbing various wards (NICU) for IPC purposes • **Established AMS committee** to oversee-provide guidance on appropriate antibiotic use. • **Lab now screens for ESBL, MRSA** and other resistant phenotypes

Lessons Learned

- Finding of ESBLs, carbapenemase producing and fluroquinolone resistant Gram negatives and MRSAs- therapeutic options will be limited in several hospitals
- High risk clones, and indications of outbreaks- outbreaks have gone un-noticed
- IPC teams acted on the genomic data and not just antibiograms.
- AMS teams had genomic evidence to support their guidelines.
- WGS must complement AST- to know how or where resistance is spreading
- Data utility depends on metadata: ward, date, clinical condition, etc. is essential for making IPC/AMS decisions from genomic data

Lessons Learned

- Hospital managers and clinicians don't need the raw sequence information, they need:

✓ *What was found*

✓ *What it means*

✓ *What should be done next*

Audience	Primary Concern	Key Message Example
Clinicians	Which drugs work	Carbapenems ineffective; switch to colistin.
Administrators	Risk, cost, safety	Outbreak confirmed — isolate and decontaminate.
IPC	Transmission control	Same clone in Ward B; screen patients.
AMS	Prescribing patterns	Increase in ESBLs — update empiric therapy.

Reflections

- WGS is not only about reading DNA-. It's also about rewriting the story of infection prevention and stewardship

- Continuous engagement/sharing of data with hospital staff is required to support IPC and AMS- to tackle AMR

- If we want to win against AMR, we must turn AMR data into action

AMR DATA IN ACTION SAVES LIVES

Acknowledgements

- Prof. Rene S. Hendriksen, (DTU)
- Dr. Pernille Nilsson (DTU)
- Dr. Christa Twyford Gibson (DTU)
- Dr. Natasia Rebeka Thornval (DTU)
- Prof. Iruka Okeke (UI)
- Dr. Marco van Zwetselaar (KCRI)
- Dr. Anthony Smith (NICD)
- Dr. Niamh Lacy-Roberts (DTU)
- Dr. Yakhya Dieye (IPD)

NMIMR SEQAFRICA Team

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- Felicia Owusu
- Agnes Oclu
- Justice Danso
- Angela Appiah Kubi
- Gabriella Acquah

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- Prof. Abraham Anang, Immediate Past Director, NMIMR
- Prof. Kwadwo Ansah Koram, Past Director, NIMIMR
- Management staff, NMIMR

All hospital administrators/ laboratories and Lab staff at sentinel sites

NMIMR SEQAFRICA TEAM