

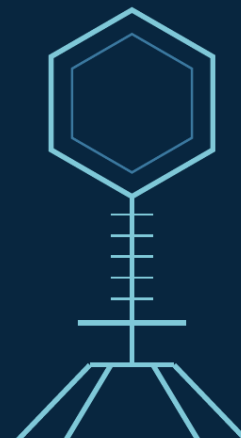


SLOVENIA-KENYA PHAGE SUMMIT | NAIROBI 2026

ABSTRACT BOOK

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08

SELECTED ORAL
PRESENTATION ABSTRACTS

Slovenia-Kenya Phage Summit - Nairobi 2026

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ABSTRACT

01

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

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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

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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, $\Delta=+8.7\%$, $P<0.001$), 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 xenorhabdus tailocins, and we elucidate their cellular targets, and establish their candidacy as antibacterial precision antibiotics. To determine cellular targets of xenorhabdus tailocins, we in silico serotyped 42 *Xenorhabdus* strains with known susceptibilities to 37 xenorhabdus 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 xenorhabdus tailocins that inhibit these strains. We showed that xenorhabdus 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 xenorhabdus 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 xenorhabdus tailocins. Four GBS, two multidrug resistant *Enterococci* and one drug-resistant *Pseudomonas* were inhibited. Hence, xenorhabdus tailocins are an apt platform for creation of precision antibiotics against antimicrobial-resistant pathogens.