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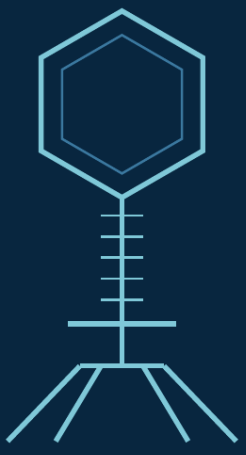
ABSTRACT BOOK

Day 2 - Slovenia-Kenya Phage Science Conference

Research, Innovation and Applications





07 OCTOBER 2026
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KENYATTA NATIONAL HOSPITAL
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08 SELECTED ORAL PRESENTATION ABSTRACTS

Table of Contents

ABSTRACT NO.	ALL AUTHORS	ABSTRACT TITLE	PAGE
01	Linda Guantai, Angela Makumi, Amos Lucky Mhone, Josiah Odaba, Arshnee Moodley, Moses Masika, Sylvain Moineau, Nicholas Svitek	**Kenyan Salmonella Phages Can Reverse Antibiotic Resistance in Field Strains of Salmonella enterica***	4
02	Ndinda Kavesu, Johnstone O. Neondo, Angela Makumi, Sylvain Moineau, Nicholas Svitek, Juliah A. Khayeli	**Phages to the Rescue: Harnessing Bacteriophages for Livestock Disease Control. ***	4
03	Omukunda Caleb Kepha, Josiah Odaba, Steven Ger Nyanjom, Sylvain Moineau, Juliah Khayeli, Nicholas Svitek, and Angela Makumi.	**Isolation and Characterization of Lytic Bacteriophages Against Caprine Mastitis-Associated Staphylococcus species as Potential Biocontrol Agents. ***	5
04	Rachael Njoroge, Humphrey Jumba, Nelly Njiru, Nicholas Svitek, Angela Makumi, Sylvain Moineau, Regina G. Mwatha, Zoë A. Campbell	**Gender considerations for equitable development and adoption of bacteriophage technology for goat mastitis in Kenya ***	6
05	Elkana Mudi, Ely Aboka, Jonathan Mutinda, Dr James Munyao	**Integrating MDR Escherichia coli Surveillance with Phage Bioprospecting in Nairobi's Informal Settlements ***	6
06	Zahra Salehi, Samaneh Bagheri, Samuel Kariuki Ndegwa, Ivy J. Mutai, Linet Lusimba, Ely Aboka, Nelson Wachira, Alice Auko Owiti, James Munyao Kingoo, Abtin Shajiee, Mohammad Javad Rasaee, Erfan Khodadad Shams Abadi	**How safe is your phage? Lessons from ten genome analysis ***	6
07	Meshack Tweya Omwega, Moses Gachoya, Martin Georges, Justin Nyasinga, James Wachira, Collins Kigen, Kevin Kamanyi, Lillian Musila	**In Silico Characterization of Phage Lytic Proteins and Rational Cocktail Design of Phages Against Multidrug-Resistant Pseudomonas aeruginosa ***	7
08	Ryan M. Awori, Tamanna Jafara, Farrah Bashey, Heidi Goodrich-Blair	**Selective inhibition of pathogens decorated with rhamnose by phage tail-like nanomachines ***	7
09	Emmanuel T. Issangya, Victor V. Mosha, Debora C. Kajeguka	**In Vitro Evaluation of Bacteriophage Efficacy against Multidrug-Resistant Pseudomonas aeruginosa: A One Health Approach in Moshi, Tanzania**	8
10	Silas O. Awuor, Eric O. Omwenga, Eliud N. Wafula, Ibrahim I. Daud, Richard M. Mariita	**Lytic and Antibiofilm Activity of Pathogen-Specific Bacteriophages against MDR Diabetic Foot Ulcer Bacteria in Kisumu, Kenya**	8
11	Alfred Katono, Dr John Mwangi	**Phage-Fortified BSF Larvae Feed: Combating Antimicrobial-Resistant Zoonotic Bacteria in Poultry While Boosting Feed Protein in Kericho, Kenya**	9

12	Muhammed-Shadhily Olafenwa Umar, Rukayyah Muhammad, Bashir Sulaiman Muhammad, Janet Yakubu Nale, Hussaini Ibrahim Mohammed, Maryam Aminu	**From Wastewater to Therapy: Characterisation of Therapeutic Bacteriophages Targeting Multidrug-Resistant Bacteria from Ahmadu Bello University Dam**	9
13	Jordan Otieno Ongalo, Caroly Lwanga, Mercy Mututa, Francis guchu	**Isolation and characterization of lytic bacteriophages active against multidrug-resistant Staphylococcus aureus from sewage in Nairobi, Kenya**	10
14	Aboka Ely	**A Competency-Based Undergraduate Workflow for Phage Discovery and Phage Bank Development at TUK**	10
15	Gerald Githinji, Dr. Grace Gitau, Dr Peris Amwayi, Dr Jillani Ngalla	**Bioinformatic Characterization of lytic proteins in an E Coli Bacteriophage**	11
16	Endalkachew Melse, Bikila Alemu, Ashetu Fikadu, Lule Teshager, Tesfaye Kassa	**Isolation and characterization of virulent bacteriophages and their synergism with antibiotic against multidrug-resistant Klebsiella pneumoniae**	11
17	Jonathan Mutinda, Aboka Ely, Elkana Mudi, Dr. James Munyao	**Locally Recovered Klebsiella pneumoniae Lytic Bacteriophages Demonstrate Potent Antibiofilm Activity Against Established Biofilms**	12
18	Mukoma Mark Kamau, Dr. Atunga Nyachieo, Professor Antony Keberia	**Geographic and Ecological Drivers of Phage Efficacy Against Multidrug-Resistant Escherichia coli in Kenya**	12
19	Zahra Salehi	**Bridging the Gap: Perspectives on Bacteriophage-Based Biocontrol Adoption in Iran**	13
20	Abtin Shajiee, Zahra Salehi, Abdolhossein Naseri	**From Hospital Wastewater to Phage Therapy: A Lytic Bacteriophage Targeting Multidrug-Resistant Pseudomonas aeruginosa**	13
21	Samane Bagheri, Mohammad Javad Rasaee	**Isolation and Genome characterization of Salmonella Typhimurium phage**	14
22	Hafiz Anas Saeed, Nazim Hussain, Shafiq Ur Rehman	**Phenotypic, Genomic, And Therapeutic Characterization Of Bacteriophages Targeting Pcr-Confirmed Multidrug-Resistant Acinetobacter Baumannii**	14
23	Md Ramim Tanver Rahman, D. William Cameron, Robert Feibel, Melissa T Cammuso, John C. Bell, Leanne Mortimer, Yang Yu, Bradley W. M. Cook, Heidi Huttunen-Hennelly, Marisa Ann Azad	**Novel α-Helical Peptide-Phage Combination Therapy for the Treatment of Implant-Associated Staphylococcus aureus Biofilms**	15
24	Haftom Legese, Araya Gebreyesus Wasihun, Hadush Negash, Gebrecherkos Teame Gebrehiwot, Letebrhan Weldemhret, Atsbeha Gebreegziabxier Weldemariam, Hayalom Kahsay Bayrau, Mebrahtu Teweldemedhin Shfare, Tsehaye Asmelash Dejene	**Genotypic Diversity and Recent Transmission Patterns of Mycobacterium tuberculosis in Ethiopia**	15

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ABSTRACT 01

Kenyan Salmonella Phages Can Reverse Antibiotic Resistance in Field Strains of Salmonella enterica

Linda Guantai[1,2,3], Angela Makumi[1], Amos Lucky Mhone[1], Josiah Odaba[1*], Arshnee Moodley[1], Moses Masika[2], Sylvain Moineau[3,4,5], Nicholas Svitek[1,6]

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Multidrug-resistant (MDR) Salmonella enterica Enteritidis (S. Enteritidis) is a major cause of foodborne illness, and antimicrobial resistance (AMR) is a leading cause of death in sub-Saharan Africa, driving the need for alternatives to conventional antibiotics. Bacteriophages (phages) offer one such alternative, and phage-antibiotic combination therapy has been proposed to reverse antibiotic resistance while limiting bacteriophage-insensitive mutants (BIMs). We tested two S. Enteritidis-specific phages isolated from Kenyan poultry farms against six Kenyan field strains of S. Enteritidis, generating 44 BIMs, most of which showed reduced phage adsorption. Across 22 antibiotics, most BIMs (25/44) became newly susceptible to antibiotics the parent strain had resisted, 12 retained similar sensitivity, and 4 became newly resistant. One BIM (from Sal 572) gained marked susceptibility to nalidixic acid, gentamicin, and tetracycline, losing all four resistance genes tested (tetA, tetB, strA, strB). Kill-curve assays showed phage-antibiotic combinations reduced bacterial load more than either agent alone in four isolates. These findings support phage-antibiotic combination therapy as a strategy against MDR Salmonella in African settings, using locally isolated phages and field strains.

ABSTRACT 02

Phages to the Rescue: Harnessing Bacteriophages for Livestock Disease Control.

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Mastitis is an inflammation of the mammary gland, a widespread disease in dairy herds. Staphylococcus spp. are major mastitis-associated pathogens, while antimicrobial resistance (AMR) limits treatment options. This study evaluated bacteriophages as a targeted alternative for mastitis control in goats in Kiambu County, Kenya. Goat milk was screened using the California Mastitis Test, and bacterial isolates were identified using biochemical tests, MALDI-TOF mass spectrometry, and 16S rRNA sequencing. Antimicrobial susceptibility and AMR genes were assessed using Kirby-Bauer disk diffusion and PCR. Lytic bacteriophages were isolated from environmental samples and characterized for plaque morphology, pH and temperature stability, and one-step growth kinetics. Individual phages and a cocktail were evaluated for in vitro antibacterial activity. Mastitis-associated Staphylococcus spp. exhibited multidrug resistance and carried clinically important AMR genes. The isolated phages showed broad pH and temperature stability and effective activity against susceptible isolates. The phage cocktail produced greater bacterial growth inhibition than individual phages. Locally isolated bacteriophages demonstrated potential against AMR Staphylococcus associated with goat mastitis and warrant further evaluation as a biological alternative to antibiotics. Bacteriophages could contribute to reduced antibiotic use, mitigation of AMR, and more sustainable dairy goat production in Kenya.

ABSTRACT 03

Isolation and Characterization of Lytic Bacteriophages Against Caprine Mastitis-Associated Staphylococcus species as Potential Biocontrol Agents.

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Mastitis is a disease affecting lactating goats and causes economic losses in small ruminant production systems. This study aimed to isolate and characterize lytic bacteriophages active against mastitis-associated Staphylococcus species from goats in Kajiado and Narok counties, Kenya. 427 goat milk samples were screened using the CMT test, yielding 41 Staphylococcus species, 12 of which were multidrug-resistant. Five lytic bacteriophages (Gr44, Gr70, PigHouse1large, PigHouse1small, and PigHouse2) were isolated and evaluated for their host range, EOP, adsorption, MOI, bacterial killing, pH, temperature, milk, and storage stability. The phages exhibited variable infectivity against S. aureus, S. capitis, S. caprae, S. epidermidis and S. xylosus, with EOP values of 0.141-1.946. Adsorption was rapid, with Gr44 achieving 99% adsorption within 5 minutes. Killing assays suppressed S. aureus growth while selected cocktails controlled growth for 24 hours. Phage activity was retained across the tested pH and temperature ranges and in different milk types, with log reductions reaching 7.8 for Gr44 in goat milk and 7.9 for PigHouse1small in whole cow milk. After four weeks at 4°C, 29.6-44.5% of their initial titres were retained. The phages overall demonstrated broad anti-Staphylococcus activity, rapid adsorption, and measurable stability under several conditions, thus supporting their further investigation as candidates for phage-based control of caprine mastitis.

ABSTRACT 04

Gender considerations for equitable development and adoption of bacteriophage technology for goat mastitis in Kenya

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Considering gender needs early in animal health technology development is important for equitable uptake. Bacteriophage technology is being developed to help goat keepers to manage mastitis. Considering gender dynamics in designing and disseminating bacteriophage technology can make it accessible and useful to women and men goat keepers once commercialized. This study aims to identify gender needs to consider when developing bacteriophage technology and to recommend equitable delivery approaches for different production systems. We conducted an exploratory qualitative study in Bomet, Kajiado, and Kiambu counties, representing semi-intensive, extensive, and intensive goat production systems, respectively. We conducted fifteen (7 with men and 8 with women) gender-disaggregated focus group discussions with goat keepers and 16 key informant interviews with animal health professionals. Data were analyzed thematically using NVivo and interpreted through an intersectional lens. Lack of withdrawal period was a preferred attribute by women and men across the production systems. Across production systems, women preferred a phage product designed for prevention and sold as a shelf-stable milking salve to apply while milking; this would reduce the cost and difficulties of engaging male vets. The findings provide practical recommendations for researchers and development actors to consider in developing phage products that can equitably benefit livestock keepers.

ABSTRACT 05

Integrating MDR Escherichia coli Surveillance with Phage Bioprospecting in Nairobi's Informal Settlements

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Antimicrobial resistance (AMR) surveillance and phage bioprospecting are often conducted separately despite sharing environmental reservoirs and bacterial targets. We developed an integrated workflow linking MDR Escherichia coli surveillance in Nairobi's Mukuru and Kibera informal settlements with phage discovery and characterization. Phage bioprospecting has already yielded 15 E. coli phages, 3 of which were characterised for physicochemical stability, one-step growth, and lytic activity. Phages retained infectivity from -20 to 50°C and across pH 5-11, with complete loss of viability at 70°C. One-step growth analysis indicated a 15-min latent period and an approximate burst size of 100 plaque-forming units per infected cell. The ongoing MDR E. coli surveillance will provide a phenotypically defined panel of locally circulating strains for host-range testing of the 15 phages, linking phage activity to resistance phenotypes identified through surveillance. DNA extraction and whole-genome sequencing are planned to assess phage taxonomy, lytic potential and genetic safety. By linking surveillance with an already established phage collection, this workflow demonstrates how a single environmental AMR investigation can generate both epidemiological information and locally sourced phage candidates for further development.

ABSTRACT 06

How safe is your phage? Lessons from ten genome analysis

Zahra Salehi [1*], Samaneh Bagheri [1], Samuel Kariuki Ndegwa[2,3], Ivy J. Mutai[3,4], Linet Lusimba[3,5], Ely Aboka[2,3], Nelson Wachira[3,6], Alice Auko Owiti[3,5], James Munyao Kingoo[3,7], Abtin Shajiee [1], Mohammad Javad Rasaee [1], Erfan Khodadad Shams Abadi[1]

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Bacteriophage genome analysis is essential for evaluating candidate phages by assessing genome quality, lifestyle, host, taxonomy, and safety-related genes such as AMR and virulence genes. In this study, ten phage genomes were systematically screened using a sequential bioinformatics-based exclusion strategy. Genome quality and viral identity were assessed first, followed by prediction of lifecycle, host, taxonomy, genomic features, and safety. Tools included ViralVerify, CheckV/Phagenomics, PhageAI, PhageLeads, PhageGE, PhageScope, ViPTree, DeepHost, CHERRY, taxMyPhage, PhaGCN, ResFinder, and Phagenomics. Candidates with uncertain viral identity, low genome quality, or temperate characteristics were excluded. HM137666.1, despite a high-quality genome, virulent lifestyle, and predicted Escherichia coli host, was excluded due to a potential DfrA52 trimethoprim-resistance gene detected by Phagenomics. NC_001825.1 showed a complete high-quality genome, virulent lifecycle, concordant prediction of Streptococcus pneumoniae as host, consistent taxonomy, and no AMR or virulence genes, and was prioritized as the most suitable candidate. PhageScope provided the most comprehensive assessment, while PhageScope, Phagenomics, PhageLeads, and PhageAI were the most useful tools for assessing phage therapeutic suitability. Experimental validation is required before therapeutic application.

ABSTRACT 07

In Silico Characterization of Phage Lytic Proteins and Rational Cocktail Design of Phages Against Multidrug-Resistant Pseudomonas aeruginosa

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Bacteriophage lytic proteins and rationally designed cocktails are two complementary strategies against multidrug-resistant Pseudomonas aeruginosa (MDRPA). We first mined five broad-host-range lytic phages, identifying two lytic architectures: an endolysin-holin-spanin cassette conserved across four phages (LytE, LytH, LytS1), and a distinct lytic transglycosylase-spanin system in a divergent phage (LytT, LytS2). LytE and LytT, prioritised for peptidoglycan-degrading activity, underwent in silico characterization (physicochemical profiling, AlphaFold3, docking, MHC I/II immunogenicity/allergenicity), identifying LytE as the stronger candidate on stability and low predicted immunogenicity. Separately, we screened all possible three-phage combinations of the five phages by Omnilog kinetics against strain PA01 (inhibition 16.1–84.1%), then applied a Highest Single Agent independence model to distinguish true synergy. This identified Cocktail D (Phages 1, 3, 4) as synergistic (84.1% observed vs 75.4% expected, Δ=+8.7%, P<0.001), while four combinations were antagonistic (Δ to −24.2%). Cocktail D was then validated against seven genetically distinct MDRPA strains, reducing biofilm biomass by 29–63% (P<0.001), and in Galleria mellonella larvae achieved 80–90% survival across treatment regimens (P<0.001), with no adverse effects. These findings suggest lead standalone protein candidate and a synergistic cocktail candidate for preclinical development.

ABSTRACT 08

Selective inhibition of pathogens decorated with rhamnose by phage tail-like nanomachines

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Precision antibiotics are an effective means to curb antimicrobial resistance. Xenorhabdus bacteria produce bactericidal phage tail-like nanomachines called xenorhabdicin tailocins, and we elucidate their cellular targets, and establish their candidacy as antibacterial precision antibiotics. To determine cellular targets of xenorhabdicin tailocins, we in silico serotyped 42 Xenorhabdus strains with known susceptibilities to 37 xenorhabdicin tailocins. Only the O antigen locus encoded lipopolysaccharide variations and two strains encoded O antigen L-rhamnose. Since this is a non-mammalian sugar, we identified xenorhabdicin tailocins that inhibit these strains. We showed that xenorhabdicin tailocins target O antigen sugars, by creating mutants with O antigen locus gene deletions, and observing drastic differences between mutant and wild type strains in tailocin susceptibility. Through sugar competition assays, we showed that xenorhabdicin tailocins target L-rhamnose, and through tailocin locus gene deletions, we identified a rhamnose-specific tail fibre. Since rhamnose decorates Group B Streptococci (GBS), Enterococci, and Pseudomonas, we screened clinical isolates from these genera for inhibition by rhamnose-specific xenorhabdicin tailocins. Four GBS, two multidrug resistant Enterococci and one drug-resistant Pseudomonas were inhibited. Hence, xenorhabdicin tailocins are an apt platform for creation of precision antibiotics against antimicrobial-resistant pathogens.

ABSTRACT 09

In Vitro Evaluation of Bacteriophage Efficacy against Multidrug-Resistant Pseudomonas aeruginosa: A One Health Approach in Moshi, Tanzania

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Pseudomonas aeruginosa is an opportunistic pathogen associated with multidrug resistance and biofilm formation. Bacteriophages offer a potential alternative to antibiotics. This study assessed resistance, biofilm formation, and lytic phage activity against P. aeruginosa.

A cross-sectional study was conducted in Moshi, Tanzania. A total of 716 human, animal, and environmental samples were screened using standard microbiological methods. Antimicrobial susceptibility was assessed by disc diffusion, biofilm formation by microtiter plate assay, and bacteriophages were isolated using the double-layer agar technique. Plaque assays assessed lytic activity, host range, and phage titres. Data were analyzed using descriptive statistics and non-parametric tests, with $p < 0.05$ considered significant.

Out of 716 samples, 93 (12.99%) were P. aeruginosa. Ciprofloxacin showed the highest resistance, 37 (39.8%). 11 (11.8%) isolates were MDR, including 9 (9.7%) strong biofilm producers. Lytic bacteriophages showed high specificity against P. aeruginosa. Phage treatment significantly reduced bacterial growth ($p < 0.05$) and biofilm biomass, with greater reductions among moderate and weak biofilm producers ($p < 0.01$).

Lytic bacteriophages showed significant antibacterial and anti-biofilm activity against P. aeruginosa, including MDR isolates, supporting their potential as an alternative approach to antimicrobial resistance.

ABSTRACT 10

Lytic and Antibiofilm Activity of Pathogen-Specific Bacteriophages against MDR Diabetic Foot Ulcer Bacteria in Kisumu, Kenya

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ESKAPE pathogens drive antimicrobial resistance (AMR) and difficult-to-treat infections. This study evaluated the in-vitro lytic and antibiofilm activity of pathogen-specific bacteriophages against MDR diabetic foot ulcer (DFU) pathogens in Kisumu County, Kenya.

Five lytic phages targeting E. coli, K. pneumoniae, S. aureus, A. baumannii, and P. aeruginosa were isolated from hospital wastewater and characterized for host range, stability, MOI, and growth kinetics. Planktonic killing and biofilm assays were performed.

Phage susceptibility ranged from 50–100%. Complete susceptibility occurred among tested K. pneumoniae and A. baumannii. Planktonic reductions were 3.0–3.8 $\log_{10}$ CFU/mL, with vB_PaeP-05 (3.8) and vB_AbaP-04 (3.6) showing the greatest activity. All phages showed antibiofilm activity.

Locally isolated phages demonstrated promising lytic and antibiofilm activity against MDR DFU pathogens, supporting further genomic, formulation, combination, and preclinical evaluation.

ABSTRACT 11

Phage-Fortified BSF Larvae Feed: Combating Antimicrobial-Resistant Zoonotic Bacteria in Poultry While Boosting Feed Protein in Kericho, Kenya

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Antimicrobial growth promoters (AGPs) used in poultry farming drive antimicrobial resistance (AMR) in zoonotic bacteria such as Salmonella, E. coli, and Campylobacter, while conventional protein feed sources remain costly. This study investigates whether Black Soldier Fly (BSF) larvae reared on chicken manure and decaying organic matter can acquire lytic bacteriophages effective against these pathogens, and whether a dried, phage-fortified BSF larvae cocktail can replace AGPs. Research questions: (1) Can BSF larvae reared on poultry manure and decaying substrates harbor phages capable of controlling pathogenic poultry bacteria? (2) How does bacterial load in poultry fed the phage-BSF cocktail compare with poultry fed conventional AGPs? Phages will be isolated, characterized, and propagated by the Microbiology Club, University of Kabianga, then incorporated into dried larval meal. A controlled feeding trial, supervised by Dr. John Mwangi, will compare bacterial load, AMR prevalence, and growth performance across phage-cocktail, AGP, and control groups. Findings will be validated with smallholder farmers around Kabianga, Kericho County, Rift Valley. The study aims to deliver a low-cost, locally producible, antibiotic-free intervention that reduces AMR zoonotic risk while addressing poultry feed protein shortages, supporting One Health goals in Kenyan poultry production.

ABSTRACT 12

From Wastewater to Therapy: Characterisation of Therapeutic Bacteriophages Targeting Multidrug-Resistant Bacteria from Ahmadu Bello University Dam

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The global rise in antimicrobial resistance (AMR) underscores the need to understand links between clinical pathogens, environmental reservoirs, and bacteriophages as potential therapeutics. This study investigated multidrug resistance (MDR) in Escherichia coli, Klebsiella pneumoniae, and Staphylococcus aureus from Ahmadu Bello University dam wastewater and evaluated lytic phages targeting them. Isolates were identified via conventional culture and biochemical methods, with susceptibility tested by Kirby–Bauer disk diffusion (CLSI guidelines). Lytic phages were isolated from raw wastewater using enrichment, spot tests, and plaque assays. Extensive MDR was observed. E. coli showed 100% resistance to Augmentin, Amoxicillin, Chloramphenicol, Septrin, and Streptomycin (MAR Index = 0.556). Environmental K. pneumoniae from S1/S2 showed lower resistance (MAR Index = 0.285), whereas the S3 isolate was resistant to all tested antibiotics (MAR Index = 1.000). Clinical S. aureus isolate S.A1 showed complete resistance (MAR Index = 1.000), while S.A2 and S.A3 recorded MAR indices of 0.300 and 0.200. Lytic phages were isolated only against K. pneumoniae. These findings demonstrate widespread MDR in isolates while identifying wastewater as a source of K. pneumoniae phages, highlighting the value of wastewater surveillance for AMR monitoring and phage discovery.

ABSTRACT 13

Isolation and characterization of lytic bacteriophages active against multidrug-resistant Staphylococcus aureus from sewage in Nairobi, Kenya

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Multidrug-resistant (MDR) Staphylococcus aureus, including MRSA, is a WHO high-priority pathogen and a major cause of resistant infections in Kenyan hospitals and communities. Because bacteriophages are host-specific and geographically structured, locally sourced phage collections are needed, yet anti-staphylococcal phages active against Kenyan MDR S. aureus remain poorly characterized. We isolated lytic phages against MDR S. aureus from sewage in Nairobi, Kenya. Fifty sewage samples were collected across Nairobi, enriched in tryptic soy broth using a local S. aureus propagation host, screened by double-layer agar, and plaque-purified. Lytic activity was screened by spot testing against 25 biochemically confirmed MDR S. aureus isolates. MDR was defined as non-susceptibility to at least one agent in three or more antimicrobial classes. Fifteen samples (30%) yielded lytic phages, from which 15 distinct isolates were established, each producing clear plaques on the propagation host. Preliminary screening indicates lytic activity against multiple MDR isolates, while systematic host-range and efficiency of plating analyses are ongoing. These findings demonstrate that Nairobi sewage is a productive source of lytic anti-staphylococcal phages active against local MDR and S. aureus. Host-range profiling, genome sequencing, and phage cocktail development will further characterize these isolates and support their potential application in phage therapy and biocontrol research in Kenya.

ABSTRACT 14

A Competency-Based Undergraduate Workflow for Phage Discovery and Phage Bank Development at TUK

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Antimicrobial resistance requires both new interventions and a skilled workforce capable of generating them. We implemented an eight-week competency-based authentic research pilot at the Technical University of Kenya (TUK), in collaboration with the Phage Hunters Training & Research Program, involving 54 undergraduate students. The pilot aimed to develop a competency-based phage isolation workflow capable of generating characterised bacteriophages for future phage-bank development. Students sampled commonly sold beverages and fruit juices around the university as a food-safety investigation, isolating and identifying bacterial contaminants and assessing their antimicrobial susceptibility. PCR was used to characterise selected isolates, after which drug-resistant isolates were prioritised as bacterial hosts for phage isolation. The workflow recovered diverse bacterial species, including E. coli, K. pneumoniae, S. Typhi, E. cloacae, P. aeruginosa, P. mirabilis and S. aureus, and yielded 38 bacteriophages from Nairobi's wastewater. Students developed practical competencies spanning environmental sampling, bacterial isolation and identification, antimicrobial susceptibility testing, PCR, phage isolation, and research troubleshooting. The pilot demonstrates how competency-based education can integrate authentic discovery research to build undergraduate competencies while developing practical capacity for AMR research and development.

ABSTRACT 15

Bioinformatic Characterization of lytic proteins in an E Coli Bacteriophage

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Infections caused by diarrhoeagenic E. coli are a vital public health concern in developing countries because they are closely linked to high morbidity and mortality in young children 0- 5 years old. Most antibiotics used in the treatment of E. coli infections are shared between veterinary practice and human medicine leading to misuse and resistance. To address the increasing threat of antibiotic resistance, bacteriophages (phages) and their related enzymes have gained increasing attention as antibiotic alternatives. The objective of this study therefore was to characterize E. coli bacteriophage phage-lytic proteins using bioinformatics analysis. The study found the phage had 10 lytic proteins, five endolysin, three holin and and two spanin. The different lytic proteins identified were able to cluster in their respective clades using the maximum likelihood phylogenetic tree. Using protein mapping, the study was able to identify the compartmental topology, the protein types, whether the N and C terminal were present, the domain family present, whether the protein binding domain were present and the number of amino acids of each lytic protein. Holin transmembrane domain were also predicted and identifies. Modelling of the lytic proteins was done and thereafter protein - protein docking was carried our using Swiss model and clusterpro software.

ABSTRACT 16

Isolation and characterization of virulent bacteriophages and their synergism with antibiotic against multidrug-resistant Klebsiella pneumoniae

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The rise of multidrug-resistant (MDR) Klebsiella pneumoniae poses a global public health and economic threat, necessitating alternative therapies. Bacteriophages specifically infect bacteria, but understanding phage-host interactions with antibiotics is essential for effective use. Ten MDR K. pneumoniae isolates were selected, and three were randomly used for lytic phage isolation and enrichment. Four wastewater samples were collected once from four sites at Jimma Medical Center. Three lytic phages were isolated by spot assay, purified and quantified by plaque assay. Biological characteristics were assessed by spot/plaque assays; checkerboard assays evaluated phage-antibiotic synergy and biofilm disruption. KpPhage57, KpPhage56, and KpPhage85 showed potent lytic activity against MDR clinical isolates, with titers of 1.80×10^9, 1.60×10^8, and 5.0×10^10 PFU/ml, respectively. All were stable at 4–50°C and pH 4–11, with almost similar lytic activity and narrow host ranges; KpPhage56 had a relatively broader host range. KpPhage56 and KpPhage85 synergized with gentamicin (FICI 0.087 and 0.077, respectively), indicating promising candidates for future phage therapy. All three phages disrupted K. pneumoniae biofilm at MOI 10. These lytic and synergistic effects support further study of the phages, with gentamicin, as candidates for therapy of MDR K. pneumoniae and biofilm-associated infections, including wound and catheter-associated infections.

ABSTRACT 17

Locally Recovered Klebsiella pneumoniae Lytic Bacteriophages Demonstrate Potent Antibiofilm Activity Against Established Biofilms

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Antibiotic-resistant Klebsiella pneumoniae causes healthcare-associated infections from medical devices such as catheters, with biofilms contributing to persistence and treatment failure. Bacteriophages offer an alternative approach to biofilm-associated AMR. We isolated 10 lytic K. pneumoniae bacteriophages from wastewater in informal settlements in Nairobi and evaluated their activity against established biofilms. Samples were screened against K. pneumoniae, followed by plaque purification and characterization of lytic activity, titre, host range, thermal stability, and one-step growth. The recovered phages had titres of 6.0 × 10^7 to 6.0 × 10^11 PFU/mL and lytic activity against 75% of the tested K. pneumoniae clinical isolates. One-step growth showed a 30-minute latent period and a burst size of 150 phage particles per infected cell. Lytic activity was retained from -20°C to 50°C, lysis was turbid at 50°C, and no lysis was detected at 70°C. Treatment of mature established K. pneumoniae biofilms with four phages over 24 hours reduced biofilm biomass by 80% relative to untreated controls. The isolated phages have demonstrated depolymerase-associated activity against K. pneumoniae biofilms. Whole-genome sequencing is underway to assess genomic safety and identify candidate depolymerase and receptor-associated determinants. These findings support further investigation of locally recovered phages targeting K. pneumoniae biofilms associated with indwelling medical devices.

ABSTRACT 18

Geographic and Ecological Drivers of Phage Efficacy Against Multidrug-Resistant Escherichia coli in Kenya

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Multidrug-resistant (MDR) Escherichia coli is a critical public health threat in Kenya. Bacteriophage therapy offers a promising alternative. However, its efficacy is constrained by geographic and ecological barriers. This study will investigate genetic differentiation among MDR E. coli populations, driven by geographic distance and ecological barriers such as the Great Rift Valley. It will then investigate whether any observed genetic differentiation among MDR E. coli correlates with variation in phage efficacy.
MDR E. coli isolates will be collected from five Kenyan regions (Nairobi, Nakuru, Kisumu, Mombasa, Isiolo). Lytic phages will be isolated from Nairobi wastewater. Phage efficacy will be quantified using Efficiency of Plating (EOP). Multi-Locus Sequence Typing (MLST) will characterize bacterial genetic diversity and differentiation (FST). Population genetic analyses will test for Isolation by Distance and the Rift Valley as a barrier to gene flow.
Generalized Linear Mixed Models (GLMMs) will correlate genetic differentiation with phage efficacy.
The study will determine whether genetic differentiation explains phage efficacy decay across Kenya's ecological gradients. Findings will inform region-specific phage deployment. It will provide a basis for incorporating population genetics into phage therapy development.

ABSTRACT 19

Bridging the Gap: Perspectives on Bacteriophage-Based Biocontrol Adoption in Iran

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Although phage-based biocontrol is a promising alternative for bacterial plant diseases, its adoption in Iran faces practical barriers. Semi-structured interviews with 10 agricultural experts and pesticide distributors explored their perceptions. Participants showed limited familiarity with phage products, with copper-based pesticides remaining the familiar default option. They emphasized the need for greater awareness and education among professionals, distributors, and farmers. Concerns were raised about cost and affordability, shelf life, stability, and storage requirements. Some suggested that early adoption could be facilitated by engaging technology-oriented agricultural professionals open to emerging approaches. Finally, participants stressed the importance of clear regulatory frameworks and registration pathways. Overall, successful adoption in Iran will depend not only on scientific development but also on awareness, economic feasibility, product stability, early-adopter engagement, and supportive regulation.

ABSTRACT 20

From Hospital Wastewater to Phage Therapy: A Lytic Bacteriophage Targeting Multidrug-Resistant Pseudomonas aeruginosa

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The emergence of multidrug-resistant (MDR), extensively drug-resistant (XDR), and pandrug-resistant (PDR) Pseudomonas aeruginosa (PA) and its ability to form biofilms are responsible for hospital-acquired infections, diabetic wound infections, lung infections, and burn infections. Each year, 32,600 cases of multidrug-resistant (MDR) P. aeruginosa are reported, resulting in 2,700 deaths.
Phages are viruses that are highly specific to bacteria, unlike broad-spectrum antibiotics, and do not negatively affect the human microbiota. In our study, a phage was isolated from hospital wastewater in Iran against P. aeruginosa, which was resistant to amikacin, ciprofloxacin, imipenem, cefoxitin, and gentamicin but sensitive to ceftazidime. The isolate was obtained from a burn infection and was purified through four rounds using the double-layer agar method. The phage titer was determined to be 10^{-9} PFU/mL.
The phage was tested to determine its host range against 13 MDR P. aeruginosa isolates obtained from wound and burn infections. Among the 13 isolates, five were lysed by the phage. In addition, its specificity was examined against Klebsiella, Staphylococcus aureus, Shigella, Escherichia coli O157, and uropathogenic E. coli (UPEC), and no lysis zones were observed.
The isolated phage could be a potential candidate for phage therapy against P. aeruginosa infections but further analysis are needed.

ABSTRACT 21

Isolation and Genome characterization of Salmonella Typhimurium phage

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One of the main pathogenic bacteria causing food poisoning is Salmonella. Here, we report the successful isolation and characterization of a lytic bacteriophage infecting Salmonella enterica subsp. enterica serovar Typhimurium. Transmission electron microscopy (TEM) revealed that the phage possesses an icosahedral head and a long, non-contractile tail. We also determined its complete genome sequence and predicted proteome. The phage exhibits specific lytic activity against Salmonella and harbors a linear dsDNA genome of 42,786 bp with a G+C content of 49.77% and 62 predicted coding sequences. The lysis cassette contains the full complement of proteins required to lyse a Gram-negative host (including endolysin, holin, and spanin), organized into three functional units, while the tail and adsorption module comprises ten proteins. The absence of integrase and recombinase genes indicates a strictly virulent (lytic) lifestyle. Phylogenomic analysis places this phage within the family Siphoviridae and genus Jerseyvirus. These features make this phage a promising candidate for phage-based biocontrol of Salmonella and a valuable source of endolysins for antibacterial enzyme development.

ABSTRACT 22

Phenotypic, Genomic, And Therapeutic Characterization Of Bacteriophages Targeting Pcr-Confirmed Multidrug-Resistant Acinetobacter Baumannii

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Acinetobacter baumannii is a WHO-classified critical-priority pathogen that causes hospital-acquired infections, especially in intensive care units. As treatment options decline, bacteriophages are making a comeback as an alternative to antibiotics, but phages from molecularly confirmed clinical isolates in Pakistan remain limited.
Objective: The objective of this study was to molecularly confirm MDR A. baumannii strains, isolate a lytic bacteriophage against them, characterize it phenotypically and genomically, and evaluate its therapeutic efficacy in a murine model.
Clinical isolates were identified using conventional microbiological methods, susceptibility testing and Vitek 2 analysis and then molecularly confirmed using in-house designed primers targeting five genes by PCR and real-time PCR. A bacteriophage named ABP-AS was isolated and characterized. Genomic DNA was isolated and subjected to whole genome sequencing, and therapeutic efficacy was evaluated in murine model.
ABP-AS formed clear plaques with halo zones and achieved a titer of 4.2×10^{9} PFU/mL. It was strictly lytic and lysed 8/23 (34.8%) MDR isolates. The phage remained stable across pH 5-8 and −25°C to 50°C. Treated mice showed improved clinical condition and disease severity.
ABP-AS exhibited high lytic activity, stability and therapeutic efficacy, thus being a promising candidate for phage therapy against molecularly confirmed MDR A. baumannii.

ABSTRACT 23

Novel α-Helical Peptide-Phage Combination Therapy for the Treatment of Implant-Associated Staphylococcus aureus Biofilms

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Periprosthetic joint infection (PJI) is a major complication of arthroplasty, in which implant-associated biofilms drive bacterial persistence and antimicrobial tolerance. Bacteriophage (phage) and antimicrobial peptides (AMPs) kill bacteria through distinct, potentially complementary mechanisms, providing a rationale for combination therapy. We rationally designed cationic α-helical AMPs and tested them alone and in combination with a lytic phage against Staphylococcus aureus, one of the most frequently isolated PJI pathogens. Activity was assessed by minimum inhibitory concentration (MIC), growth kinetics, and time-kill assays; antibiofilm activity was evaluated against mature biofilms and in an implant-relevant Kirschner-wire (K-wire) model. The lead peptide, M-5W0A, had an MIC of 4 µg/mL and demonstrated concentration-dependent antibacterial activity. Against biofilms, the phage-peptide combination reduced viable counts by 64% versus untreated controls and showed greater activity than either monotherapy. In the K-wire model, the combination reduced viable S. aureus counts by 62% versus untreated controls. These findings support phage-peptide combination therapy as a complementary strategy for treating implant-associated S. aureus biofilms and warrant further development for difficult-to-treat PJI.

ABSTRACT 24

Genotypic Diversity and Recent Transmission Patterns of Mycobacterium tuberculosis in Ethiopia

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Mycobacterium tuberculosis complex (MTBC) remains a major cause of morbidity and mortality. Despite low mutation rates, considerable genotypic variation influences disease progression and drug resistance. This systematic review and meta-analysis synthesized evidence on MTBC genotypic diversity and transmission in Ethiopia.
Electronic databases (PubMed, Web of Science, Google Scholar, Cochrane) and grey literature were searched for Ethiopian studies using spoligotyping, MIRU-VNTR, or WGS. Random-effects meta-analyses, I^2 heterogeneity assessments, and subgroup analyses were performed using R (v4.5.2).
Twenty-four studies (3,601 isolates) were included. The most frequent Spoligotype International Types were SIT149 (58.3%) and SIT53 (50.0%). Lineage 4 (Euro-American) predominated, followed by Lineage 3 (Delhi/CAS); Lineages 1, 2, 5, and Lineage 7 (Ethiopia-specific) were less frequent. Distribution varied across regions (Amhara, Oromia, Tigray), reflecting high heterogeneity. Orphan strains reached 91.1% in some studies. Overall pooled clustering and recent transmission index (RTI) were 57% and 45%, respectively.
MTBC in Ethiopia exhibits substantial genetic diversity and high transmission, dominated by Lineage 4. High clustering and RTI highlight active spread with regional variation, underscoring the need for strengthened molecular surveillance.