

Identification and genomic analysis of a novel bacteriophage belonging to a new virus family infected with *Vibrio alginolyticus*

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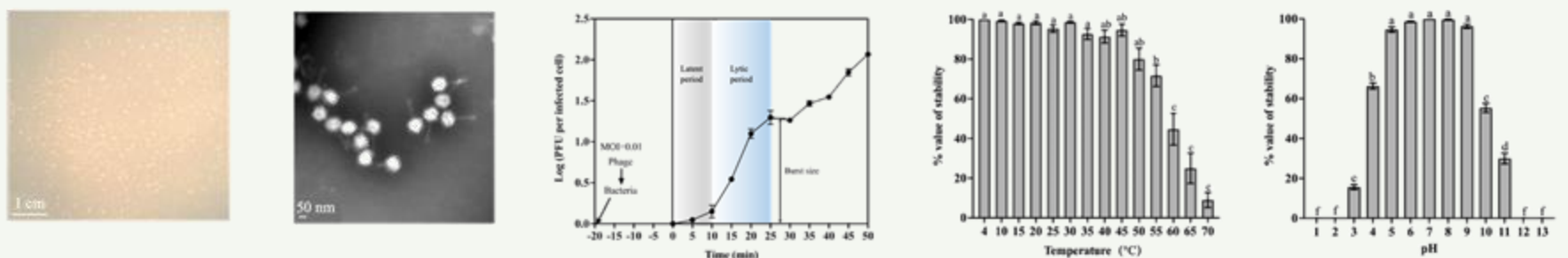
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Background

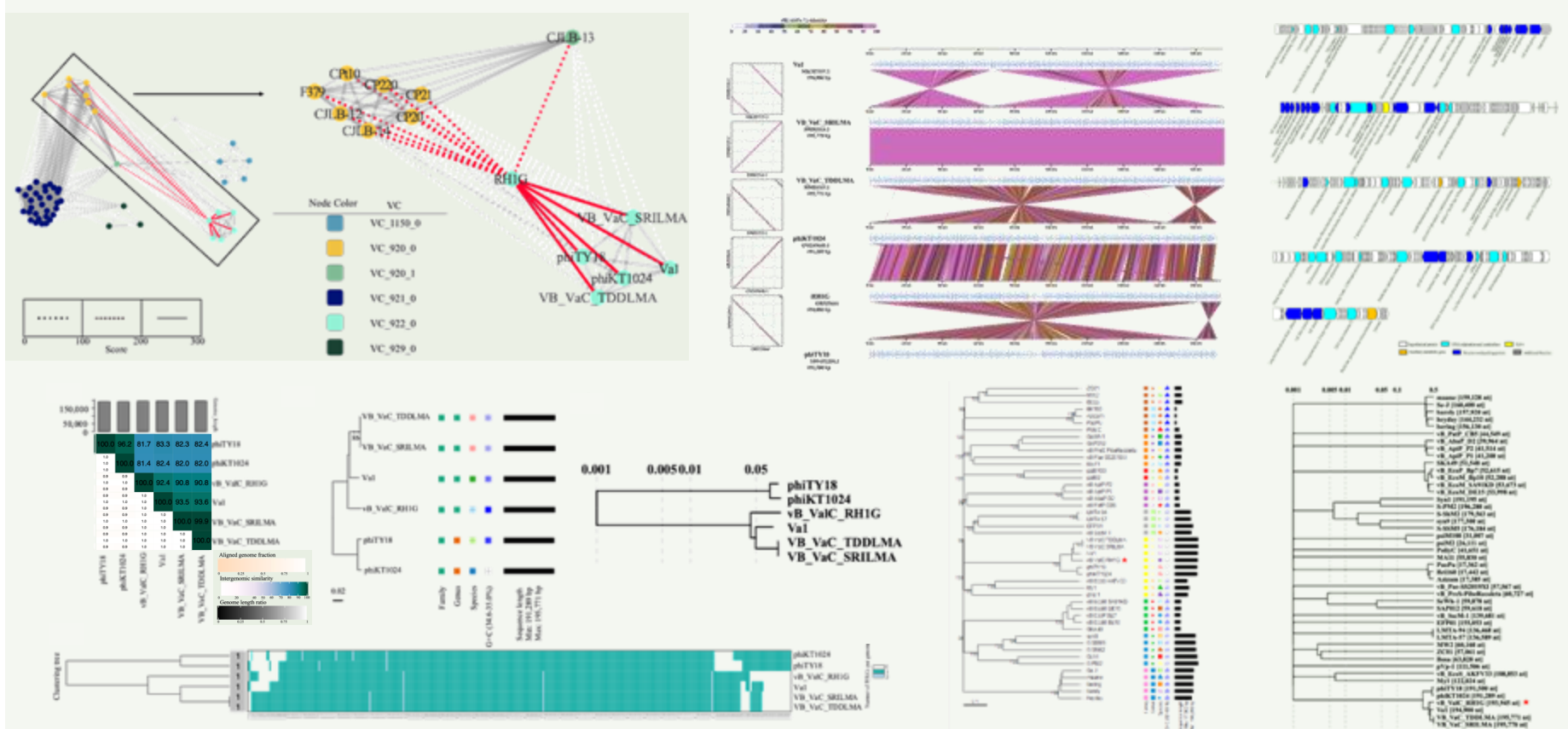
- *Vibrio* has a very fast growth rate and a very short generation time.
- Pathogenic bacteria develop resistance to antibiotics.
- Phage therapy is a promising method to solve the drug resistance of pathogenic bacteria.

The objective of this study was to isolate a novel strain of *Vibrio alginolyticus* phage from natural water sources, specifically targeting the isolation of a unique strain, and subsequently evaluate its potential application as a biocidal agent based on its distinctive physiological and genomic characteristics.

Results and discussions



Phage vB_ValC_RH1G has a short latency period and high burst size, and shows good adaptability to fluctuations in environmental factors.



Phage vB_ValC_RH1G is grouped in the same evolutionary clade as five other phages, including Va1, phiKT1024, phiTY18, VB_ValC_TDDLMA, and VB_ValC_SRILMA, and is distinct from all known phages approved by the International Committee for the Classification of Viruses (ICTV) for the purpose of Caudoviricetes.

Conclusion

- Based on the results of phage physiological properties and genomic characterization, it was concluded that phage vB_ValC_RH1G could be involved in phage therapy as a biocidal agent.
- It is proposed that RH1G be grouped with five other phages into a new family for the purpose of Caudoviricetes.

Supplementary research



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