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Genomic Insights into Bacteriophage PaFZ4: A Potential Alternative to Antibiotics for MDR *Pseudomonas aeruginosa*

Zuhayr Mahtab, Fahmida Haque, Sohidul Islam, Ishrat Jabeen and Sabbir R. Shuvo*

Department of Biochemistry & Microbiology, North South University, Dhaka, Bangladesh

sabbir.shuvo@northsouth.edu

INTRODUCTION & AIM

- **Multidrug-Resistant *Pseudomonas aeruginosa*:**

P. aeruginosa is a Gram-negative opportunistic pathogen responsible for severe hospital-acquired infections. In Bangladesh, multidrug-resistant (MDR) strains pose a growing threat due to resistance to a wide range of antibiotics[1].

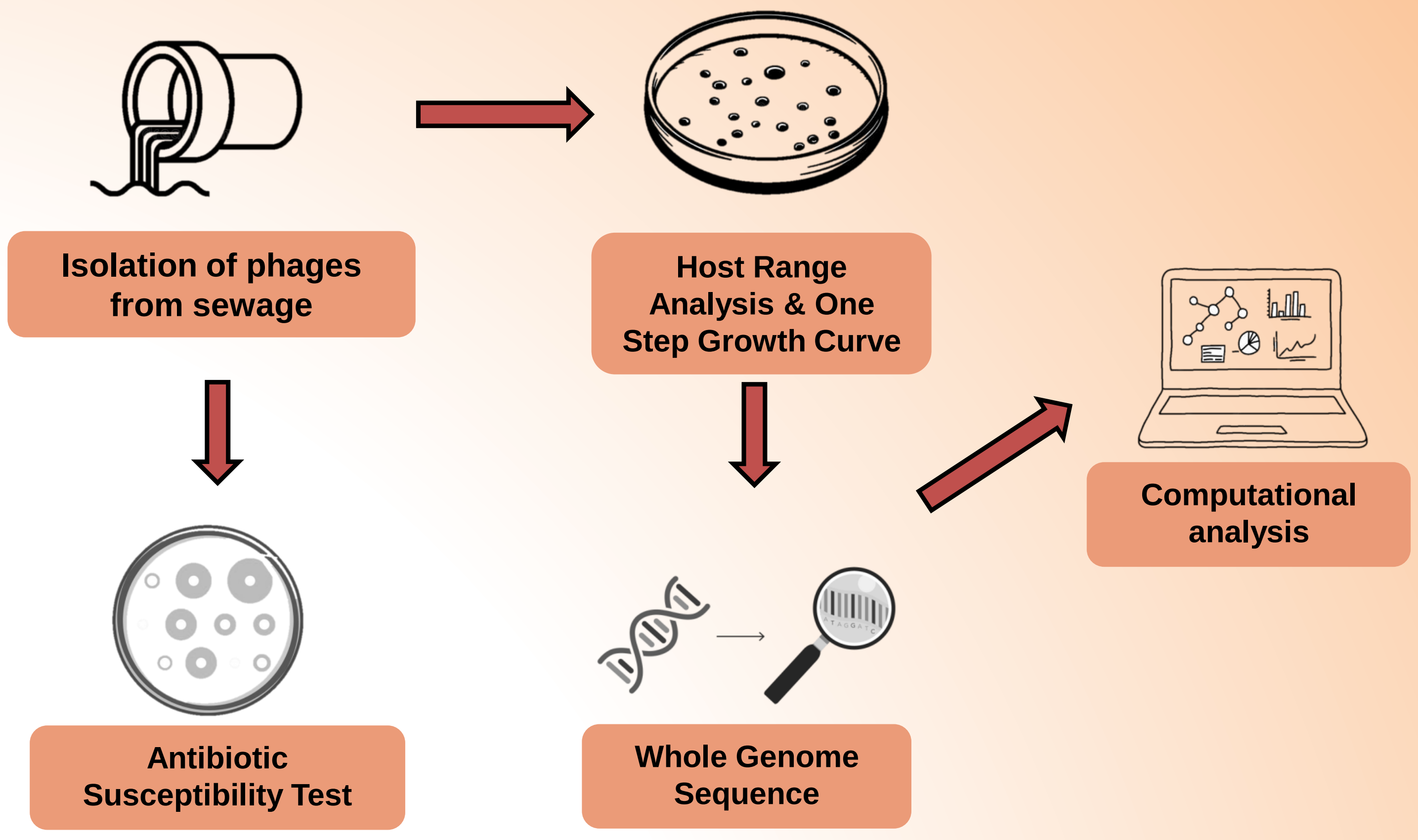
- **Bacteriophages:**

Bacteriophages (phages) are viruses that specifically infect and lyse bacteria. With rising antibiotic resistance, phage therapy is emerging as a promising strategy to combat MDR bacterial infections[2].

- **Aim of the Study:**

To isolate, characterize, and perform genomic analysis of a novel lytic bacteriophage (PaFZ4) targeting MDR *P. aeruginosa* from hospital wastewater in Dhaka, Bangladesh.

METHOD



Isolation of phages from sewage

Host Range Analysis & One Step Growth Curve

Computational analysis

Antibiotic Susceptibility Test

Whole Genome Sequence

RESULTS

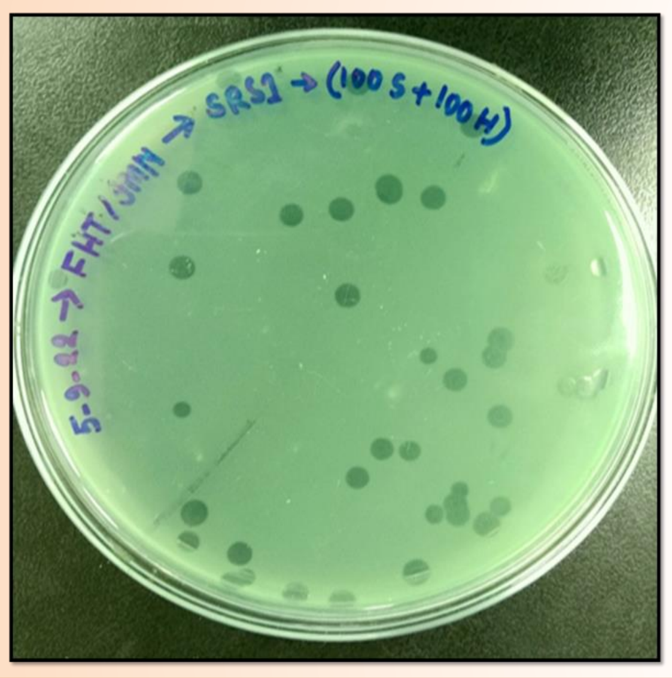


Figure 1: Isolation of Bacteriophage

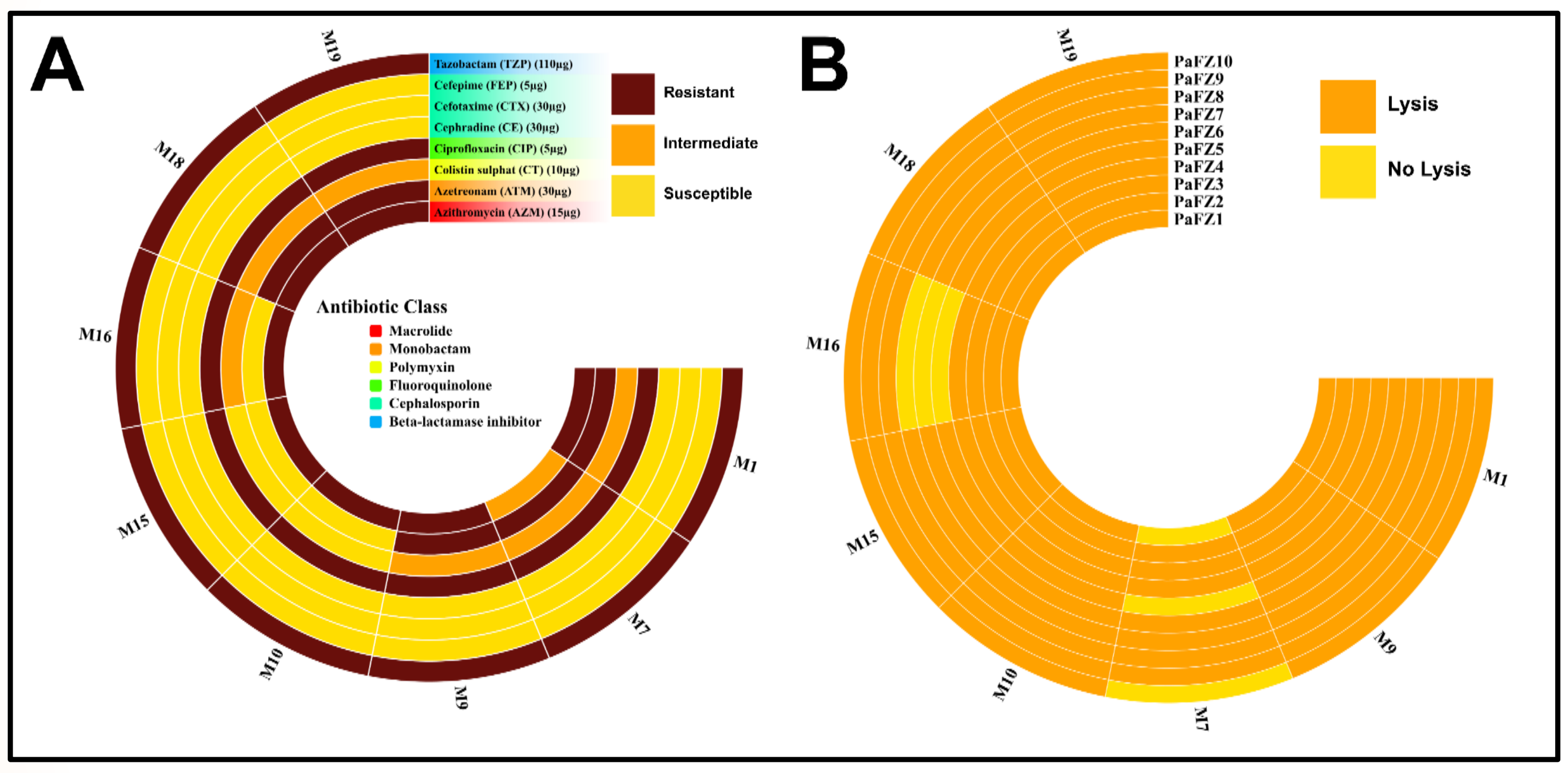


Figure 2: A) Antibiotic susceptibility test for *P. aeruginosa*
B) Host range analysis of isolated phages against *P. aeruginosa*

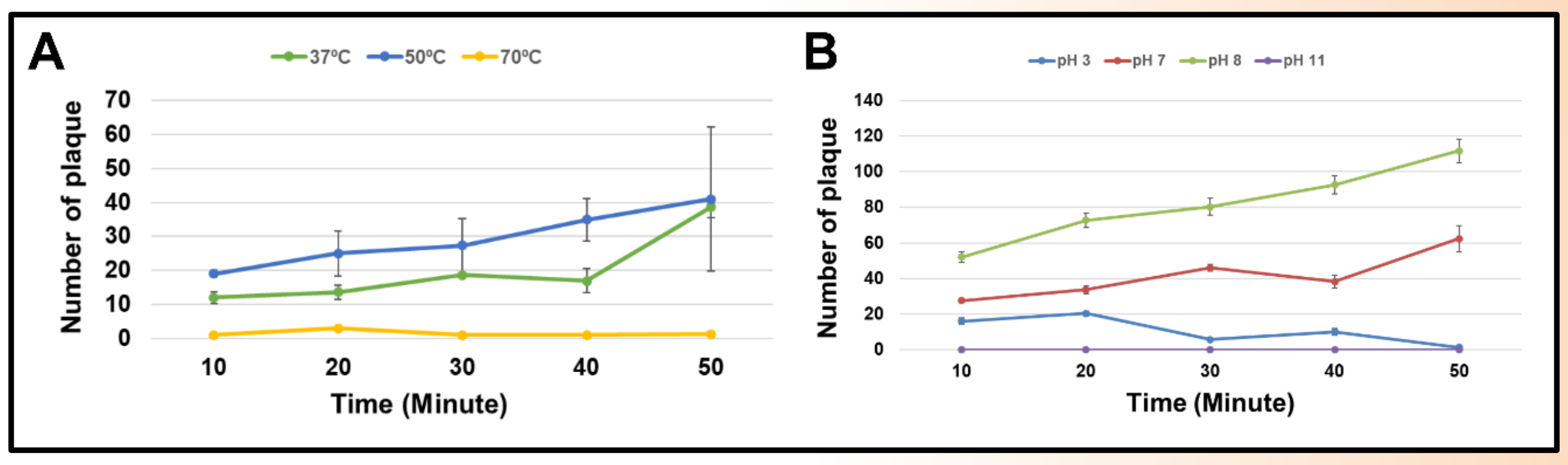


Figure 3: One step growth curve (A) Different pH, (B) Different temperatures

Table 1: Genomic Data	
Genome Length	43,208
CG %	62.3
Contig	1
CDS	59
Contig L50	1
Contig N50	43,208
rRNA	0
tRNA	0
Miscellaneous RNA	0
Coverage	645x
Completeness	100%

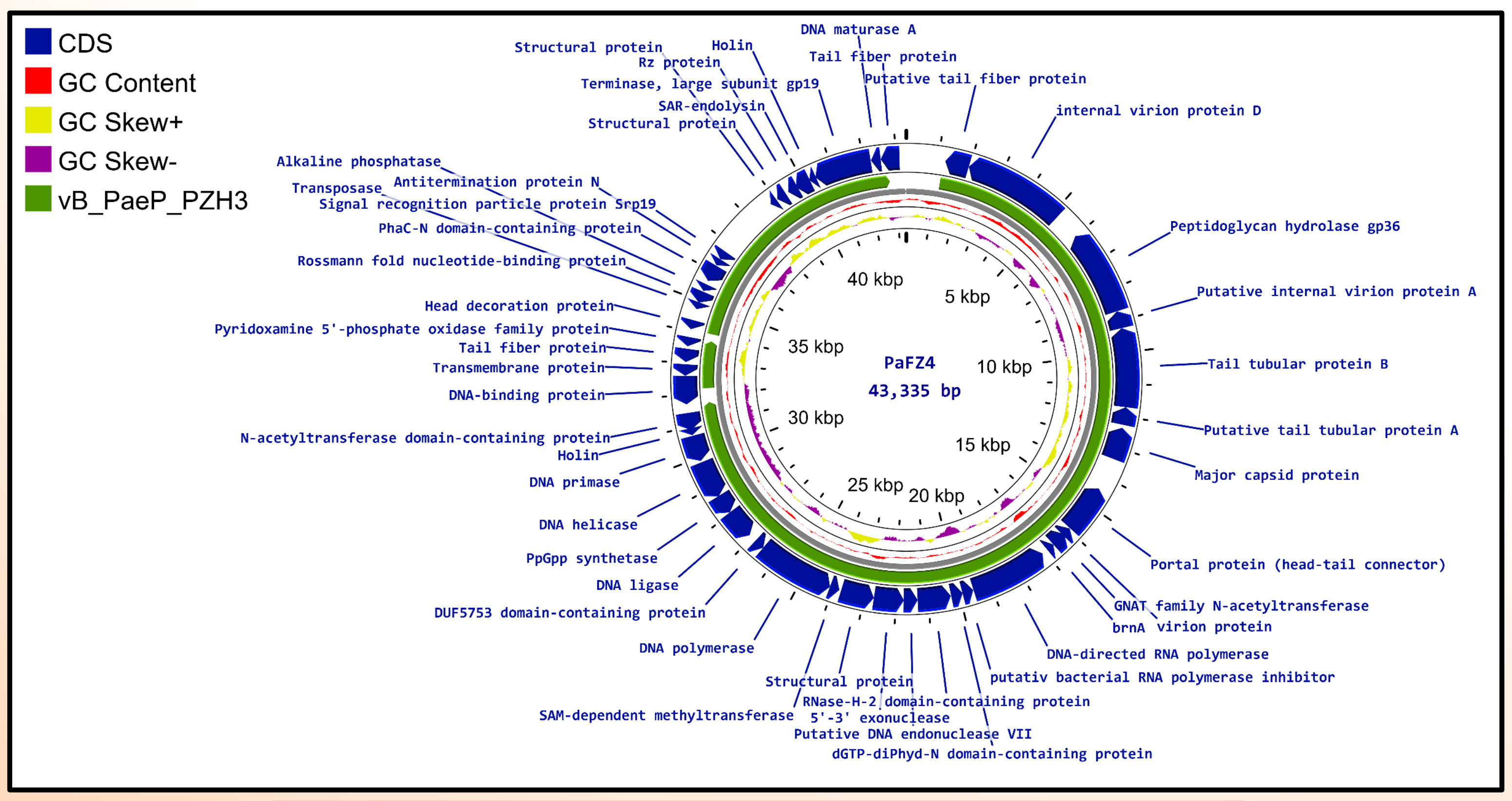


Figure 4: Sequence Alignment of PaFZ4 Phage with vB_PaeP_PZH3

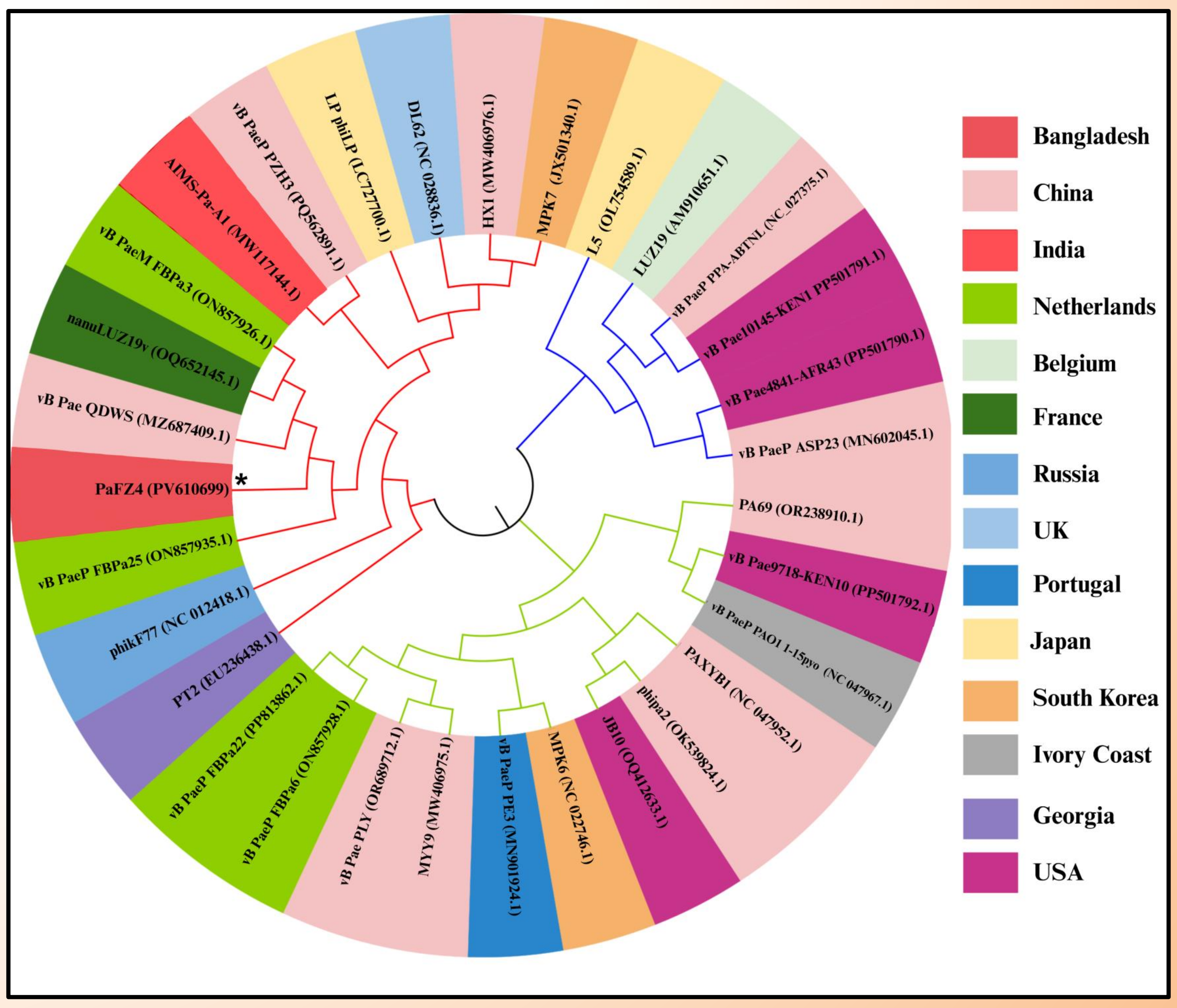


Figure 5: Phylogenetic Analysis of Phage PaFZ4 with 30 closet related phage from NCBI

CONCLUSION

- Bacteriophage PaFZ4 exhibited potent lytic activity against all eight tested MDR *P. aeruginosa* strains, indicating a broad host range
- MOI (Multiplicity of Infection) value of 7.3, suggesting efficient bacterial infection.
- No virulence or antibiotic resistance genes were detected, supporting its safety for therapeutic use.
- Phylogenomic analysis confirmed that PaFZ4 belongs to the genus *Phikmvvirus* within the family Autographiviridae and shares close evolutionary relationships with phages isolated from the Netherlands, China, and France.

FUTURE WORK / REFERENCES

- In vivo studies and clinical trials of phage therapy
- Expanded host range and resistance studies
- Scalability and production for clinical use

1. Alam, Mohammad Morshad, et al. "Prevalence of multidrug resistance bacterial isolates from infected wound patients in Dhaka, Bangladesh: a cross-sectional study." International Journal of Surgery Open 28 (2021): 56-62.
2. Liu, Chengxi et al. "Phage-Antibiotic Therapy as a Promising Strategy to Combat Multidrug-Resistant Infections and to Enhance Antimicrobial Efficiency." Antibiotics (Basel, Switzerland) vol. 11,5 570. 25 Apr. 2022, doi:10.3390/antibiotics11050570

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