

PhaseMix





ANTIBIOTICS

Powerful medications

**Main ways in which
antibiotics target
bacteria**

1

Prevent

Reproduction

2

Kill

Bacteria



So, why do
antibiotics fail



BIOLOGICAL CAUSES

01

SELECTIVE PRESSURE

- ANTIBIOTIC-RESISTANT
- DOMINANCE

02

MUTATION

- RAPID-DIVISION
- DEVELOPED RESISTANCE

03

GENE TRANSFER

- MULTI-BACTERIAL INTERACTION
- CONJUGATION

SOLUTION?

PHAGE THERAPY



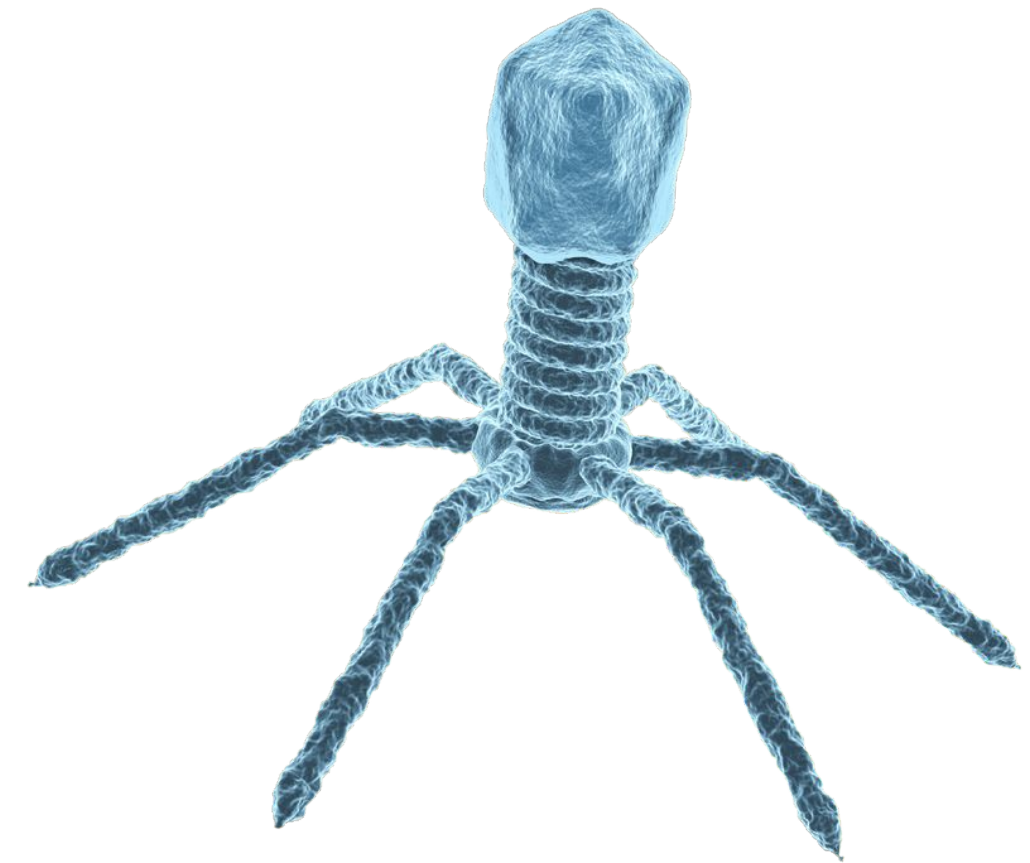
BACTERIOPHAGES

WHAT ARE THEY?

- **Phages** are **viruses** that infect bacteria.
- **Ubiquitous** and **abundant** in the environment.
- Basic structure: a head, a sheath and a tail fibre.
- **Dr. Felix d'Herelle**, a French microbiologist, discovered bacteriophages in 1917.

HOW DO THEY WORK?

- Phages connect to their victim with tail fibres and **puncture the surface** of the bacteria.
- Phage injects its genetic information into the bacteria and **hijacks the cellular mechanism** to make copies of itself.
- Finally, it produces endolysin, a powerful enzyme that **punches a hole** in the bacteria.
- The pressure is so high that the **bacteria bursts and dies** while releasing the phages.



Overuse of antimicrobials has led to the development of **drug-resistant bacteria**.

WHO agrees that **AMRs** are an **urgent issue** requiring a global, coordinated action plan to address.

WHY?

In 2019, The **Lancet** said that antibiotic-resistant **superbugs** caused an estimated **1.2 million deaths**.

In addition to death and disability, prolonged illness results in **longer hospital stays**, the need for more **expensive medicines** and financial challenges for those impacted.

PHAGE THERAPY OFFERS AN ALTERNATIVE TO ANTIBIOTICS FOR TREATING BACTERIAL INFECTIONS.

WHY?

- **Overuse** of antimicrobials have led to the development of **drug resistant bacteria**.
- In 2019, **The Lancet** said that antibiotic-resistant **superbugs** caused an estimated **1.2 million deaths**.
- **WHO** agrees that **AMRs** are an **urgent issue** requiring a global, coordinated action plan to address.
- In addition to death and disability, prolonged illness results in longer **hospital stays**, the need for more **expensive medicines** and financial challenges for those impacted.

Phage therapy offers an **alternative to antibiotics** for treating bacterial infections.

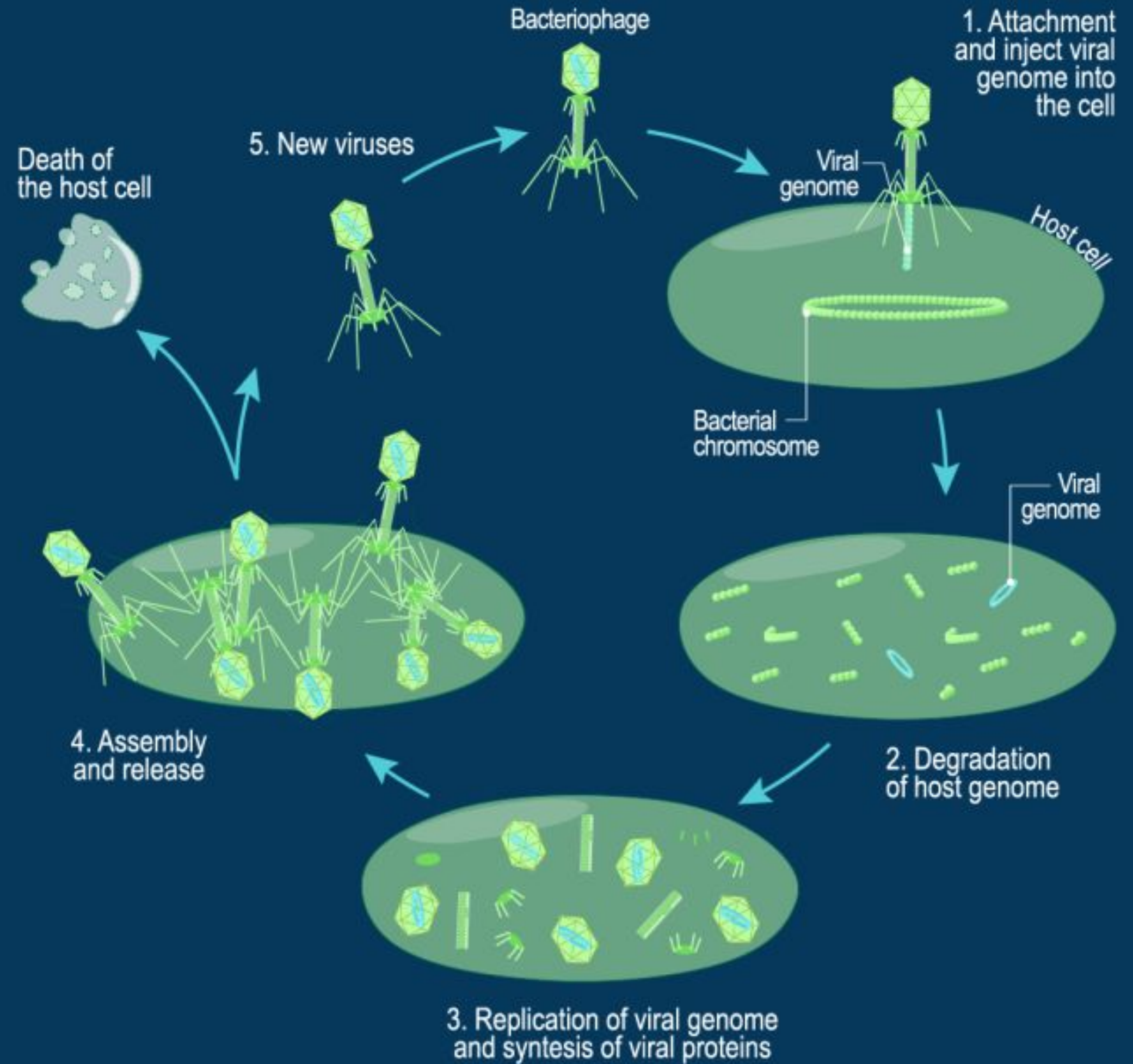
LIFE CYCLE

01

LYSOGENIC
CYCLE

LYTIC
CYCLE

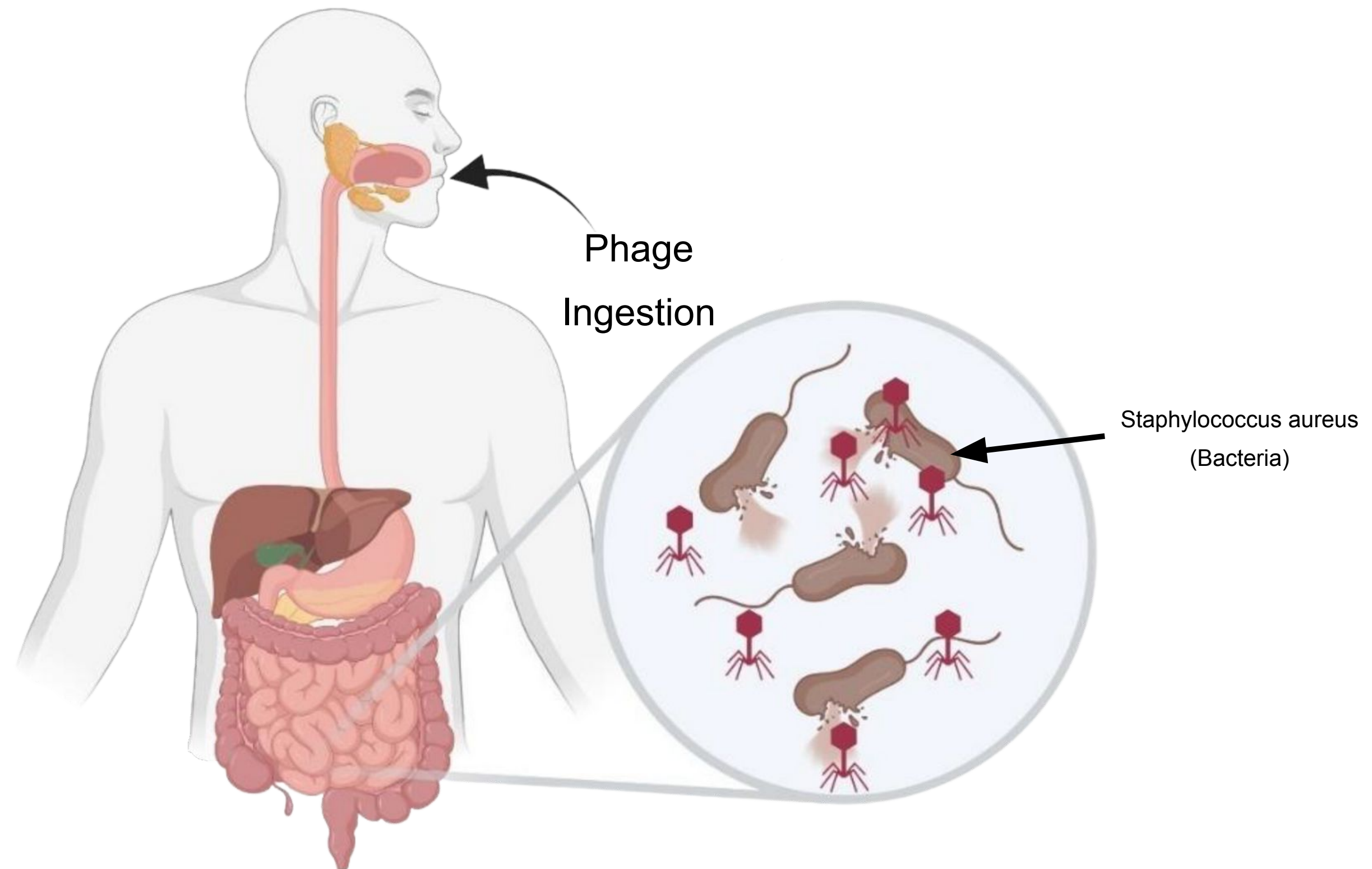
02



BUT, ARE
THEY
EFFECTIVE?



INTERACTION

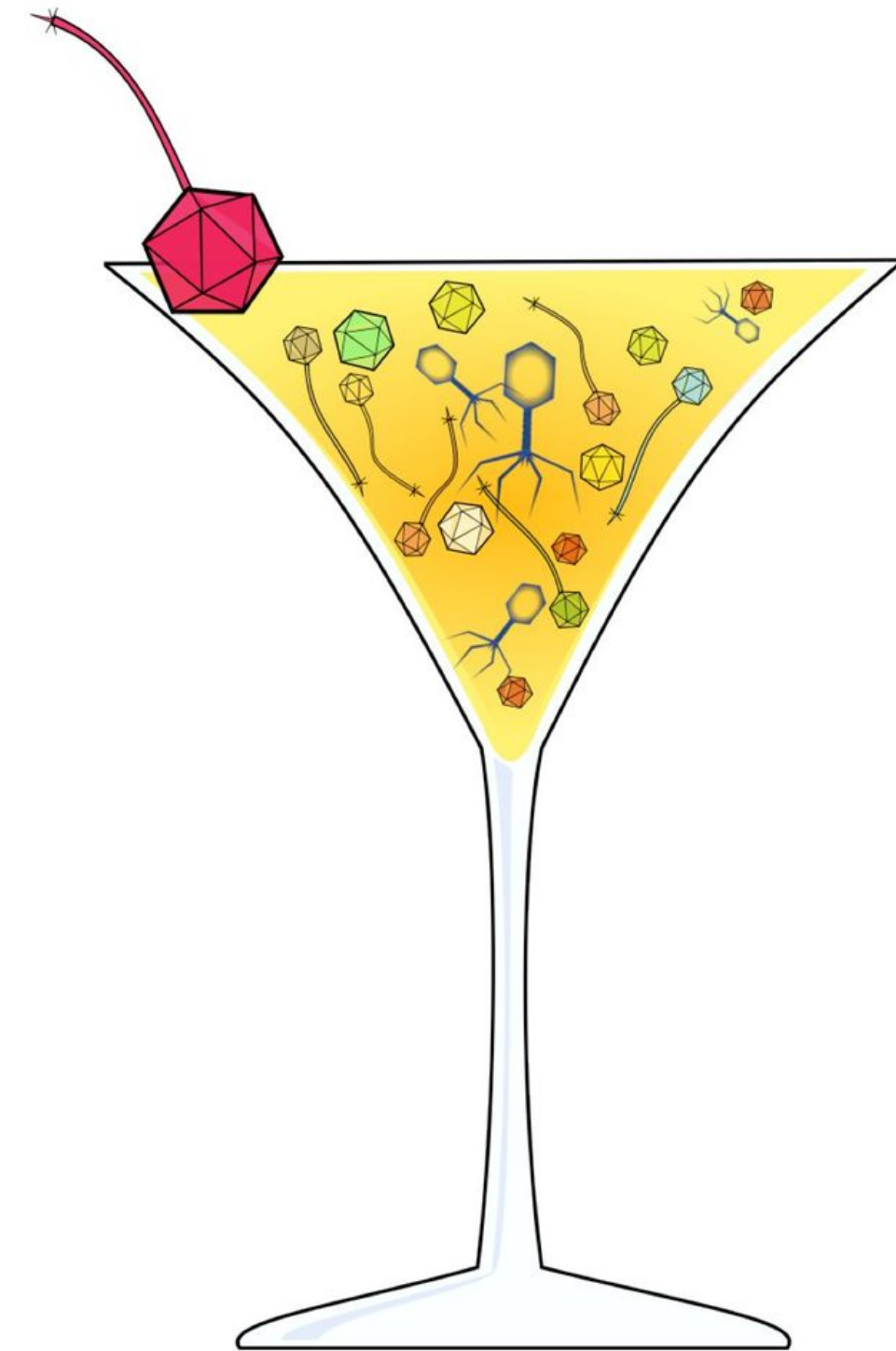


COCKTAIL

(Not the one you would expect)

A Phage Cocktail is a mixture of different bacteriophages that target a specific bacterial strain.

- INCREASES EFFECTIVENESS
- CUSTOMIZABLE
- REDUCES RESISTANCE
- SELF-REPLICATING



DOES IT HELP?

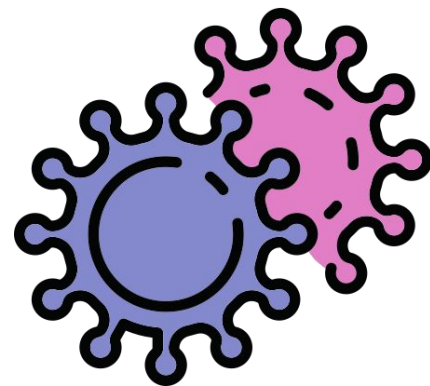
1

**INCREASE
EFFECTIVENESS**



2

**INCREASE LIKELIHOOD
OF INFECTING**



3

**PROVIDE FLEXIBILITY
AND ADAPTABILITY**



PRIOR RESEARCHES



VirHostMatcher

Categories for isolation host of viruses	Count	Category description								
Specific host name, >1 host genome match	71	Host name name on which the virus was isolated is provided is specific (Genus species with strain, serovar or subspecies) and t								
Specific host, 1 host genome match only	352	Host name on which the virus was isolated is provided is specific (Genus species with strain, serovar or subspecies) and there is								
Specific host name, no host genome match	380	Host name name on which the virus was isolated is provided is specific (Genus species with strain, serovar or subspecies) and r								
Genus species listed	600	Only the genus and species of the host on which the virus was isolated is provided								
Genus listed	24	Only the genus of the host on which the virus was isolated is is provided								
Sum	1427									
Taxonomy of host on which virus was isolated										
Virus name	Accession	Host name	Domain	Phylum	Class	Order	Family	Genus	Species	Virus hc
Salmonella phage vB_SenS-Ent1	HE775250	Salmonella enterica subsp	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Salmonella	Salmonella enterica	Specific
Salmonella phage vB_SenS-Ent3	HG934470	Salmonella enterica subsp	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Salmonella	Salmonella enterica	Specific
Salmonella phage vB_SenS-Ent2	HG934469	Salmonella enterica subsp	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Salmonella	Salmonella enterica	Specific
Escherichia phage rv5	DQ832317	Escherichia coli O157	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Enterobacteria phage fIAA91-ss	KF322032	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Enterobacteria phage WV8	EU877232	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage Phaxl	JN673056	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage ECML-117	JX128258	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage ECML-134	JX128259	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage ECML-4	JX128257	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage vB_EcoM_FFH2	KJ190158	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage Av-05	KM190144	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage phiV10	DQ126339	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage PE3-1	KJ748011	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Enterobacteria phage JLI	JX865427	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Escherichia phage vB_EcoS_FFH1	KJ190157	Escherichia coli O157:H7	Bacteria	Proteobacter	Gammaprote	Enterobacteri	Enterobacteri	Escherichia	Escherichia coli	Specific
Campylobacter phage CP30A	JX569801	Campylobacter jejuni sub	Bacteria	Proteobacter	Epsilonprotec	Campylobact	Campylobact	Campylobact	Campylobacter jejuni	Specific

<https://github.com/jessieren/VirHostMatcher/blob/master/>

Supplemental_table_virus_and_host_genomes.xlsx

STRING

#taxon_id	STRING_type	STRING_name_compact	official_name_NCBI	domain
23	mapped	Shewanella colwelliana	Shewanella colwelliana	Bacteria
48	mapped	Archangium gephyra	Archangium gephyra	Bacteria
52	mapped	Chondromyces crocatus	Chondromyces crocatus	Bacteria
54	mapped	Nannocystis exedens	Nannocystis exedens	Bacteria
69	mapped	Lysobacter enzymogenes	Lysobacter enzymogenes	Bacteria
140	mapped	Borrelia hermsii	Borrelia hermsii	Bacteria
162	mapped	Treponema phagedenis	Treponema phagedenis	Bacteria
163	mapped	Treponema bryantii	Treponema bryantii	Bacteria
183	mapped	Leptonema illini	Leptonema illini	Bacteria
192	mapped	Azospirillum brasilense	Azospirillum brasilense	Bacteria
195	mapped	Campylobacter coli	Campylobacter coli	Bacteria
202	mapped	Campylobacter mucosalis	Campylobacter mucosalis	Bacteria
211	mapped	Helicobacter sp. CLO-3	Helicobacter sp. CLO-3	Bacteria
216	mapped	Helicobacter muridarum	Helicobacter muridarum	Bacteria
238	mapped	Elizabethkingia meningoseptica	Elizabethkingia meningoseptica	Bacteria
244	mapped	Planomicrobium okeanoikoites	Planomicrobium okeanoikoites	Bacteria

<https://stringdb-static.org/download/species.v11.5.txt>

Actinobacteriaophage DB

Column1	Host	Cluster	Subcluster	Finished Sequence?	Temperate?	Archive Titer	In GenBank?	Accession #	Published in a Paper?
20ES	Mycobacterium smegmatis mc ² 155	A	A2	TRUE	TRUE		TRUE	KJ410132	FALSE
	244 Mycobacterium smegmatis mc ² 155	E	None	TRUE	TRUE		TRUE	DQ398041	TRUE
32HC	Mycobacterium smegmatis mc ² 155	Z	None	TRUE	TRUE		TRUE	KJ028219	FALSE
39HC	Mycobacterium smegmatis mc ² 155	B	B6	TRUE	FALSE		TRUE	KJ433973	FALSE
40AC	Mycobacterium smegmatis mc ² 155	A	A17	TRUE	TRUE		TRUE	KJ192196	FALSE
40BC	Mycobacterium smegmatis mc ² 155	B	B6	TRUE	FALSE		TRUE	KJ433975	FALSE
A3Wally	Microbacterium foliorum NRRL B-24224	GD	None	TRUE	None		TRUE	MZ150783	FALSE
Aaronocolus	Streptomyces griseus ATCC 10137	BD	BD1	TRUE	TRUE		TRUE	KT124227	FALSE
Abba	Arthrobacter globiformis B-2979	AO	AO3	TRUE	FALSE		TRUE	MT024868	FALSE
AbbeyMikolon	Streptomyces lividans JI 1326	BL	None	TRUE	TRUE		TRUE	MG593800	FALSE
AbbyDaisy	Arthrobacter globiformis B-2979	AY	None	TRUE	TRUE		FALSE		FALSE
AbbyPaige	Mycobacterium smegmatis mc ² 155	A	A2	TRUE	TRUE		TRUE	MH077576	FALSE
Abbyshoes	Mycobacterium smegmatis mc ² 155	A	A1	TRUE	TRUE		TRUE	OL455898	FALSE
AbbysRanger	Mycobacterium smegmatis mc ² 155	A	A4	TRUE	TRUE	1.0x10 [^] 12 pfu/m	TRUE	MN284905	FALSE
ABCat	Mycobacterium smegmatis mc ² 155	E	None	TRUE	TRUE		TRUE	KF188414	TRUE
Abdiel	Mycobacterium smegmatis mc ² 155	A	A4	TRUE	TRUE	1.84E+08	TRUE	KY083058	TRUE
Abidatro	Arthrobacter sp. ATCC 21022	AS	AS1	TRUE	TRUE	2.2 x 10 [^] 10 pfu/i	TRUE	MF140397	FALSE
Abigail	Microbacterium foliorum NRRL B-24224	EB	None	TRUE	FALSE	1X10 [^] 10	TRUE	MZ322012	FALSE
Abinghost	Mycobacterium smegmatis mc ² 155	B	B3	TRUE	FALSE	3.0 X 10 [^] 9pfu/m	TRUE	MN444873	FALSE
Abrogate	Mycobacterium smegmatis mc ² 155	A	A1	TRUE	TRUE		TRUE	KM597531	TRUE
AbsoluteMadLa	Mycobacterium smegmatis mc ² 155	B	B1	TRUE	FALSE	1.9*10 [^] 7	TRUE	MN096366	FALSE
Abt2graduatex2	Streptomyces griseus ATCC 10137	BG	None	TRUE	FALSE		TRUE	MF975638	TRUE
ABU	Mycobacterium smegmatis mc ² 155	B	B1	TRUE	FALSE	2.00E+10	TRUE	JF704091	TRUE
Acadian	Mycobacterium smegmatis mc ² 155	B	B5	TRUE	FALSE		TRUE	JN699007	TRUE
ACFishhook	Mycobacterium smegmatis mc ² 155	A	A3	TRUE	TRUE		TRUE	MK284518	FALSE

<https://phagesdb.org/data/>

virushostdb

	A	B	C	D	E	F	G	H	I
1	Abaca bun	438782	NC_010314,NC_010315,NC_010316,NC_010317,NC_010318,NC_010319						
2	Abutilon Br	665102	NC_014138,NC_014139						
3	Abutilon m	932071	NC_015045,NC_015048						
4	Abutilon m	1046572	NC_016574,NC_016577						
5	Abutilon m	10815	NC_001928,NC_001929						
6	Actinidia cl	1776763	NC_038769,NC_038770,NC_038771,NC_038772,NC_038773						
7	Adana viru	1611877	NC_029127,NC_029128,NC_029129						
8	Adult diarr	335103	NC_007548,NC_007549,NC_007550,NC_007551,NC_007552,NC_007553,NC_007554						
9	Aedes can	2010269	NC_035216,NC_035217,NC_035222,NC_035223						
10	Aedes pse	341721	NC_007666,NC_007667,NC_007668,NC_007669,NC_007670,NC_007671,NC_007672						
11	Aeonium ri	1962503	NC_038761,NC_038762						
12	African cas	2560285	NC_055127,NC_055128						
13	African cas	10817	NC_001467,NC_001468						
14	African cas	222064	AF112352,AF112353						
15	African cas	685973	FJ751234						
16	African hor	40050	NC_005996,NC_006008,NC_006011,NC_006012,NC_006016,NC_006017,NC_006018						

https://www.genome.jp/ftp/db/virushostdb/segmented_virus_list.tsv

EXISTING MODELS

1

VirHostMatcher

genetic code
differences

2

WISH

sequencing data
comparison

3

VirSorter

viral sequences

4

ClassiPhage

genomic data

SO, WHAT WENT WRONG?

OUR MODEL

WHAT?

Predicting virus-host interactions.

HOW?

Constructing a network of contigs

Various Machine learning algorithms

Cocktail

Metagenomic

Random forests

Neural Nets

SVMs

DIFFERENCES

PhaseMix

- Predicts both **known** and **novel** virus-host interactions.
- Accounts for the **potential presence** of multiple hosts for a given virus.
- Uses **machine learning algorithms** like neural networks, support vector machines, and random forests to make accurate predictions.
- Predicts virus-host interactions with a possibly **higher AUROC score** compared to other tools.

Other Models

- Some tools like VirHostMatcher **only compare genetic data** to a database of known viruses.
- can **only detect viral sequences** based on the presence of specific genes.
- can categorize metagenomic contigs into different categories based on sequence composition and similarity to known viral genomes.
- prone to report **false positive detections**

OUR TEAM AND CREDITS

SAMEER

- Literature Review
- Presentation
- Prior Models
- Solution Model

JYOTIR

- Literature Review
- Presentation
- Phage Therapy

NAMAN

- Literature Review
- Bacteria interaction and cocktails
- Classification of Bacteria

UDIT

- Literacy Review
- Presentation
- Prior researches
- Solution Model

ANKIT

- Presentation Design
- Antibiotics
- Prior Research

NISHI

- Bacteriophages Study
- Presentation Design

AVINASH

- Bacteriophages Study
- Presentation

ARYAN

- Bacterial studies

REFERENCES

- <https://www.ncbi.nlm.nih.gov/books/NBK493185/>
- <https://bmcmicrobiol.biomedcentral.com/articles/10.1186/s12866-021-02256-5>
- <https://www.britannica.com/science/bacteriophage>
- <https://www.medicalnewstoday.com/articles/327093#evolution>
- <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9697832/>
- <https://www.ncbi.nlm.nih.gov/books/NBK493185/>



- [https://academic.oup.com/bioinformatics/article/38/
Supplement_1/i45/6617519?login=false](https://academic.oup.com/bioinformatics/article/38/Supplement_1/i45/6617519?login=false)
- <https://pubmed.ncbi.nlm.nih.gov/34819064/>
- [https://www.sciencedirect.com/science/article/a
bs/pii/S1879625721001620](https://www.sciencedirect.com/science/article/abs/pii/S1879625721001620)

Datasets

- [https://github.com/jessieren/VirHostMat
cher/blob/master/Supplemental_table_v
irus_and_host_genomes.xlsx](https://github.com/jessieren/VirHostMatcher/blob/master/Supplemental_table_virus_and_host_genomes.xlsx)
- <https://phagesdb.org/data/>
- <https://www.genome.jp/virushostdb/>
- <https://string-db.org/>

