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DEVELOPMENT

MINISTRY OF
ENVIRONMENT,
CLIMATE CHANGE
& FORESTRY

MINISTRY OF
MINING, BLUE
ECONOMY &
MARITIME AFFAIRS

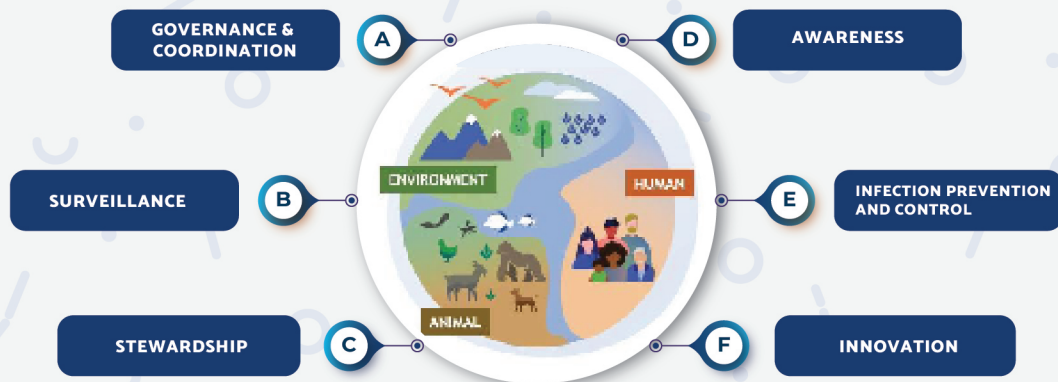


WAAW 2025

WORLD AMR AWARENESS WEEK

High Level Launch & Symposium

**Program and Book of Abstracts for
the National AMR Scientific Symposium 2025**



*Theme: **ACT NOW:** Protect Our Present, Secure Our Future*



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22. **James Wanjama Kabugu**, Kenya Fisheries Service, Fish Quality Control Laboratory – Nairobi
23. **Collins Jaguga**, National Antimicrobial Stewardship Technical Working Group (AMS TWG).
24. **Daniel Waruingi**, Zihi Institute
25. **Loyce Kihungi**, National Public Health Institute (NPHI) & NASIC

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PROGRAM

World AMR Awareness Week - WAAW 2025 KENYA NATIONAL AMR SCIENTIFIC SYMPOSIUM	
THEME: "Act Now: Protect Our Present, Secure Our Future"	
DAY 1 - Tuesday 18th November 2025	
Time	Activity
8.00 - 8.30 AM	Arrival and Registration
8.30 - 10.00 AM	WAAW week high level launch
10:00 - 10:30 AM	HEALTH BREAK & POSTER SESSION
10.30 - 1.00 PM	WAAW week high level launch
1.00 - 2.00 PM	LUNCH & POSTER SESSION
SESSION 1: SESSION 1: GOVERNANCE & COORDINATION AND INFECTION PREVENTION AND CONTROL	
SESSION CHAIR:	Willy Mwangi, Winnie Mutai, Kiplangat Sigei and Felix Kibegwa
2.00 - 2.15 PM	Antimicrobial Resistance Governance in Low- and Middle-Income Countries: The Case Study of Kenya - Mercy Mbithe Musyoka
2.15 - 2.30 PM	Between Policy and Practice: Discursive Fragmentation in Antimicrobial Resistance Governance Across National and County Levels in Kenya - Sammy Gakero Gachigua
2.30 - 2.45 PM	Prevalence and Antimicrobial Resistance Profile of Nasal Carriage of <i>Staphylococcus aureus</i> and Coagulase-Negative – Caroline Nzomo
2.45 - 3.00 PM	Q&A Plenary Discussion
3.00 - 3.15 PM	Molecular characterization and risk factors of enterotoxigenic <i>Escherichia coli</i> among children under five years in mukuru slums, Nairobi County, Kenya - Amos Thuku Njuguna
3.15 - 3.30 PM	A Qualitative Assessment of Infection Prevention and Control in four Public Hospital Newborn Units in Kenya – Edna Mutua
3.30 - 3.45 PM	Point Prevalence Survey on Antibiotic Use and Hospital-Acquired Infections at a Tertiary Referral Hospital - Ann Mercy Wanjiku
3.45- 4.00 PM	Q&A Plenary Discussion
4:00 - 4:30 PM	HEALTH BREAK & POSTER SESSION
DAY 2 - Wednesday 19th November 2025	
Time	Activity
8.00- 8.30 AM	Arrival and registration
8:30 - 9:00 AM	POSTER SESSION
SESSION 2: AMR SURVEILLANCE AND MONITORIN, IPC	
SESSION CHAIR:	Mitchelle Kasudi, and Kiplangat Sigei
9.00 - 9.15 AM	Analysis of somatic cell count, pathogen distribution and susceptibility test results in dairy cattle on smallholder farms in Kenya - Eugene Lusanji

9.15 - 9.30 AM	Antimicrobial Susceptibility Profile of <i>Escherichia coli</i> Isolates Received in National Microbiology Reference Laboratories (NMRL) for Retesting Between 2022 and 2023 - Teresia Nyaga
9.30 - 9.45 AM	Modelling antibiotic resistance in who-priority pathogens in Kenya: a machine learning and epidemiological approach - George Gitau Wanjiru
9.45 - 10.00 AM	Genomic analysis of <i>Pseudomonas aeruginosa</i> recovered from surgical site infections from a referral hospital in Western Kenya reveals dominance of high-risk subtypes - Sarah Kindiki
10.00 - 10.15 AM	Q&A Plenary Discussion
10:15 - 11:00 AM	HEALTH BREAK & POSTER SESSION
SESSION 3: YOUTH SESSION	
SESSION CHAIR:	Collins Jaguga, and Gathai Mundia
11.00 – 11.15 AM	National Youth In Action for Containment and Prevention of AMR: ACT NOW; Protect Our Present Secure Our Future – Cynthia Odhiambo , National WAAW Youth Sub Committee
11.15 - 11.30 AM	Empowering Youth as Agents of Change for Antimicrobial Resistance Prevention Through Applied Poultry Biosecurity Training in Sub-Saharan Africa– Ndege Ngere , AMR Now
11.30 -11.45 AM	Empowering the Next Generation of Scientists to Combat Antimicrobial Resistance (AMR) through Phage Research - Nelson Wachira
11.45 - 12.00 PM	Q&A Plenary Discussion
12.00 - 12.15 PM	Driving Community Change Through Youth Leadership: A Multi-Faceted Approach to Antimicrobial Resistance Awareness in Kisii County, Kenya – Odiwuor Byrone , Phoenix CBO
12.15 -12.30 PM	From University Grounds to Community Impact: Advancing AMR Awareness Through Youth Leadership and Community Engagement – Cheryl Jeruto , NUPSA
12:30 – 12:45 PM	Winning the Game Against Antimicrobial Resistance: Integrating Student Research, Sports, and Digital Advocacy for Scalable AMR Awareness - Kelvin Kipkoech , MMUSTAC
12:45 – 1:00 PM	Q&A Plenary Discussion
1.00 - 2.00 PM	LUNCH & POSTER SESSION
SESSION 4: AMR SURVEILLANCE AND MONITORING	
SESSION CHAIR:	Moses Olum and Veronicah Chuchu
2.00 - 2.15 PM	Molecular Characterization of β -Lactamase and Carbapenemase- Producing Enterobacterales in Children Under Five in Kibera, Nairobi Kenya - Beatrice Oduor
2.15 - 2.30 PM	Assessment of antibiotic resistance patterns among Patients in the intensive care unit at Kenyatta national Hospital - Levis Gitau Kimunyu
2.30 - 2.45 PM	Longitudinal assessment of child growth and extended-spectrum cephalosporin-resistant Enterobacterales colonization in infants from Kibera informal settlements - Celestine Wairimu
2.45 - 3.00 PM	Q&A Plenary Discussion
3.00 - 3.15 PM	Emerging <i>Klebsiella Pneumoniae</i> Carbapenem Resistance in a Kenyan Private Tertiary Hospital: Snapshot Pilot Prevalence Study and In Patient Risk - Dr. Peter Njenga
3.15 - 3.30 PM	Antimicrobial Resistance Patterns of <i>Escherichia coli</i> and <i>Enterococcus</i> Species Isolated from ready for market Poultry in Trans Nzoia County, Kenya - Peris Sambili
3.30 – 3.45 PM	Genotypic characterisation of carbapenemase genes among gram negative bacteria isolates at Mbagathi hospital – Dorothy Mutanu Kilonzo

3.45- 4.00 PM	Q&A Plenary Discussion
4:00 - 4:30 PM	HEALTH BREAK & POSTER SESSION
DAY 3 – Thursday 20th November 2025	
<i>Time</i>	<i>Activity</i>
8.00- 8.30 AM	Arrival and registration
8:30 - 9:00 AM	POSTER SESSION
SESSION 5: AMR SURVEILLANCE ,MONITORING AND INNOVATION	
SESSION CHAIR:	Winnie Mutai
9.00 - 9.15 AM	<i>Prevalence and Antimicrobial Resistance Profiles of Escherichia coli from Aquaculture Environments in Kenya - Dr. James Wanjama Kabugu</i>
9.15 - 9.30 AM	<i>Sporadic distribution of beta-lactamases genes in phenotypically resistant bacteria from Thika level five hospital - Simon Chege Irungu</i>
9.30 - 9.45 AM	<i>Longitudinal assessment of rectal colonization among women and children in Kibera, Kenya - Teresa Ita</i>
9.45 - 10.00 AM	<i>Linking antibiotic residue degradation to microbial dynamics and greenhouse gas emissions in manure - Arusey Chebet</i>
10.00 - 10.15 AM	Q&A Plenary Discussion
10:15 - 11:00 AM	HEALTH BREAK & POSTER SESSION
SESSION 6: AWARENESS, INNOVATION & AMU	
SESSION CHAIR:	Daniel Waruingi
11.00 – 11.15 AM	<i>Building a Culture of Antimicrobial Stewardship Among University Students: A Peer-Led Awareness Initiative at JKUAT - Victor Odira</i>
11.15 - 11.30 AM	<i>Peptaibols from Trichoderma Species as Emerging Antifungal Agents: A Mini-Review of Biotechnological Prospects for Kenya - Charity Lyavuli Akweya</i>
11.30 -11.45 AM	<i>Point prevalence survey of antibiotic use at a county referral hospital in Nairobi County – Dr. Marion Ong'ayo</i>
11.45 - 12.00 PM	Q&A Plenary Discussion
12.00 - 12.15 PM	<i>Quantification of antimicrobial use in semi-intensive broiler farms in Kenya using mass-, dose- and count-based indicators - Naomi Kemunto Peter</i>
12.15 -12.30 PM	<i>Impact of antimicrobial stewardship behaviour modification interventions on one health practice in Northern Kenyan – Esson Wambugu Njau</i>
12:30 – 12:45 PM	<i>Adherence to infection prevention practices at caesarean section: Quality improvement and antimicrobial resistance stewardship in obstetric safe surgery - Mary Muthengi</i>
12:45 – 1:00 PM	Q&A Plenary Discussion
1.00 – 1:30 PM	CLOSING REMARKS & End of symposium
1.30 - 2.30 PM	LUNCH & POSTER SESSION

ABSTRACTS

A. SURVEILLANCE AND MONITORING

Antimicrobial Susceptibility Profile of Escherichia coli Isolates Received in National Microbiology Reference Laboratories (NMRL) for Retesting Between 2022 and 2023**Teresia Nyaga¹, Josiah Njeru¹, Susan Githii², John Mburu³, Jenifer Njuhigu³, Jully Okonji⁴**¹National Public Health Laboratories ²National Antimicrobial Stewardship Committee ³National Antimicrobial Stewardship Interagency Committee⁴Association of Public Health Laboratories**Background:**

Escherichia coli is a critical pathogen identified by the World Health Organization (WHO) for antimicrobial resistance (AMR) surveillance. It is among the most frequently isolated bacterial pathogens globally and a leading cause of bacteremia in developed countries. In sub-Saharan Africa, E. coli causes an estimated 250 million infections and 65,000 deaths annually. The emergence of resistant strains poses a major public health concern, complicating treatment and underscoring the need for continuous monitoring through robust AMR surveillance programs.

Methodology:

A total of 147 E. coli isolates from urine samples were received at the National Microbiology Reference Laboratory between January and December 2023 from sentinel AMR surveillance sites. Identification was performed using Matrix-Assisted Laser Desorption Ionization Time of Flight Mass Spectrometry (MALDI-TOF MS), and antimicrobial susceptibility testing (AST) was conducted using the Vitek 2 Compact system. Each isolate was tested against antibiotics recommended in the Kenya national AMR surveillance strategy and CLSI M100 (2023) guidelines.

Results:

Of the 147 isolates, 76% were resistant to ampicillin, 65% to co-trimoxazole, and 52% to cefuroxime. Lower resistance was observed for gentamicin (18%) and meropenem (4%). Twenty-eight percent were extended-spectrum beta-lactamase (ESBL) producers, and 38% exhibited multidrug resistance (MDR).

Conclusion:

High resistance to commonly used antibiotics and the presence of ESBL and MDR strains highlight the urgent need for strengthened AMR surveillance, prudent antibiotic use, and effective infection control measures to combat antibiotic resistance in clinical settings.

Modelling Antibiotic Resistance in WHO-Priority Pathogens in Kenya: A Machine Learning and Epidemiological Approach**George Wanjiru¹, Newton Lijoodi²**¹University of Cambridge ²Moi University**Background:**

Antimicrobial resistance (AMR) poses a growing global health challenge, disproportionately affecting low- and middle-income countries where surveillance and stewardship systems are limited. In Kenya, increasing resistance among WHO-priority pathogens threatens treatment effectiveness, patient safety, and progress toward universal health coverage. To address this, data-driven approaches that integrate epidemiology and artificial intelligence (AI) are needed. This study aimed to model multidrug resistance (MDR) patterns in Kenya, identify key predictors, and develop decision-support tools to strengthen AMR surveillance and stewardship.

Methodology:

We conducted a retrospective analysis of 36,000+ isolates (2013–2023) from the Pfizer ATLAS dataset, focusing on eight WHO-priority pathogens (*E. coli*, *K. pneumoniae*, *A. baumannii*, *S. aureus*, *S. pneumoniae*, *Salmonella* spp., *Shigella* spp., and *P. aeruginosa*). Resistance was stratified by pathogen, patient type, infection source, and demographics. MDR was modeled using logistic regression and XGBoost, with interpretability supported by SHAP values. A stewardship prioritization framework was mapped to the AWaRe antibiotic classification.

Results:

Logistic regression achieved an AUC of 0.79, while XGBoost improved predictive accuracy to 0.86 (Sensitivity: 82%, Specificity: 77%). Significant predictors of MDR included inpatient status, bacterial species, older age, and infection source. SHAP analysis highlighted patient-level heterogeneity, enhancing model interpretability. Stewardship mapping revealed the highest resistance Access antibiotics (e.g. Ampicillin 95.4%, Penicillin 59.8%), followed by Watch antibiotics (e.g., Erythromycin 53.7%, Ceftazidime 50.5%), while Reserve drug Linezolid remained effective.

Conclusion:

This is the first interpretable machine learning-based mapping of MDR patterns in Kenya. The findings highlight the potential of AI-driven tools to support empirical prescribing, guide stewardship, and inform adaptive AMR policies.

Antimicrobial Resistance Patterns of *Escherichia coli* and *Enterococcus* Species Isolated from ready for market Poultry in Trans Nzoia County, Kenya

Peris Sambili^{1,2,3}

¹University of Nairobi, ²National veterinary Laboratory-Eldoret, ³National veterinary Reference laboratory -Nairobi

Background:

Antimicrobial resistance (AMR) is a growing threat to both animal and human health, particularly in food-producing animals where antibiotic use is common. This study aimed to determine the antimicrobial resistance patterns of *Escherichia coli* and *Enterococcus* species isolated from cloacal swabs of market-ready poultry (broilers, layers, and kienyeji) in Trans Nzoia County, Kenya.

Methods:

A total of 300 cloacal swabs were collected and analyzed at the National Veterinary Laboratory (NVL), Eldoret. Bacterial isolation and identification were conducted using standard microbiological procedures, and antimicrobial susceptibility testing was performed using the disc diffusion method in accordance with CLSI guidelines.

Results:

From the samples, 56 *E. coli* and 58 *Enterococcus* isolates were recovered. *E. coli* showed high sensitivity to carbapenems (98.2%), cephalosporins, and gentamicin but demonstrated high resistance to tetracycline (83.9%), trimethoprim-sulfamethoxazole (80.4%), and ampicillin (57.1%). *Enterococcus* isolates were highly sensitive to ampicillin (98.3%) and vancomycin (77.6%) but resistant to tetracycline (86.2%) and erythromycin (74.1%). Ciprofloxacin showed emerging resistance in both organisms.

Conclusion:

These findings indicate substantial resistance to commonly used antibiotics, highlighting misuse and overuse of antimicrobials in poultry production. The study emphasizes the importance of continuous AMR surveillance, enforcement of prudent antibiotic use, and improved biosecurity measures to curb the spread of resistant organisms and safeguard public health.

Analysis of somatic cell count, pathogen distribution and susceptibility test results in dairy cattle on smallholder farms in Kenya

Eugene L Ibayi¹, Linnet Ochieng¹, Lydia Kisoo^{1,2,3}, Nanna Schødt Hansen⁴, Rikke Louise Jensen⁴, Sharon Anyona¹, Abdullahi M Abdi¹, Arshnee Moodley^{1,4}, Dishon M Muloi^{1,2}

¹International Livestock Research Institute (ILRI) ²University of Liverpool ³Helmholtz Centre for Infection Research ⁴University of Copenhagen

Abstract

Quantitative analyses of somatic cell count (SCC), coupled with pathogen characterization and resistance profiling, are essential to elucidate infection dynamics and inform control strategies in dairy systems.

We performed a cross-sectional investigation of 320 lactating cows from 119 farms within a peri-urban Kenyan cooperative. Quarter milk samples (n=1261) were analysed for SCC enumeration, bacteriological culture, and antimicrobial susceptibility testing. Regression models were used to analyse host and farm-level determinants of SCC variation.

Elevated SCC were observed in cows with teat-end clearance of less than 30 cm ($\beta = 3.1$, $p = 0.04$), in mid-lactation ($\beta = 1.56$, $p = 0.03$) and late-lactation ($\beta = 1.7$, $p = 0.02$) animals, and in higher-parity cows (≥ 4 lactations; $\beta = 2.1$, $p = 0.005$). At the farm level, increased SCC was associated with muddy floors ($\beta = 2.2$, $p = 0.04$) and with routine use of antibiotic dry-cow therapy ($\beta = 1.6$, $p = 0.04$). *Streptococcus agalactiae* predominated (72.1%), with contagious mastitis comprising 73.8% of cases, and environmental mastitis 31.5%. Most Gram-positive isolates were pan-susceptible, except for high tetracycline resistance in *Strep* spp. (89.8%) and *Staph. aureus* (100%). 50% of the *E. coli* isolates were wild type.

Mastitis in smallholder dairy systems is characterised by a dual epidemiology, sustained by suboptimal udder health practices and inadequate environmental hygiene at the farm level. Integrated interventions that concurrently disrupt contagious transmission through improved milking hygiene and mitigate environmental exposure via enhanced housing and biosecurity measures, alongside antimicrobial stewardship, are essential to reduce infection pressure and safeguard productivity.

Emerging Klebsiella Pneumoniae Carbapenem Resistance in a Kenyan Private Tertiary Hospital: Snapshot Pilot Prevalence Study and In-Patient Risk

Salman Majid¹, Peter Njenga¹, Shamsa Ahmed¹, Julius Gathungu¹.

¹M.P. Shah Hospital

Background:

Carbapenem-resistant *Klebsiella pneumoniae* (CR-Kp) is a growing global threat. Surveillance data from Sub-Saharan Africa are scarce and largely from public hospitals, yet private facilities who are often heavy carbapenem users, remain understudied. To assess this threat to last-line Gram-negative therapy, M.P. Shah Hospital, Nairobi, conducted a laboratory-based study to quantify meropenem non-susceptibility and explore associations with patient status.

Objectives:

- i) i). Determine the proportion of *K. pneumoniae* isolates non-susceptible to meropenem.
- ii) ii). Assess whether inpatient status, a proxy for antibiotic pressure, predicts resistance.

Methods:

A retrospective pilot study analyzed *K. pneumoniae* cultures processed between January and December 2023. Unique isolates (n=50) were identified via VITEK 2 GN ID/AST GN83 cards, interpreted per CLSI M100 (33rd ed.). Additional agents analyzed included amikacin, ceftriaxone, ciprofloxacin, and nitrofurantoin. Variables: location, specimen type, age, sex, and MICs. Statistical analyses used Wilson 95% CIs, Fisher's exact test, and odds ratios (OpenEpi).

Results:

Of 47 isolates with MICs, 28% (13/47; 95% CI 15–40) were meropenem non-susceptible. Twelve originated from inpatients, yielding 40% non-susceptibility vs. 6% in outpatients (OR = 10.7; 95% CI 1.3–88; $p = 0.017$). Specimen type and age were not

significant. Ceftriaxone resistance was 57% (27/47), amikacin retained 78% activity, ciprofloxacin 54%, and nitrofurantoin 17%. No pan-drug-resistant isolates were detected.

Conclusion:

Nearly one in three *K. pneumoniae* isolates were meropenem non-susceptible, with a tenfold higher risk among inpatients. These findings call for carbapenem restriction, strengthened stewardship, and scalable private-sector AMR surveillance linking phenotypic and molecular data.

Point Prevalence Survey on Antibiotic Use and Hospital-Acquired Infections at a Tertiary Referral Hospital

Ann Mercy Wanjiku¹, Caroline Mwangi¹

¹Kenyatta University Teaching Research and Referral Hospital

Background:

Antimicrobial resistance (AMR) is a growing global health threat, particularly in healthcare settings where healthcare-associated infections (HAIs) contribute to prolonged hospital stays and increased mortality. Monitoring antibiotic use and HAIs are critical to optimizing antimicrobial stewardship and infection prevention.

Objective:

To estimate the prevalence of antibiotic use (AMU) and HAIs, and evaluate laboratory diagnostic utilization at a tertiary hospital in Kenya.

Methods:

A point prevalence survey was conducted in October, 2023, targeting patients in acute care inpatient wards. Sampling was based on hospital size. Trained multidisciplinary teams collected data on patient demographics, clinical details, microbiology, and antimicrobial use from medical records. Data were entered into REDCap and analyzed using R and Python.

Results:

Of 149 patients surveyed, 38% (56/149) had at least one antibiotic prescribed. Of the total 81 antibiotic prescriptions, Ceftriaxone (18.5%), meropenem (17.3%), and metronidazole (12.4%) were most commonly used. Documented indications were present in 94% of prescriptions. Culture tests were requested for 55% of patients on antibiotics. Among 135 patients assessed for HAIs, 8.1% had at least one infection—most commonly bloodstream infections (3%), urinary tract infections (1.5%), and pneumonia (0.7%). Surgical site infections were found in 18% of 34 post-operative patients.

Conclusion:

High antibiotic use and notable HAI prevalence, especially surgical site infections, highlight the need for stronger AMS-IPC collaboration, improved antimicrobial audit feedback, and better use of diagnostics to guide therapy.

Keywords: Antimicrobial resistance, Infection prevention, Antimicrobial stewardship, Healthcare-associated infections

Molecular Characterization of β -Lactamase and Carbapenemase-Producing Enterobacterales in Children Under Five in Kibera, Nairobi, Kenya

Beatrice Oduor¹, Jolly Okonji¹, Edwin Ochieng¹, Godfrey Bigogo², Alice Ouma², Isaac Ngere³, Kimberly McCarthy⁴, Patrick Munywoki⁴, Ashley Styczynski⁴, Jacqueline Safstrom⁴, Ednner Oketch⁴, Samantha Giffen⁴, Linus Ndegwa⁴, Carolyn Herzig⁴

¹Association of Public Health Laboratories Kenya ²Kenya Medical Research Institute Kenya ³Washington State University Global Health Kenya

⁴U.S. Centers for Disease Control and Prevention**Introduction:**

Antimicrobial resistance (AR) surveillance is critical for tracking resistance trends and guiding prevention and control strategies, yet it often demands substantial resources. This study integrated phenotypic and genotypic AR surveillance into Kenya's Population-Based Integrated Disease Surveillance (PBIDS) platform to assess colonization prevalence of extended-spectrum β -lactamase (ESBL) and carbapenemase-producing Enterobacterales among children under five years old.

Methods:

Rectal swabs were collected from outpatient children at a clinic in Kibera, Nairobi, during May 2025. Specimens were cultured on CHROMagar to detect extended-spectrum cephalosporin-resistant Enterobacterales (ESCrE) and carbapenem-resistant Enterobacterales (CRE). Identification and susceptibility testing were performed using VITEK 2. Real-time PCR with the Streck ARM-D kit was used to detect ESBL genes (blaCTX-M-15, blaCTX-M-14), AmpC genes (blaCMY-2, blaDHA), and carbapenemase genes (blaOXA-48, IMP, VIM, KPC, NDM).

Results:

Of 120 children enrolled, 72% (86) were colonized with ESCrE and 4% (5) with CRE. Among ESCrE-positive children, 99% (85/86) harbored ESBL-producing Enterobacterales. blaCTX-M-15 was detected in 82% (70/85), blaCTX-M-14 in 22% (19/85), while blaCMY-2 was absent. Among CRE-positive children, 60% (3/5) carried carbapenemase genes: blaNDM in one child and blaOXA-48 in two. No other carbapenemase genes were detected.

Conclusion:

These results demonstrate the feasibility of integrating molecular and phenotypic AR surveillance into existing platforms. The high prevalence of ESBL-producing ESCrE suggests community-level acquisition and ongoing transmission. In contrast, the low prevalence of carbapenemase-producing CRE indicates recent emergence, underscoring the value of genotypic data for prioritizing containment and response efforts.

Assessment of Antibiotic Resistance Patterns Among Patients in the Intensive Care Unit at Kenyatta National Hospital

Levis Gitau Kimunyu¹, George Mugendi²

¹BPharm, University of Nairobi ²University of Nairobi

Background:

Antimicrobial resistance poses a significant threat to global health, especially in intensive care units (ICUs) where the risk of resistant infections is highest due to the compromised immunity of patients. ICU patients face a high risk of contracting nosocomial infections caused by resistant microorganisms. In Kenya, there is limited current, context-specific data on resistance patterns in ICU settings.

Objectives:

The primary objective of this study was to assess resistance patterns in bacterial strains found in ICU patients to commonly used antibiotics at KNH.

Method:

This retrospective cross-sectional study reviewed laboratory records of blood, pus, and urine samples from ICU patients at KNH from January 2022 to December 2023. The study included 390 patient records selected through universal sampling. Data were collected using a predesigned form and analyzed with SPSS software, which performed descriptive, univariate, and correlation analyses. Results were presented using tables and pie charts.

Results:

The study identified *Klebsiella pneumoniae* (27.9%) and *Escherichia coli* (25.1%) as the most prevalent isolates. High resistance

rates were observed for ampicillin (61.5%) and ceftriaxone (62.6%), while lower resistance was noted for meropenem (25.4%) and amikacin (10.0%). A slight increase in resistance was seen between 2022 and 2023, emphasizing the growing challenge of antimicrobial resistance.

Conclusion:

The findings highlight the urgent need for antimicrobial stewardship programs and infection control measures in ICUs. Further research is required to monitor resistance trends and optimize empirical antibiotic use.

Genotypic Characterisation of Carbapenemase Genes Among Gram Negative Bacteria Isolates at Mbagathi Hospital

Felix Mutwiri Mbuui¹, Dorothy Kilonzo², Hellen Kamwaro², Cyrus Matheka³

¹Kisii University ²Mbagathi Hospital ³Makueni Hospital.

Introduction:

The World Health Organization has identified carbapenem-resistant Gram-negative bacteria (CR-GNB) as high-priority pathogens due to limited treatment options, high morbidity, and high mortality. Molecular surveillance of resistance genes is vital for enhancing infection control and antimicrobial stewardship, particularly in resource-limited settings like Kenya, where routine molecular testing is uncommon.

Objectives of the Study:

To investigate the molecular characteristics of carbapenem resistance genes in Gram-negative bacterial isolates from archived clinical samples at Mbagathi County Referral Hospital.

Methodology:

Phenotypically confirmed Gram-negative isolates, preserved at -80°C in Tryptone Soy Broth with 15% glycerol, were revived and examined. Genomic DNA extraction was performed using the boiling method, followed by multiplex real-time PCR (Streck ARM-D® β -lactamase kit) to identify key carbapenemase genes: NDM, KPC, OXA-48, VIM, and IMP, with the additional capacity to detect the DHA gene. A Cq range of 10–26, along with internal control amplification, served as the positivity threshold.

Results:

The NDM gene was most prevalent, found in 25 out of 32 isolates (78.1%). A single isolate (3.1%) displayed both NDM and DHA. High NDM rates were observed in *Klebsiella pneumoniae* (73.1%), *Acinetobacter baumannii* (100%), and *Escherichia coli* (100%).

Conclusion:

NDM is the predominant carbapenemase in Mbagathi County, with the absence of other significant carbapenemases indicating regional resistance patterns. Continued molecular surveillance is essential for monitoring resistance mechanisms in Kenya.

Keywords: Carbapenem resistance, Gram-negative bacteria, NDM, VIM, OXA-48, IMP, DHA, molecular surveillance

Prevalence and Antimicrobial Resistance Profiles of *Escherichia coli* from Aquaculture Environments in Kenya

James Wanjama Kabugu¹, Johnstone Masinde¹, John Karanja¹, Beatrice Nyambuti¹, Auleria Apopo¹

¹Kenya Fisheries Service

Introduction:

Antimicrobial Resistance (AMR) in bacterial pathogens is a global public health crisis. Aquaculture systems serve as environmental reservoirs for the spread of resistance genes. This study investigated the occurrence and AMR profiles of *E. coli* isolates from aquaculture environments in Kiambu, Nairobi, and Machakos counties.

Methods:

A total of 129 samples were collected, comprising 70 pond water, 49 Nile tilapia, and 10 catfish, across the three counties. *E. coli* isolates were recovered on EMB Agar and confirmed using standard biochemical tests. Antimicrobial Susceptibility Testing (AST) was performed using the Kirby-Bauer disc diffusion method against 12 antibiotics. Beta-lactams (Ampicillin, Cefotaxime, Cefepime), aminoglycosides (Streptomycin, Gentamycin), and fluoroquinolones (Nalidixic Acid, Levofloxacin), following CLSI M100 standards.

Results:

The study confirmed the widespread distribution of *E. coli* across all analyzed sources and counties. The AST results revealed high levels of resistance to Ampicillin, Tetracycline, and Streptomycin across various sample types. Resistance to Ampicillin was high in both pond water (Kiambu, Nairobi, and Machakos) and tilapia (Kiambu and Machakos). Equally, isolates showed high susceptibility to Chloramphenicol, Cefepime, and Gentamycin. Multidrug resistance (MDR) to three or more antibiotic classes was identified, demonstrating variability in AMR prevalence dependent on the specific location and sample type. The presence of MDR *E. coli* in aquaculture environments, its presence across the different counties and sample matrices, is a potential public health risk.

Conclusion:

These findings underscore the need for implementing effective, collaborative containment strategies to mitigate the spread of AMR. Also, promote the prudent use of antimicrobials in both animal and human health sectors.

Keywords: *E. coli*, AMR, aquaculture, pond water, Nile tilapia, catfish, Kenya.

Longitudinal assessment of child growth and extended-spectrum cephalosporin-resistant Enterobacterales colonization in infants from Kibera informal settlements.

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Background:

Infants in informal settlements are frequently exposed to antimicrobial-resistant bacteria through contaminated environments. Extended-spectrum cephalosporin-resistant Enterobacterales (ESCrE) are of particular concern due to resistance to commonly used β -lactam antibiotics, limiting treatment options. This study documented longitudinal growth patterns and ESCrE colonization among infants in Kibera, Nairobi.

Methods:

Infants aged ≤ 9 months were followed through 24 biweekly visits. Anthropometric measurements (length/height and weight) and stool samples for ESCrE testing were collected at each visit. Growth indices—length-for-age and BMI-for-age—were calculated using WHO standards. Children who completed ≥ 12 visits ($n = 133$) were included in the analysis.

Results:

The cohort comprised 65 females and 68 males. Normal growth predominated, with few and transient episodes of stunting or wasting. Among females, 12% experienced stunting, mainly between 8–15 months; among males, 15% exhibited stunting and 6% severe stunting, often within the first six months. Most children maintained normal BMI-for-age; 6% of females were overweight and 3% wasted, while 11% of males experienced repeated wasting and 20% were at risk of overweight. ESCrE colonization was frequent throughout follow-up. At baseline, 58.5% of females and 83.8% of males were colonized, and by five months all participants were colonized at least once. Persistent colonization (≥ 3 consecutive months) occurred in 95.4%

of females and 95.6% of males.

Discussion and Conclusion:

This study demonstrates early, frequent, and persistent ESCrE colonization among infants, with near-universal colonization by five months of age. Despite high colonization, growth outcomes were largely normal, suggesting colonization occurs independently of nutritional deficits. Interventions improving water, hygiene, and sanitation practices are essential to reduce early-life acquisition and transmission in densely populated settings.

Sporadic Distribution of Beta-Lactamases Genes in Phenotypically Resistant Bacteria From Thika Level Five Hospital.

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¹Centre for Research in Infectious Diseases, Mount Kenya University, Thika, Kenya

Abstract

This study investigates the prevalence and distribution of beta-lactamase and carbapenemase genes in gram-negative bacteria isolated from Thika Level Five Hospital, Kenya. Both phenotypic screening and PCR analysis were employed to identify the presence of blaTEM, blaCTX-M, blaNDM, blaOXA, and blaPER genes among clinical isolates. The results revealed a sporadic distribution pattern, with blaTEM showing the highest occurrence (12/44), suggesting its major contribution to antimicrobial resistance in the sampled bacteria. Other genes such as blaCTX-M, blaNDM, blaOXA, and blaPER were also detected at lower frequencies, indicating a diverse genetic basis for resistance. These genes were distributed across multiple bacterial species, including *Escherichia coli*, *Acinetobacter baumannii*, and *Enterobacter cloacae*, emphasizing the potential for horizontal gene transfer among pathogens.

The variability in gene occurrence highlights the multifactorial nature of resistance mechanisms, suggesting the coexistence of both enzymatic and non-enzymatic factors. This complexity poses significant challenges for infection control and effective antibiotic therapy. The findings underscore the urgent need for continuous molecular surveillance, proper antimicrobial stewardship, and implementation of targeted interventions to monitor resistance trends and guide clinical decision-making. Such strategies are essential to mitigate the growing threat of antimicrobial resistance in hospital environments and to preserve the efficacy of existing antibiotics for future use.

B. APPROPRIATE USE OF ANTIMICROBIALS

Point Prevalence Survey of Antibiotic Use at a County Referral Hospital in Nairobi County

Marion Ong'ayo¹, Angela Motanya¹, Dorothy Kilonzo¹

¹Mbagathi County Referral Hospital

Background:

Antimicrobial resistance is one of the top ten global public health threats contributing to approximately 1.3 million deaths annually. The misuse and overuse of antibiotics is the major contributing factor to AMR. Establishing how antibiotics are used in the hospital setting is critical in optimizing antibiotic use and preventing resistance.

Methodology:

The survey adopted a modified WHO Methodology for Point Prevalence Survey on Antibiotic Use in Hospitals which was customized for country context. Data was collected from patient files of patients admitted in 9 wards before 8am on the day of survey. Data was collected over a two day period using the Kobocollect tool kit. Analysis was done using descriptive

statistics.

Results:

148 patients on antibiotics were surveyed. The prevalence of antibiotic use was 54%. Majority (60%) were on 2 antibiotics. Ceftriaxone was the most prescribed antibiotic at 25.5%, 51% of the antibiotics utilized were from the Access category and 46.3% from Watch category. The highest indication for antibiotic use was in respiratory tract infections (39.4%), followed by prophylaxis (21.2%), then blood stream infections (16.1%). 93% of antibiotics were administered intravenously. Culture and antimicrobial sensitivity test requests were done for only 6.1% of the patients.

Conclusion:

Preference for broad spectrum antibiotics, low utilization of specimen cultures to guide therapy, high rates of antibiotic use suggest antibiotic use in this hospital is not optimal. Antimicrobial stewardship programs, policies and guidelines should be tailored to address these areas.

Adherence to infection prevention practices at cesarean section: Quality improvement and antimicrobial resistance stewardship in obstetric safe surgery

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¹Jhpiego¹ Department of Health-Nakuru²

Background:

Antimicrobial resistance (AMR) remains a growing global health threat, while in maternal health, the burden of AMR is particularly concerning due to the high rates of Cesarean Sections (CS), as it increases the risk of postpartum infections by 5-20 times as compared to vaginal delivery. The World Health Organization (WHO) recommends an infection prevention (IP) bundle at CS (prophylactic antibiotics, vaginal cleansing, and surgical skin preparation) that minimizes the use of antibiotics postoperatively. The Global Surgery-funded Obstetric Safe Surgery (OSS) project in Nakuru County, Kenya, aimed at aligning antibiotic prescribing practices at CS with WHO guidelines.

Methodology:

Fifteen trainers of trainers and 25 healthcare providers from five OSS implementing sites were trained on the use of IP bundles, mentorships were done by 12 mentors (July to October 2025) and data has been analyzed. Community post-CS discharge follow-up enhanced referrals and prevented escalation into resistant cases.

Results:

A total of 1752 CSs were performed in the first quarter of implementation. IP bundles adherence rate as per SSC rose from 0% to 88.2%, reducing extended antibiotic use from a regimen of 3-day intravenous antibiotics and 5-day oral antibiotics to a prophylactic regimen of one intravenous dose pre-operatively and post-operatively.

Conclusion:

Implementation of comprehensive, standardized, systems-based interventions bridges policy and practice, contributing to the global fight against antimicrobial resistance.

Access Pathways and Practices in Antimicrobial Use: Insights from Kibera in Nairobi, Kenya

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¹LVCT Health

Background:

Inadequate access to formal healthcare and weak regulation of antimicrobial distribution contribute to inappropriate antimicrobial use in many low-resource urban settings. The widespread misuse of antimicrobials which fuels the growing threat of antimicrobial resistance is common in Kenya's urban informal settlements. This study examined patterns of access and use of antimicrobials within the Raila Community of Kibera, an informal settlement in Nairobi, Kenya.

Methods:

A cross-sectional quantitative household survey was conducted among 684 participants living in Kibera. Data were collected using structured questionnaires on sources of antimicrobials, prescription practices, and treatment behaviors. Descriptive statistics were used to summarize access pathways and usage patterns.

Results:

Among the respondents, 81% reported that they or a family member had used antimicrobials in the previous 12 months. Among these, 37.4% had obtained antimicrobials without a prescription, with chemists and pharmacies being the most common sources (58.1%). The common reasons for using antimicrobials were treatment of fever (34.5%) and management of respiratory infections (33.3%). Incomplete treatment courses were frequently reported (33.2%), primarily due to participants feeling better in the treatment course (38%) and also, due to ignorance of the consequences (18.1%). Further, 34.3% of respondents admitted sharing leftover antimicrobials, often to save money.

Conclusion:

The findings highlight both economic and systemic barriers to appropriate antimicrobial access and use, motivated by unregulated access and significant reliance on self-medication. Strengthening access to affordable, supervised healthcare and enforcing antimicrobial stewardship measures are critical to prevent misuse, reduce risk of resistance, and improve patient outcomes.

Quantification of antimicrobial use in semi-intensive broiler farms in Kenya using mass-, dose- and count-based indicators

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Abstract

The widespread antimicrobials use (AMU) is a major driver of antimicrobial resistance (AMR), which eventually undermine the effectiveness of essential medicines. We quantified AMU and described its patterns, timing, and dosing practices in semi-intensive broiler farms in Kenya, while assessing the association between mortality and antibiotic use. We followed 73 semi-intensive broiler farms for up to six production cycles. Daily data were collected using farm recording forms capturing daily flock size, mortality, and medicine use, with empty medicine packages retained in medicine waste bins. AMU was quantified using mass-, dose - and count based metrics across 310 production cycles. Antibiotics were used in 68% cycles, often in combinations of up to four classes, predominantly during early rearing phase. Over half of the farms used antibiotics in all cycles, though quantities varied. The total quantity used was 397 mg/PCU, with variable contributions from different active ingredients. Dosing ratios fluctuated daily, reflecting alternating periods of correct, under-, and overdosing. As well as calculated treatment durations were longer than both farmer-reported and recommended periods. Daily AMU (mg/PCU) declined significantly with bird age ($P<0.01$) and was higher during the cold and wet season. Cycle-level mortality ranged between 2.4 to 6.9% and daily mortality between 0.12 to 0.29%. Daily mortality was significantly associated with AMU ($P=0.009$) daily dosing ($P=0.039$), revealing frequent multi-antibiotic use, heterogeneous pattern, inconsistent dosing, and deviation from recommended treatment practices.

Impact of antimicrobial stewardship behaviour modification interventions on one health practice in Northern Kenyan pastoralist communities

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Background:

The field of “One Health” aims to integrate the health of ecosystems, people, and animals, with antimicrobial resistance (AMR) being a vital aspect, highlighted by 4.95 million deaths in 2019 due to bacterial AMR. Despite its global significance, research on AMR’s role in One Health is limited in regions like Northern Kenya, where traditional pastoralist communities have historically inhabited.

Objective:

This study evaluates the knowledge, attitudes, beliefs, and practices regarding antimicrobial use among these communities before and after implementing behavioral interventions.

Methodology:

The methodology involved collecting data through semi-structured questionnaires and focused group discussions across five pastoralist communities in Laikipia, Isiolo, and Meru counties, both before and after the interventions. These interventions included training four female elders as Antimicrobial Stewardship (AMS) guardians and educating the pastoralists.

Results:

The results showed that initially, 51 pastoralists participated in the pre-survey, which increased to 104 in the post-survey. Pre-survey data indicated that most pastoralists obtained antibiotics informally from local markets. However, by the post-survey, a majority reported sourcing antibiotics from licensed veterinary outlets. Additionally, there was a significant improvement in knowledge about AMR, as well as a notable reduction in the immediate consumption of meat and dairy products following antimicrobial administration. Many farmers acknowledged consulting the trained female AMS guardians prior to antibiotic use in the post-survey.

Conclusion:

The study concludes that cost-effective behavioral change interventions, including capacity building and empowering female elders as AMS community champions, are effective in instigating significant behavioral changes in pastoralist communities in lower- and middle-income countries.

C. GOVERNANCE AND COORDINATION

Between Policy and Practice: Discursive Fragmentation in Antimicrobial Resistance Governance Across National and County Levels in Kenya

Sammy Gakero Gachigua¹, Anne Ngunjiri¹, Stephen Mulupi¹, Jane Thiomi¹

¹LVCT Health

Background:

Antimicrobial resistance (AMR) poses a growing public health threat in Kenya, demanding coordinated policy responses across multiple governance levels. Within the country’s devolved health system, where 47 county governments manage service delivery while the national government steers policy, regulation, and referral services, AMR has become a complex site of negotiation between global biomedical agendas and local governance realities.

Methods:

The study draws on qualitative data from key informant interviews (KIIs) with 14 policymakers, technical officers, and public health administrators across the national, Nairobi county, and Lang'ata sub-county levels.

Analytic Framework: Guided by critical discourse analysis (CDA), the paper interrogates how language frames AMR within policy discourse – what is named, prioritized, or rendered invisible – and how these framings construct and reproduce power asymmetries in policy processes.

Results:

Findings reveal a predominantly centralized, top-down AMR policy discourse shaped by global biomedical narratives. National-level actors largely define AMR in technical terms, emphasizing surveillance and containment, while county and sub-county actors foreground contextual and social dimensions. This discursive hierarchy produces fragmentation, obscuring community-level realities and constraining collaborative stewardship across governance tiers.

Implications:

To effectively intervene on AMR, clarity in language and framing is critical: how the problem is named determines how it is governed. Bridging national–county discursive divides through dialogical and context-sensitive frameworks can make invisible issues visible, integrate local knowledge, and strengthen Kenya's devolved response to AMR.

Antimicrobial Resistance Governance in Low- and Middle-Income Countries: The Case Study of Kenya

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Background:

Governance is a key building block of health systems, critical for establishing strategic visions, policies, oversight, and ensuring accountability. Building on these tenets, the Global and National Action Plans on AMR Containment have been adopted. However, governance remains under-researched, particularly in antimicrobial resistance (AMR) context. Literature highlights a sub-optimal operationalization of AMR governance in Low-and Middle-Income Countries (LMICs). In this study, we investigate the drivers of its sub-optimal operationalization in Kenya.

Methodology:

We conducted a qualitative study, engaging officers from the One Health (OH) sectors responsible for AMR governance in three counties in Kenya. Data was collected through Key informant interviews and non-participant observations of AMR governance activities and was analysed thematically.

Results:

Some counties have well-defined AMR governance structures, such as the County Antimicrobial Stewardship Interagency Committee (CASIC) or the One Health (OH) committee, demonstrating cross-sector collaboration. Where there is no CASIC, some AMR containment activities are integrated into routine work processes. Across the counties, duplication of mandates and lack of clarity on AMR governance roles and responsibilities leads to unintended neglect of governance functions. The environment sector is the least active in AMR governance. Identified areas of improvement in AMR governance include: 1) alignment of vision across the OH sectors, 2) communication, coordination, and collaboration within and across OH sectors, 3) accountability, monitoring, and feedback mechanisms, 4) enhancing AMR visibility and awareness to leadership and the public, and 5) financial and implementation sustainability.

Conclusions:

To enhance AMR governance, aligned priorities, enhanced collaboration and coordination, and sustained shared commitment remain pivotal.

D. INFECTION PREVENTION AND CONTROL

Molecular Characterization and Risk Factors of Enterotoxigenic Escherichia Coli Among Children Under Five Years in Mukuru Slums, Nairobi County, Kenya**Amos Njuguna¹, John M. Maingi², Cecilia Mbae¹, Phelgona Otieno¹, Kelvin Kering¹, Winfred Mbithi¹, Christine Kioko¹, Rahma Osman¹, Evans Kibet¹, Samuel Kariuki¹**¹Kenya Medical Research Institute (KEMRI) ²Kenyatta University (KU)**Introduction:**

Enterotoxigenic Escherichia coli (ETEC) is a significant cause of diarrheal morbidity and mortality among children under 5 years, particularly in low and middle-income countries. This study aimed to determine the prevalence of ETEC and associated risk factors among children under five presenting with diarrhea in health facilities in Mukuru slums of Nairobi, Kenya, where poor sanitation and hygiene practices are prevalent.

Methods:

Using a cross-sectional design, we recruited 387 children under five years presenting with acute diarrhea. Total nucleic acid was extracted from stool samples and analyzed using a PCR-based customized TaqMan Array Card, which included three ETEC toxin genes (LT, ST_H, and ST_p) and six ETEC colonization factors. A structured questionnaire was employed to collect participants information.

Findings:

ETEC was detected in 148/387 samples, yielding a prevalence of 38.2% (95% CI: 34.2–42.2%). Both heat-labile and heat-stable (LT/ST) enterotoxin genes were the most common (43%) followed by heat-labile (30%), and heat-stable (27%). Colonization factors were present in 52% (77/148) of ETEC-positive samples. Children aged 13–24 months had significantly elevated odds of infection (aOR = 2.48; 95% CI: 1.36–4.52, $p = 0.003$), as well as those aged 25–36 month (aOR = 2.12, $p = 0.025$), 37–48 months (aOR = 2.45, $p = 0.013$), and 49–59 months (aOR = 2.59, $p = 0.027$). Households lacking access to private flush toilets exhibited a tripled risk (aOR = 3.04; 95% CI: 1.38–6.71, $p = 0.006$) of ETEC positivity.

Conclusion:

These findings highlight the urgent need for targeted public health interventions, including improved sanitation and hygiene practices and vaccine introduction, to mitigate the burden of ETEC-related diarrhea among high-risk populations in disease endemic settings.

Prevalence and Antimicrobial Resistance Profile of Nasal Carriage of Staphylococcus aureus and Coagulase-Negative Staphylococcus spp. among Health Workers in Selected Hospitals in Makueni County**Caroline Nzomo¹, Sepha Mabeya², Samuel kariuki³, Susan Githii⁴, Gavin Orangi¹**¹Makueni County Referral Hospital ²Jomo Kenyatta University of Agriculture and Technology ³Kenya Medical Research Institute (KEMRI)⁴National Public Health Institute**Background:**

Staphylococcus aureus is a common cause of hospital-acquired infections, and nasal colonization among healthcare workers (HCWs) poses a potential risk for transmission to patients and colleagues.

Methods:

A cross-sectional study was conducted among 294 HCWs at Makueni County Referral Hospital and Makindu Sub-County Hospital. Nasal swabs were collected and processed for isolation and antimicrobial susceptibility testing of *S. aureus* and coagulase-negative *Staphylococcus* spp.

Results:

Twenty-three (7.6%) nasal swabs were positive for *S. aureus*, with higher prevalence at Makueni County Referral Hospital (9.9%) than Makindu (2.4%) ($p = 0.48$). Colonization rates by cadre were: clinical officers (15.1%), medical officers (13.2%), patient caretakers (8.3%), nurses (3.5%), and laboratory staff (2%). The highest prevalence occurred in the Neonatal Unit (21%) and among HCWs with less than five years of experience (13%). Of the 23 isolates, eight (34.8%) were methicillin-resistant (*S. aureus*, MRSA), and all were multidrug resistant (MDR). Notably, 53.3% of methicillin-susceptible isolates (MSSA) also exhibited MDR.

Conclusion:

Nasal carriage of *S. aureus* among HCWs in Makueni County was relatively low, but the high rate of MDR isolates, including MRSA, is of concern.

Recommendations:

Clinical officers and less-experienced HCWs, including interns, were the most affected groups. Thorough infection prevention and control (IPC) orientation, continuous mentorship, and reinforcement of best practices are recommended for new staff, while experienced HCWs should model and sustain good IPC behaviors.

A Qualitative Assessment of Infection Prevention and Control in four Public Hospital Newborn Units in Kenya

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Introduction:

Newborn Units (NBUs) are the first extrauterine environments for small and sick newborns. The standards of Infection Prevention and Control (IPC) in NBUs thus affect the recovery and wellbeing of hospitalized newborns. In this study, we assess the implementation of IPC measures in four public hospital NBUs in Kenya.

Methods:

We conducted a qualitative study combining in-depth interviews with clinicians, nurses and hospital support staff, focus group discussions with mothers of hospitalized newborns, and non-participant observations of how IPC measures are implemented in the NBUs. Data was analysed thematically using Nvivo 12.

Results:

Routine cleaning of ward environment, newborn care technologies and feeding items is dependent on availability of cleaning supplies (water, soap, sodium hypochlorite) and persons to conduct cleaning tasks. In NBUs, hygiene related tasks are shared by mothers, health care workers, and hospital support staff. NBU infrastructure, such as the space available for service provision, functionality of sinks, taps, and toilets affect the quality of hygiene. For instance, overcrowding in NBUs and sharing of equipment such as incubators make cleaning difficult, while broken sinks or taps compromise hand washing. Health care worker and mothers' handwashing behaviour is affected by individual practices and availability of soap and water for hand washing, and sanitizer and gloves for healthcare workers, which are essential when handling, treating, and feeding babies.

Conclusion:

In NBUs, availability of IPC resources, the infrastructure, and healthcare worker and mothers' behaviour affect

implementation of IPC measures and should be addressed concurrently to enhance wellbeing of hospitalized newborns.

E. INNOVATION (RESEARCH AND DEVELOPMENT)

Linking antibiotic residue degradation to microbial dynamics and greenhouse gas emissions in manure

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Abstract

The widespread use of antibiotics in livestock poses environmental and public health risks due to their persistence in manure. This study examined the fate of Tylosin (100, 700 mg kg⁻¹), Enrofloxacin (29, 200 mg kg⁻¹), and Oxytetracycline (229, 1600 mg kg⁻¹) in cattle manure under aerobic incubation for 110 days, and their impacts on microbial communities and associated CH₄ and N₂O emissions. Antibiotics were quantified by LC-MS/MS, and microbial DNA analyzed via shotgun metagenomics. All antibiotics showed biphasic degradation, with rapid loss in the first 21 days: Tylosin degraded most (99.0%), followed by Enrofloxacin (83.4%) and Oxytetracycline (73.3%). Microbial community alpha diversity was stable, but shifts were separated primarily by antibiotic class. Treatment explained ~21% of between-sample variation ($p = 0.001$). Concentration explained an additional ~3%. False Discovery Rate-corrected correlations linked functional groups to greenhouse gas fluxes: Pseudomonadota and Bacteroidota were positively associated with both gases, CH₄ ($\beta = 0.51$) N₂O ($\beta = 0.47$). Ignavibacteriota showed the strongest positive associations, CH₄ ($\beta = 0.62$), N₂O ($\beta = 0.61$), whereas Planctomycetota were negatively associated ($\beta = -0.85$), and Verrucomicrobiota $\beta = -0.31$. There was a temporal recomposition from Proteobacteria to Bacteroidota modulated by the treatments. Methanogens were more evident at later storage of manure. Critical human-associated antibiotic-resistant genes detected in manure were capabemems, methicillin, vancomycin, and aminoglycosides. Overall, the persistence of antibiotics in manure and their effects on emission-related microbes highlight environmental and climate risks. Improved manure management and prudent antibiotic use are essential to reduce emissions and antimicrobial resistance.

Longitudinal assessment of rectal colonization among women and children in Kibera, Kenya

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Introduction:

Extended-spectrum cephalosporin-resistant Enterobacterales (ESCrE) pose a major public health threat, with individuals carrying them being at high risk of difficult to treat infections. Despite the high risk of resistant infections among colonized individuals, the dynamics of human colonization by ESCrE are poorly understood in low- and middle-income countries.

Methods:

We conducted a 12-month longitudinal study of 133 households in Kibera, an informal settlement in Kenya. Each household constituted one adult and one child participant whose stool samples were collected every two weeks and tested for the presence of ESCrE.

Results:

All participants were colonized at least once during the study period. Of the 133 women, 25 (19%) were colonized with ESCrE every time they provided a sample. Ninety-three (70%) were persistently colonized. However, none remained uncolonized throughout the study. The average colonization frequency was 16 times. Children had an average colonization frequency of 14 times, with only 27 (21%) of the children demonstrating colonization with ESCrE every time they provided a sample, while 73 (55%) were persistently colonized over the study. Moreover, with each sample provided, simultaneous colonization was observed in only 11 pairs (8%) of the 133 mother-child pairs. Overall, nearly half of the pairs, 61 (46%), were simultaneously colonized for at least 6-months.

Conclusion:

High prevalence of ESCrE was observed in this population, suggesting varied transmission dynamics. Investments in data-driven surveillance are therefore needed to develop targeted interventions to mitigate the public health threat posed by ESCrE.

Peptaibols from *Trichoderma* Species as Emerging Antifungal Agents: A Mini-Review of Biotechnological Prospects for Kenya

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Abstract

Antifungal resistance (AFR) is an escalating yet under-recognized component of the global antimicrobial resistance (AMR) crisis. Fungal pathogens such as *Candida*, *Aspergillus*, and *Fusarium* are increasingly resistant to azoles and polyenes, prompting the search for novel antifungal compounds. *Trichoderma* species, well known for their biocontrol activity, produce short linear peptides called peptaibols that exhibit potent antifungal and membrane-permeabilizing effects. Global studies show that *T. asperellum*, *T. harzianum*, and *T. longibrachiatum* secrete peptaibols such as trichotoxins, and asperelines that inhibit major fungal pathogens with >80 % growth suppression through ion-channel disruption and cell leakage [1–4].

This mini-review synthesizes current evidence on *Trichoderma*-derived peptaibols and explores their translation to Kenya's context. Solid-state fermentation using locally abundant cereals such as sorghum and millet, widely cultivated in Machakos, Kitui, and Meru counties, could provide a cost-effective substrate for scalable peptaibol production [2,5]. Comparative data indicate that solid-state systems yield higher metabolite and enzyme levels than submerged fermentation, suggesting feasibility for small-scale biotech applications in resource-limited settings.

Trichoderma-based peptaibols could thus serve as sustainable antifungal leads within Kenya's AMR Action Plan 2025 framework. Further integration of molecular screening and predictive analytics of peptaibol biosynthetic clusters will be key to guiding scale-up and regulatory adoption.

Keywords: Peptaibols, *Trichoderma*, antifungal resistance, and biotechnology.

F. PUBLIC AWARENESS AND EDUCATION

Building a Culture of Antimicrobial Stewardship Among University Students: A Peer-Led Awareness Initiative at JKUAT

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Background:

University students, particularly those studying science and health-related courses, are future professionals who will influence how antimicrobials are used in Kenya. However, awareness of antimicrobial resistance (AMR) and responsible antibiotic practices remains limited among young adults.

Objective:

This study aimed to assess the impact of a peer-led awareness program on students' knowledge and attitudes toward antibiotic use and AMR.

Methods:

An intensive six-weeks campaign was implemented at JKUAT college of health sciences, combining interactive lectures, quizzes, posters, and social media discussions led by trained student researchers. A short survey was administered before and after the campaign to evaluate changes in understanding and self-reported behavior regarding antibiotic use.

Results:

After the intervention, there was a marked increase in correct knowledge of antibiotic use (from 54% to 82%) and a significant drop in students who reported purchasing antibiotics without a prescription (from 32% to 14%). Participants described the peer-led approach as relatable and motivating.

Conclusion:

Engaging university students through peer-driven awareness programs is an effective, low-cost strategy to promote responsible antimicrobial use. Integrating similar initiatives into higher education settings can contribute to sustained AMR prevention efforts and align with Kenya's National Action Plan on AMR (2023–2027).

Genomic analysis of *Pseudomonas aeruginosa* recovered from surgical site infections from a referral hospital in Western Kenya reveals dominance of high-risk subtypes.

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Abstract

We set out to analyze the genome sequences of 13 *Pseudomonas aeruginosa* isolates recovered from Surgical Site Infections (SSIs) at a level 5 referral facility in western Kenya. These strains of *P. aeruginosa* displayed multiple resistance to amikacin, ciprofloxacin, piperacillin, and ceftazidime. Our findings show that multi-drug efflux pumps are the dominant antimicrobial resistance mechanism, whereas antibiotic inactivation and target protein alteration mechanisms were identified but are less common. Genomic analyses revealed substantial variability in the size and number of insertion sequences (IS) and genomic islands (GIs). IS3 carrying various virulence genes and transposases was the most common. Virulence in laboratory strains of *P. aeruginosa* is largely under the control of quorum sensing (QS). However, we noted several mutations in key QS regulators among the strains studied here, and this correlated well with the production of key QS signal molecules. High-risk multi-locus sequence types ST274 and ST244 dominated among the isolates. Our findings suggest the need for enhanced surveillance of *P. aeruginosa* and the robust implementation of infection prevention and control measures in healthcare facilities in sub-Saharan Africa.

G. YOUTH SESSION

National Youth in Action for Containment and Prevention of AMR: ACT NOW; Protect Our Present Secure Our Future

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¹Kenya National Public Health Institute (NPHI)

²AMR Now³Quadripartite Technical Working Group on Youth Engagement on AMR⁴WAAW Youth Event Sub-Committee**Background:**

Antimicrobial resistance (AMR) is a growing global health threat, requiring coordinated multisectoral action. In Kenya, the National Youth in Action for AMR initiative was established in 2019 and integrated into the WAAW Youth Sub-Committee to empower young people to lead AMR prevention and containment efforts. The initiative focuses on strengthening youth capacity, promoting grassroots awareness, and fostering youth-led innovation, advocacy, and collaboration using a One Health approach.

Objectives:

To strengthen youth knowledge and skills in AMR, antimicrobial stewardship, and One Health; to promote youth-led awareness, advocacy, and behavior-change initiatives at national and community levels; to support youth-driven innovation and research addressing AMR prevention and containment; and to build a coordinated national network of youth AMR champions.

Methodology:

The initiative employs multi-platform engagement, including annual webinars, X-Space conversations, youth competitions, community engagement calls, and collaboration with counties, academic institutions, and development partners. Activities involve capacity-building sessions, digital advocacy, community outreach, innovation challenges, and participation in national and global AMR forums.

Results:

Since 2020, over 2,000 youth have been trained through webinars, and more than 1,300 participants engaged through X-Space discussions. Community engagement calls have generated over 100 youth-led reports showcasing grassroots AMR interventions. The annual youth innovation competition has attracted 200+ creative entries, with some recognized internationally. Strengthened partnerships have enabled youth participation in initiatives such as the Trinity Challenge and Quadripartite Youth Engagement Working Group.

Conclusion:

Youth engagement is a powerful driver of AMR containment in Kenya. Strengthening capacity-building, funding, collaboration, digital outreach, and establishing a national youth AMR network will enhance sustainability, amplify youth voices, and accelerate progress toward AMR prevention and a healthier future.

Empowering Youth as Agents of Change for Antimicrobial Resistance Prevention Through Applied Poultry Biosecurity Training in Sub-Saharan Africa

N. Ngere^{1,7}, W. Ndaga², A. Saheed³, W. Akello^{2,5}, H. Abdulbasit⁴, B. Adeyeye⁴, R. Omani⁶, J. Asin⁸

¹AMR Now ²African Youth AMR Alliance Task Force (AYARA-TF) ³International Veterinary Students Association (IVSA) Nigeria

⁴AMR Interservice Training Program (AMR-ITP) ⁵Makerere University ⁶University of Liege ⁷Kisii University

⁸Ecumenical Pharmaceutical Network

Background:

Antimicrobial resistance is an urgent global health challenge. Young people are an underutilized resource in the fight against AMR, particularly in Sub-Saharan Africa, where nearly 70% of the population is under 30. The poultry value chain provides an entry point because it is widely practiced and characterized by weak biosecurity and frequent antimicrobial misuse. Strengthening youth capacity in poultry biosecurity can improve antimicrobial use and livestock health.

Objective:

To equip youth with practical skills in poultry biosecurity, antimicrobial resistance prevention, and Social and Behavior

Change Communication.

Methods:

A Trinity Challenge seed grant supported development of a 12-session curriculum covering poultry production systems, disease pathways, biosecurity measures, antimicrobial use drivers, vaccination, nutrition, and farmer engagement. The curriculum employed adult learning principles, incorporating participatory methods, problem-solving tasks, and farm observation exercises. A 6-week virtual program was delivered in September and October 2025 across Nigeria, Kenya, and Uganda. Participants were trained to use the Poultry Farm Visit Conversation Guide and Farmer Commitment Card. Field implementation is ongoing.

Results:

A total of 631 youths from 29 countries expressed interest (Nigeria 41%, Kenya 31%, Uganda 4%, others 24%). Screening enrolled 250 participants (Nigeria 41.9%, Kenya 33.2%, Uganda 7.4%, others 17.5%). Twelve sessions totaling 25 hours were delivered. One hundred and eighty participants completed the program (72%), and 120 qualified as Biosecurity Champions (67%). Reflections indicated improved understanding and readiness for farmer engagement.

Conclusion:

This initiative demonstrates a feasible model for empowering youth as agents of change for antimicrobial resistance prevention through applied poultry biosecurity training.

Empowering the Next Generation of Scientists to Combat Antimicrobial Resistance (AMR) through Phage Research

Nelson Wachira¹, Ely Aboka¹

¹Phage Hunters Training and Research Program

Abstract

Phage Hunters Training and Research Program (PHTRP) implemented a multifaceted intervention (July 2024–Oct 2025) to raise awareness and build technical capacity in phage research as a response to antimicrobial resistance (AMR). The program combined three pillars: global outreach and advocacy (multiple LinkedIn Live and panel discussions engaging experts, policymakers and public audiences across >10 countries); a sustained Journal Club that mentored 20 undergraduates from five Kenyan universities to develop critical literature skills and capstone proposals; and a flagship 10-day hands-on Phage Genome Analysis & Comparative Genomics workshop that trained 31 participants in wet-lab phage isolation, genome sequencing, annotation, comparative genomics and phylogenetics. Activities reached 500+ people, produced award-winning student teams in national and Food and Agriculture Organization of the United Nations (FAO) challenges, and forged institutional partnerships (e.g., Kenya Institute of Primate Research, Technical University of Kenya) and international phage networks. Financial and infrastructure limits constrained scale but were mitigated through partnerships and grassroots fundraising. By linking mentorship, practical training and advocacy, PHTRP established a reproducible, sustainable pipeline to accelerate phage discovery and policy engagement against AMR in low-resource settings.

Driving Community Change Through Youth Leadership: A Multi-Faceted Approach to Antimicrobial Resistance Awareness in Kisii County, Kenya

Odiwuor Byrone¹, Violet Otieno¹, Obed Apiri¹, Joseph Kioko¹

¹Phoenix Community Based Organization, Kisii, Kenya

Abstract

Antimicrobial Resistance (AMR) poses a critical global health threat, implicated in over 1.27 million deaths annually. In response, Phoenix Community Based Organization (CBO) initiated a sustained, multi-year AMR cause program from

2023-2025, targeting diverse demographics in Kisii County through a One Health approach. The objective of the CBO is to promote responsible antimicrobial use and proper hygiene through community awareness, education, and behavioral change communication, leveraging youth as key change agents.

The intervention employed an integrated strategy combining physical and digital platforms. Key activities included an AMR symposium for 300 students and health workers; age-appropriate mentorship for 1,200 primary school students; a 58km cycling campaign with 40 youth champions; a regional online campaign engaging 625 East Africans; sensitization of 35 influential motorcycle taxi operators; and an Antimicrobial Guardian Pledge.

The program directly engaged over 1,800 individuals, educating 1,500 students and distributing 2,000 informational materials. It successfully established sustainable structures, including school AMR clubs and a network of youth champions. The innovative integration of physical activity, cross-border collaboration, and leveraging existing community networks proved highly effective in generating widespread engagement and personal accountability.

This model demonstrates the powerful impact of a youth-led, multi-pronged approach to raising AMR awareness. Its success underscores the value of innovative and sustainable interventions that move beyond traditional campaigns. Future efforts will focus on program expansion, deeper healthcare partnerships, and hosting a regional youth AMR summit to amplify its impact.

From University Grounds to Community Impact: Advancing AMR Awareness Through Youth Leadership and Community Engagement

Cheryl Jeruto¹, Collins Kioko¹, Gail Auma¹, Bitange Faith¹, Saad Ibrahim¹, Dennis Wambugu¹

¹Nairobi University Pharmacists Students' Association

Abstract

The World Antimicrobial Awareness Week commemoration in November 2024, organized by the Nairobi Pharmacists Students' Association (NUPSA), was an initiative aimed at strengthening awareness and promoting action against Antimicrobial Resistance (AMR), under the theme 'Educate, Advocate and Act Now!'. The activities engaged pharmacy students, health science students, and the community as a whole. The program combined media outreach, webinars, social media campaigns, digital competition, and community engagement to promote responsible antimicrobial use and the one health approach. Media outreach was conducted through a UNC TV panel discussion and a YouTube live stream. The interdisciplinary virtual webinar inspired students from various faculties to take up the role of championing AMR advocacy. The social media campaign and digital competition extended AMR awareness beyond the campus environment. A physical champions training equipped student volunteers with skills to educate the community effectively on AMR. The AMR sensitization walk targeted the Kenyatta market community, where volunteers engaged residents and business owners on practical ways to prevent AMR. Overall, the hybrid model ensured a wide reach, strong youth participation, and a meaningful community impact.

Winning the Game Against Antimicrobial Resistance: Integrating Student Research, Sports, and Digital Advocacy for Scalable AMR Awareness

Kelvin Kipkoech¹, Mercy Chepkoech¹, Fredrick Ochieng¹, Antony Sifuna¹, Peter Nyongesa¹, Lindsay Olima²

¹Masinde Muliro University of Science and Technology, Kakamega, Kenya

²Kakamega County Antimicrobial Stewardship Interagency Committee, Kenya

Background:

Antimicrobial resistance (AMR) is a growing global health threat requiring innovative, community-driven interventions. Youth play a key role in antimicrobial stewardship (AMS) as influencers, early adopters of positive health behaviours, and future One Health advocates. The Masinde Muliro University Students Antimicrobial Stewardship Chapter (MMUSTAC)

conducted a series of youth-led activities during World Antimicrobial Awareness Week (WAAW) 2024, to strengthen AMR awareness, promote responsible antimicrobial use and generate evidence for targeted interventions.

Methods:

Activities included an AMR-themed football tournament, awareness walk, virtual X Space session, radio talk show, and two research projects. The tournament engaged students and healthcare professionals incorporating AMR education materials and expert-led discussions. The AMR walk reached Kakamega residents with printed educational materials. A multidisciplinary expert panel led the X Space session focused on AMR and One Health principles. Two cross-sectional studies assessed antibiotic practices and hand hygiene among students via surveys, observation, and digital analytics. Both studies were presented at international conferences.

Results:

More than 6,000 individuals were reached across various platforms. The football tournament engaged over 500 participants, AMR walk reached over 1,000 people while X Space attracted more than 2,000 virtual attendees. The talk show at Lubao FM expanded outreach to thousands of listeners. The research findings provided actionable data to inform interventions.

Conclusion:

Youth-led, innovative, and evidence-based approaches significantly strengthen AMS awareness and engagement. Empowering youth is essential for sustainable AMR prevention.



LIST OF POSTERS

A. SURVEILLANCE AND MONITORING

Antimicrobial Susceptibility Profile of Escherichia coli Isolates Received in National Microbiology Reference Laboratories (NMRL) for Retesting Between 2022 and 2023**Teresia Nyaga¹, Josiah Njeru¹, Susan Githii², John Mburu³, Jenifer Njuhigu³, Jolly Okonji⁴**¹National Public Health Laboratories ²National Antimicrobial Stewardship Committee ³National Antimicrobial Stewardship Interagency Committee⁴Association of Public Health Laboratories**Modelling Antibiotic Resistance in WHO-Priority Pathogens in Kenya: A Machine Learning and Epidemiological Approach****George Wanjiru¹, Newton Lijoodi²**¹University of Cambridge ²Moi University**Antimicrobial Resistance Patterns of Escherichia coli and Enterococcus Species Isolated from ready for market Poultry in Trans Nzoia County, Kenya**Peris Sambili^{1,2,3}¹University of Nairobi, ²National veterinary Laboratory-Eldoret, ³National veterinary Reference laboratory -Nairobi**Analysis of somatic cell count, pathogen distribution and susceptibility test results in dairy cattle on smallholder farms in Kenya****Eugene L Ibayi¹, Linnet Ochieng¹, Lydia Kisoo^{1,2,3}, Nanna Schødt Hansen⁴, Rikke Louise Jensen⁴, Sharon Anyona¹, Abdullahi M Abdi¹, Arshnee Moodley^{1,4}, Dishon M Muloi^{1,2}**¹International Livestock Research Institute (ILRI) ²University of Liverpool ³Helmholtz Centre for Infection Research ⁴University of Copenhagen**Emerging Klebsiella Pneumoniae Carbapenem Resistance in a Kenyan Private Tertiary Hospital: Snapshot Pilot Prevalence Study and In-Patient Risk****Salman Majid I¹, Peter Njenga¹, Shamsa Ahmed¹, Julius Gathungu¹.**¹M.P. Shah Hospital**Point Prevalence Survey on Antibiotic Use and Hospital-Acquired Infections at a Tertiary Referral Hospital****Ann Mercy Wanjiku¹, Caroline Mwangi¹**

¹Kenyatta University Teaching Research and Referral Hospital

Molecular Characterization of β -Lactamase and Carbapenemase-Producing Enterobacterales in Children Under Five in Kibera, Nairobi, Kenya

Beatrice Oduor¹, Jully Okonji¹, Edwin Ochieng¹, Godfrey Bigogo², Alice Ouma², Isaac Ngere³, Kimberly McCarthy⁴, Patrick Munywoki⁴, Ashley Styczynski⁴, Jacqueline Safstrom⁴, Ednner Oketch⁴, Samantha Giffen⁴, Linus Ndegwa⁴, Carolyn Herzig⁴

¹Association of Public Health Laboratories Kenya ²Kenya Medical Research Institute Kenya ³Washington State University Global Health Kenya

⁴U.S. Centers for Disease Control and Prevention

Assessment of Antibiotic Resistance Patterns Among Patients in the Intensive Care Unit at Kenyatta National Hospital

Levis Gitau Kimunyu¹, George Mugendi²

¹BPharm, University of Nairobi ²University of Nairobi

Genotypic Characterisation of Carbapenemase Genes Among Gram Negative Bacteria Isolates at Mbagathi Hospital

Felix Mutwiri Mbuui¹, Dorothy Kilonzo², Hellen Kamwaro³, Cyrus Matheka³

¹Kisii University ²Mbagathi Hospital ³Makueni Hospital.

Prevalence and Antimicrobial Resistance Profiles of Escherichia coli from Aquaculture Environments in Kenya

James Wanjama Kabugu¹, Johnstone Masinde¹, John Karanja¹, Beatrice Nyambuti¹, Auleria Apopo¹

¹Kenya Fisheries Service

Longitudinal assessment of child growth and extended-spectrum cephalosporin-resistant Enterobacterales colonization in infants from Kibera informal settlements.

Celestine Wairimu¹, Sylvia Omulo¹

¹Washington State University (WSU) Global Health, Kenya

Sporadic Distribution of Beta-Lactamases Genes in Phenotypically Resistant Bacteria From Thika Level Five Hospital.

Simon Chege Irungu¹, Anthony Kipkoech¹, Racheal Kimani¹, Bernard Kanoi¹, Jesse Gitaka¹

¹Centre for Research in Infectious Diseases, Mount Kenya University, Thika, Kenya

B. APPROPRIATE USE OF ANTIMICROBIALS

Point Prevalence Survey of Antibiotic Use at a County Referral Hospital in Nairobi County

Marion Ong'ayo¹, Angela Motanya¹, Dorothy Kilonzo¹

¹Mbagathi County Referral Hospital

Adherence to infection prevention practices at cesarean section: Quality improvement and antimicrobial resistance stewardship in obstetric safe surgery

Muthengi Mary¹, Wekesa Doreen², Muia Christine¹, Kiiru Samuel¹ and Ruto Daisy¹

¹Jhpiego¹ Department of Health-Nakuru²

Access Pathways and Practices in Antimicrobial Use: Insights from Kibera in Nairobi, Kenya

Bernard Nyauchi¹, Anne Ngunjiri¹, Sammy Gachigua¹, Hanington Olum¹, Jane Thiomi¹

¹LVCT Health

Quantification of antimicrobial use in semi-intensive broiler farms in Kenya using mass-, dose- and count-based indicators

Naomi Kemunto^{1,2}, Dishon Muloi^{1,3}, Soren Saxmose², Arshnee Moodley^{1,2}

¹International Livestock Research Institute (ILRI) ²University of Copenhagen ³University of Liverpool

Impact of antimicrobial stewardship behaviour modification interventions on one health practice in Northern Kenyan pastoralist communities

Njau Esbon¹, Kubai Edna¹, Kibue Duncan¹, Obolensky Lucy^{2,3}, Doig Iain^{2,4}, Beattie Miriam⁵,

¹Nanyuki Teaching and Referral Hospital (NTRH) ²Dharura Global Emergency Care ³Plymouth University Peninsula Schools of Medicine and Dentistry, UK ⁴Bristol Royal Infirmary; ⁵Royal Cornwall Hospitals Trust, UK

C. GOVERNANCE AND COORDINATION

Between Policy and Practice: Discursive Fragmentation in Antimicrobial Resistance Governance Across National and County Levels in Kenya

Sammy Gakero Gachigua¹, Anne Ngunjiri¹, Stephen Mulupi¹, Jane Thiomi¹

¹LVCT Health

Antimicrobial Resistance Governance in Low- and Middle-Income Countries: The Case Study of Kenya

Mercy Musyoka¹, Nancy Odinga¹, John M. Kiragu², Anita Musiega², Hai Hoang Tuan Ngo⁴, Anh Phuong Nghiem⁴, Trang Thu Vu⁴, Edwine Barasa^{2,3}, Sassy Molyneux³, Sonia Lewycka^{3,4}, Edna Mutua¹

¹Health Services Unit, KEMRI Wellcome Trust Research Programme, Nairobi, Kenya ²Health Economics Research Unit, KEMRI Wellcome Trust Research Programme, Nairobi, Kenya ³Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford ⁴Oxford University Clinical Research Unit, National Hospital for Tropical Diseases

D. INFECTION PREVENTION AND CONTROL

Molecular Characterization and Risk Factors of Enterotoxigenic Escherichia Coli Among Children Under Five Years in Mukuru Slums, Nairobi County, Kenya

Amos Njuguna¹, John M. Maingi², Cecilia Mbae¹, Phelgona Otieno¹, Kelvin Kering¹, Winfred Mbithi¹, Christine Kioko¹, Rahma Osman¹, Evans Kibet¹, Samuel Kariuki¹

¹Kenya Medical Research Institute (KEMRI) ²Kenyatta University (KU)

Prevalence and Antimicrobial Resistance Profile of Nasal Carriage of Staphylococcus aureus and Coagulase-Negative Staphylococcus spp. among Health Workers in Selected Hospitals in Makueni County

Caroline Nzomo¹, Sepha Mabeya², Samuel kariuki³, Susan Githii⁴, Gavin Orangi¹

¹Makueni County Referral Hospital ²Jomo Kenyatta University of Agriculture and Technology ³Kenya Medical Research Institute (KEMRI)

⁴National Public Health Institute

A Qualitative Assessment of Infection Prevention and Control in four Public Hospital Newborn Units in Kenya

Nancy Odinga¹, Caroline Waithira¹, Justinah Maluni¹, Gloria Ngaiza², Onesmus Onyango¹, Vincent Kagonya¹, Michuki Maina¹, Sebastian Fuller², Mike English², Sassy Molyneux^{1,2}, Dorothy Oluoch¹, Edna Mutua¹

¹KEMRI-Wellcome Trust Research Programme ²Health Systems Collaborative, Nuffield Department of Medicine, University of Oxford

E. INNOVATION (RESEARCH AND DEVELOPMENT)

Linking antibiotic residue degradation to microbial dynamics and greenhouse gas emissions in manure

Arusey Chebet^{1,2}, Fredrick Gudda³, Linnet Ochieng¹, Fredrick Ng'ang'a¹, Syphyline Kebeney⁴, Dishon Muloi^{1,5}, Wilson Ngetich², Sonja Maria Leitner¹, Yaovi Gildas Hounmanou⁶, Arshnee Moodley^{1,6}

¹International Livestock Research Institute ²University of Eldoret ³Aga Khan University ⁴Moi University ⁵University of Liverpool

⁶University of Copenhagen

Longitudinal assessment of rectal colonization among women and children in Kibera, Kenya

Teresa Ita¹, Sylvia Omulo¹, Paul G. Allen^{2,3}

¹Washington State University Global Health-Kenya; ²School for Global Health - Washington State University

³University of Nairobi Institute of Tropical and Infectious Diseases.

Peptaibols from Trichoderma Species as Emerging Antifungal Agents: A Mini-Review of Biotechnological Prospects for Kenya

Charity Lyavuli Akweya¹, Winnie Mutai¹, Marianne Mureithi^{1,3}

¹Department of Medical Microbiology & Immunology, University of Nairobi ²CAFE SEA EACCR-EDCTP

³KAVI-Institute of Clinical Research (KAVI-ICR).

F. PUBLIC AWARENESS AND EDUCATION

Building a Culture of Antimicrobial Stewardship Among University Students: A Peer-Led Awareness Initiative at JKUAT

Victor Odira^{1,2} ¹Health Rights Advocacy Forum (HERAF) ²Jomo Kenyatta University of Agriculture and Technology

Genomic analysis of *Pseudomonas aeruginosa* recovered from surgical site infections from a referral hospital in Western Kenya reveals dominance of high-risk subtypes.

Sarah Kindiki¹, Sabella Kiprono¹, Oleg Reva², Peter Kuloba¹, Nicholas Mogoi¹, Martin Welche³, Anthony Sifuna¹

¹Masinde Muliro University of Science and Technology ²University of Pretoria; ³University of Cambridge



Antibiotics
Antivirals
Antifungals
Antiparasitics

