Phage-Amplified Diagnostics Against MDR Bacterial Pathogens for Forward-Deployed ID and AST

MHSRS 2026 — Fighting the Invisible Enemy: Combating Antibiotic-Resistant Bacteria in Combat Wounds

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Acknowledgments and Disclosures

Collaborators, contributors, and funding support

- Biswajit Biswas, MS, PhD — U.S. Naval Medical Research Command
- FDA/CDC Antibiotic Resistance Isolate Bank
- U.S. Army WRAIR/MRSN Multidrug-Resistant Organism Repository

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The Diagnostic Gap in Combat Wound Infection

MDR/XDR ESKAPE pathogens at Role 2+ care environments

- MDR/XDR ESKAPE pathogens are a leading cause of combat-associated wound infections
- Direct threat to warfighter survivability and return to duty
- Unmet gap: no culture-independent ID or susceptibility testing in austere, forward-deployed settings

To address the MDR threat, Role 2+ casualty care needs:

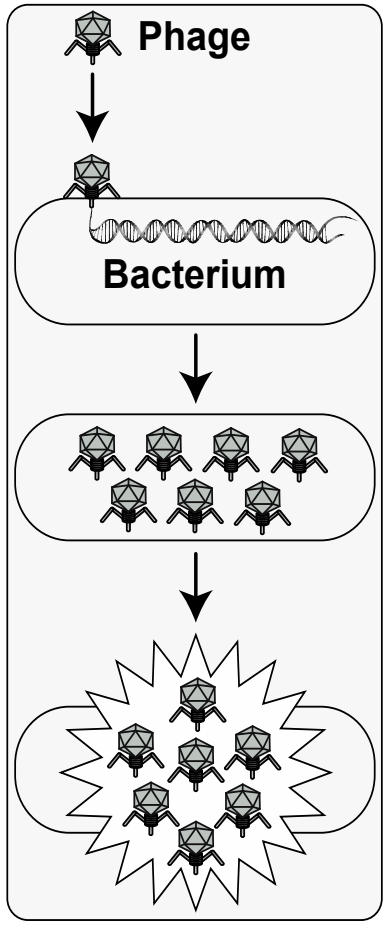
Rapid, portable, *phenotypic,* culture-free, cloud-independent answers

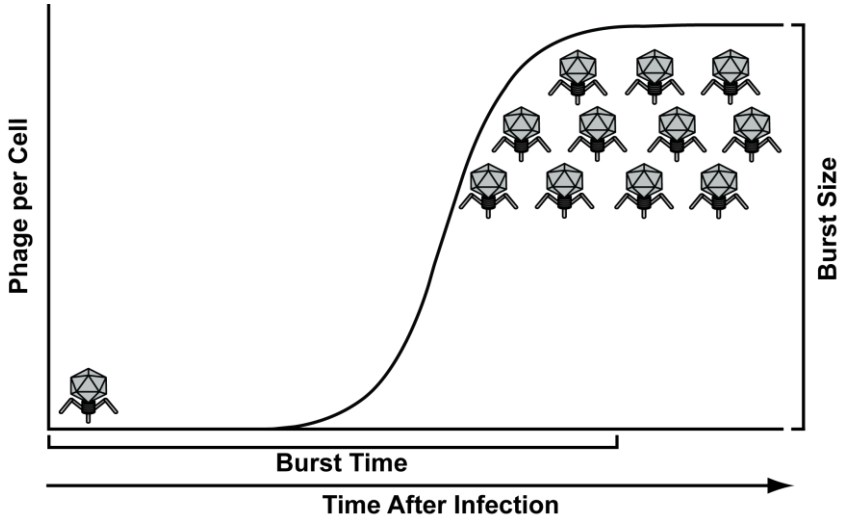
— Streamlined workflow that is executable with minimal expertise/cold chain requirements

— Not a lab-dependent culture or genotypic inferred result

Bacteriophage biology, exploited

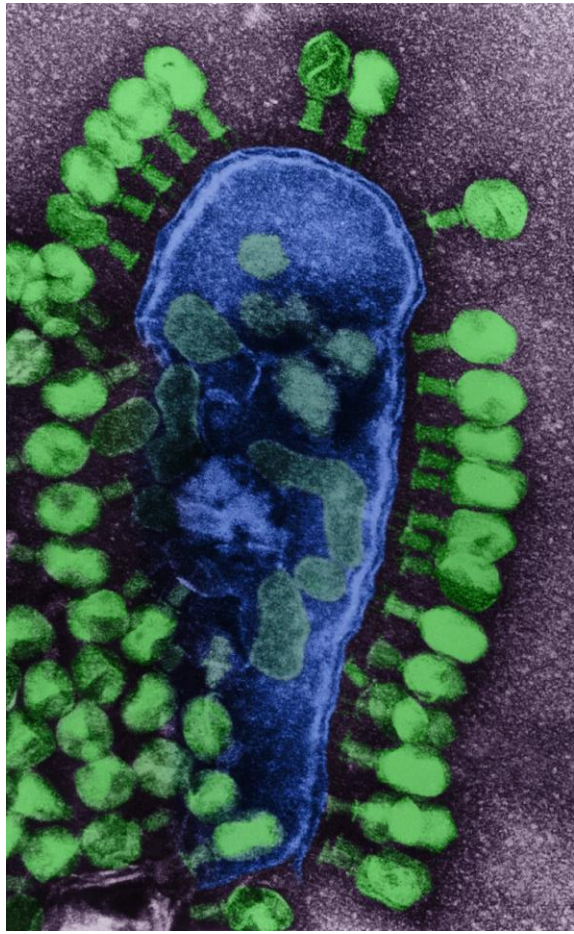
- Bacteriophages (phage) are viruses that infect and kill bacteria
- Used therapeutically against the ESKAPE pathogens for at least a century
- Cobio harnesses that natural infection cycle as an amplifiable *diagnostic signal* (detection platform agnostic)





Latency: ~15-25 min

Burst: 10^2-10^4 x *per cell*

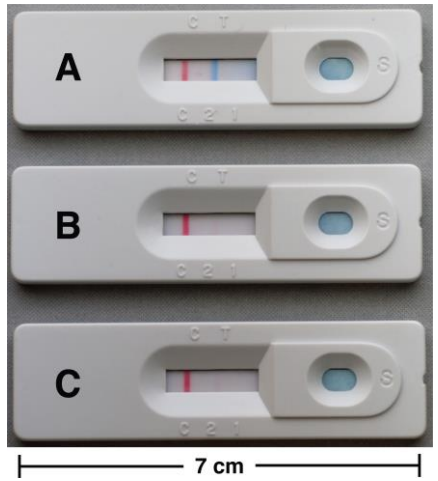


Same Amplification Signal, Different Readouts

Phage amplification is platform agnostic. Two prior Cobio readouts, both against biothreat agents.

Lateral flow immunoassay: *B. anthracis*

Gamma phage amplification read on a COVID style cassette.



Limits of detection

cfu/mL	1 Hr	2 Hr	3 Hr	4 Hr
1×10^2	-	-	+	+
1×10^3	-	-	+	+
1×10^4	+	+ +	+ + +	+ + + +
1×10^5	+ +	+ +	+ + + +	+ + + + +

\+ detectable + + + + + strongly detected

Cox et al. J Microbiol Methods 2015

One force multiplier, any readout the mission allows.
Paper at the point of injury.

Mass spectrometry in the lab.

Nanopore forward at Role 2+.

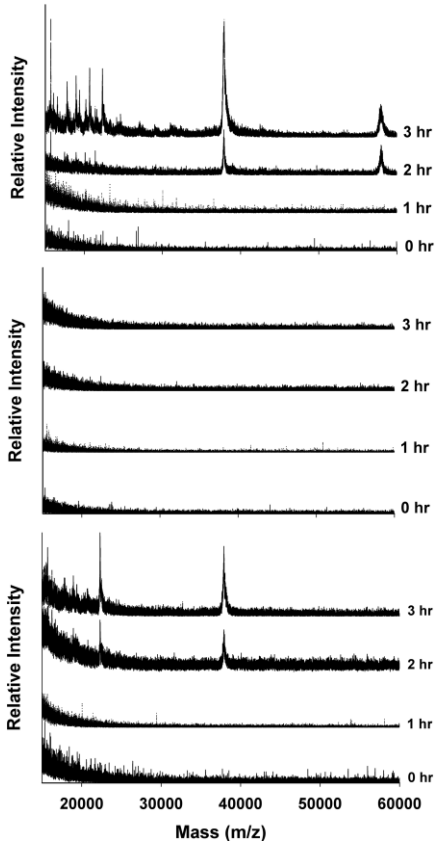
MALDI-TOF MS: *B. pseudomallei*

Phenotypic susceptibility in 3 hr, independent of resistance mechanism.

Bp82 + ϕX216
No antibiotic
Capsid peak by 2 hr

Bp82 + ϕX216
10 µg/mL ceftazidime
No amplification. Susceptible.

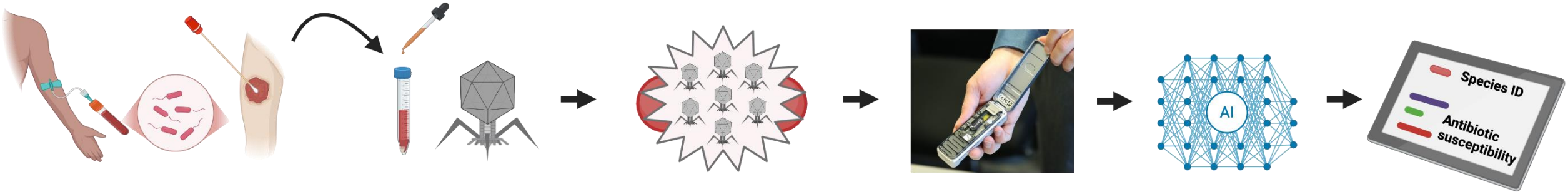
Bp82.3 + ϕX216
15 µg/mL ceftazidime
Amplification in resistant strain



Cox et al. Bacteriophage 2014; 4: e29011

Cobio PhAAST Platform

The tyranny of time (and low cell burden)



Clinical Sample

Blood draw or wound swab at the point of injury

Phage Cocktail

Species-specific phage cocktail added to specimen

Phage Amplification

Phage replicate exponentially only inside living target bacteria

Fieldable Nanopore Sequencer

Handheld sequencer detects amplified phage signal on-device

AI Signal Processing

Read-Until adaptive sampling + edge-AI deliver species ID

Simple Results Reporting

Binary ID + susceptibility result in under 7 hours

No cloud connectivity • Role 2+ forward-deployable • U.S. Army field-demonstrated sequencing platform* • <7 hr sample-to-answer

Cobio U.S. Patent #: 12,601,740 • Prototype under active validation toward DoD capability requirements

*U.S. Army Research, Development and Engineering Command Chemical & Biological (RDECOM C&B) Center, Aberdeen Proving Ground, MD.

Phage Sourcing and Validation

Cocktail Development

- Isolated and characterized *de novo* from wastewater
- Optimized as cocktails for broad, overlapping host range
- No dependence on outside phage repositories — wastewater isolation alone provided sufficient diversity

National and Global Validation Panels

- CDC Antibiotic Resistance Isolate Bank
- WRAIR/MRSN Multidrug-Resistant Organism Repository
- Six priority ESKAPE pathogens screened for lytic efficiency

The ESKAPE Pathogens

E	S	K	A	P	E
Enterococcus faecium & faecalis	*Staphylococcus aureus*	*Klebsiella pneumoniae*	*Acinetobacter baumannii*	*Pseudomonas aeruginosa*	*Enterobacter spp.*

Validated Lytic Efficiency

Against priority MDR/XDR ESKAPE pathogens. CDC ARIB and WRAIR/MRSN panels.

P. aeruginosa

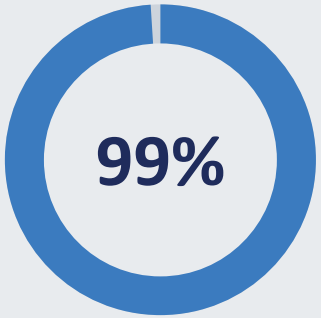
n = 112

***S. aureus* (MRSA/MSSA)**

n = 129

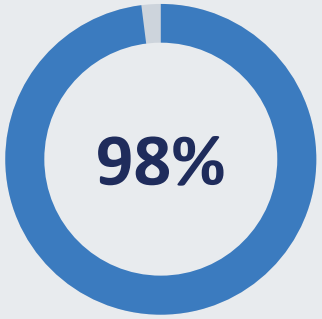
***E. faecalis & faecium* (VRE/VSE)**

n = 102



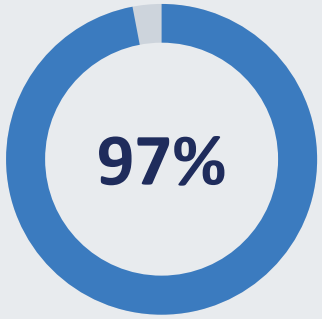
K. pneumoniae

n = 130



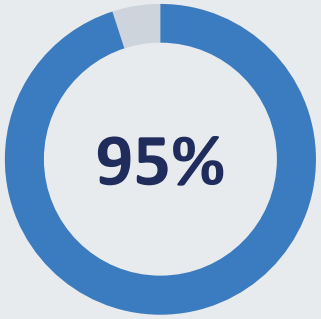
E. coli

n = 169



A. baumannii

n = 169



Translational Significance

From validated phage biology to a forward-deployed diagnostic

- Validated broad-spectrum lytic activity establishes a robust biological foundation for PhAAST
- Phage-amplification kinetics generate a detectable Nanopore signal; Read-Until adaptive sampling enables binary susceptibility calls
- Directly addresses the DoD diagnostic gap for combat wound infections at Role 2+
- Prototype validation is ongoing toward DoD capability requirements

Thank You

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