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Review Article

The Coevolution of Virophages and Their Hosts: A Comprehensive Review

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ABSTRACT

Virophages are small, satellite viruses that depend on the replication machinery of their host viruses. While originally thought to be rare and unique to certain environments, the discovery of numerous virophages has led to an increased understanding of their importance in regulating viral dynamics and their potential impact on ecosystems. This paper provides a comprehensive review of the coevolutionary relationship between virophages and their hosts. We examine the evolutionary history of virophages, their role in modulating viral communities, and the mechanisms underlying their interactions with host viruses. Additionally, we discuss the potential implications of virophages for human health and biotechnology. Through an analysis of current research, we highlight the gaps in knowledge and identify promising avenues for future studies.

Keywords: *Virophages, Coevolutionary, Viruses*

INTRODUCTION

Virophages are viruses that depend on other viruses, known as host viruses, for their replication [1]. Discovered in 2008, these small satellite viruses were originally thought to be rare and found only in certain environments [2]. However, recent research has shown that virophages are widespread and play a significant role in the regulation of viral dynamics [3]. The coevolutionary relationship between virophages and their hosts has become an area of intense research interest due to its potential impact on ecosystems and human health. This paper aims to provide a comprehensive review of the current understanding of the coevolution of virophages and their hosts, including their evolutionary history, ecological significance, and potential applications in biotechnology [4].

Literature Review:

The coevolution of virophages and their hosts is a rapidly expanding field of research, as scientists seek to understand the ecological and evolutionary significance of these enigmatic viral entities. In this section, we provide a comprehensive and critical review of the existing literature on the topic [5].

Virophages were first discovered in 2008, and are defined as small, satellite viruses that replicate within the cytoplasm of their host cells, often in association with larger viruses [6]. Their name derives from their ability to interfere with the replication of their associated viruses, acting as a form of viral parasite [7]. Virophages have been identified in a wide range of ecosystems, including aquatic environments, soil, and the human gut microbiome. Despite their ubiquity, the ecological and evolutionary significance of virophages remains poorly understood [8].

A key question in the study of virophages is their evolutionary history. Recent research has suggested that virophages are part of a larger group of mobile genetic elements known as transpovirons, which are found within the genomes of giant viruses [9]. This suggests that virophages and giant viruses have coevolved over long periods of time, and may have played an important role in shaping the evolution of these viruses. However, there is still much to learn about the evolutionary relationships between virophages, giant viruses, and other mobile genetic elements [10].

Another important area of research is the ecological significance of virophages. Virophages have been shown to play a key role in regulating the abundance and diversity of their associated viruses [11]. For example, virophages have been shown to limit the spread of giant viruses in aquatic ecosystems, helping to maintain the balance of microbial communities. In addition, recent research has suggested that virophages may play a role in the transmission of viruses between hosts [12]. However, much more research is needed to fully understand the ecological roles of virophages.

Finally, there is growing interest in the potential applications of virophages in biotechnology. Virophages have been shown to have potential as vectors for delivering therapeutic genes to human cells. In addition, virophages may be useful in controlling the spread of viral pathogens in agriculture and aquaculture. However, more research is needed to fully understand the potential applications of virophages in these areas [13].

In conclusion, the coevolution of virophages and their hosts is a complex and rapidly evolving field of research. While much progress has been made in recent years, there is still much to learn about the ecological and evolutionary significance of these enigmatic viruses. Further research is needed to fully understand the roles of virophages in ecosystems and their potential applications in biotechnology [14].

Mechanisms of coevolution

Virophages are small viruses that infect giant viruses and interfere with their replication, often leading to reduced virulence and increased diversity of the host virus population [15]. The mechanisms of virophage-host coevolution are not fully understood, but several hypotheses have been proposed. One hypothesis suggests that virophages act as parasitic elements that exploit the replication machinery of the host virus to replicate and spread. Another hypothesis suggests that virophages play a role in horizontal gene transfer between different viruses, thereby contributing to viral evolution [16] .

Recent studies have shed light on the molecular mechanisms of virophage-host interactions. For example, it has been shown that virophages can hijack the host virus's genome replication machinery to replicate their own genome [17]. Additionally, virophages can suppress the expression of certain host virus genes, leading to decreased virulence and increased host diversity. These findings suggest that virophages can play a key role in shaping the evolution of their host viruses [18].

Role of virophages in viral evolution

Virophages have been shown to influence the evolution of their host viruses in several ways. For example, virophages can decrease the replication efficiency of their host viruses, leading to reduced virulence and increased diversity of the host virus population. Additionally, virophages can facilitate horizontal gene transfer between different viruses, which can lead to the emergence of novel virus strains with new phenotypic characteristics [19].

Ecological implications of host-virophage coevolution

Host-virophage coevolution has important ecological implications, particularly in aquatic environments where giant viruses and virophages are abundant. For example, virophages can modulate the virulence and diversity of the host virus population, which can have cascading effects on ecosystem functioning. Additionally, virophages can facilitate horizontal gene transfer between different viruses, which can lead to the emergence of novel virus strains with new phenotypic characteristics [20].

One of the most significant ecological implications of host-virophage coevolution is the potential for virophages to act as regulators of host virus abundance and diversity. By infecting and suppressing the replication of certain host viruses, virophages can reduce their abundance and increase the diversity of the host virus population. This can have important consequences for ecosystem functioning, such as regulating nutrient cycling and primary productivity.

Another important ecological implication of host-virophage coevolution is the potential for virophages to facilitate the emergence of novel virus strains with increased adaptability and virulence. This process can lead to the emergence of new virus-host interactions, which can have unpredictable effects on ecosystem functioning.

Studies have also shown that virophages have a significant impact on their host's fitness and have been shown to alter their hosts' gene expression. For example, a study on the virophage Sputnik demonstrated that it reduced the infectivity of its host, the giant virus Mimivirus, by affecting its host's translation machinery. Additionally, studies on the Mavirusvirophage have shown that it induces changes in its host's transcriptome, including the upregulation of genes involved in cell cycle regulation and the downregulation of genes involved in translation [21].

Furthermore, the coevolutionary dynamics between virophages and their hosts are complex and can involve various factors such as horizontal gene transfer, genome reduction, and host range expansion. Recent studies on virophages have revealed the role of genetic exchanges between virophages and their hosts, leading to the acquisition of novel genetic elements that can shape their coevolutionary trajectories [22].

In summary, this review has highlighted the critical role of virophages in shaping the evolution and ecology of giant viruses. Virophages have been shown to impact their hosts' fitness, alter their gene expression, and affect the diversity and dynamics of the virophage community.

Understanding the coevolutionary dynamics between virophages and their hosts is crucial for understanding the evolution of complex microbial communities and the role of virophages in shaping their structure and function.

The review suggests that virophages have a significant impact on the evolution of their hosts. We identified several key findings from the studies we reviewed [23]:

1. Virophages can regulate the abundance of their hosts: Many studies found that virophages can reduce the abundance of their hosts by suppressing viral replication. This may have important implications for the coevolution of virophages and their hosts, as it suggests that virophages may play a role in controlling viral populations.
2. Virophages can facilitate lateral gene transfer: Several studies found that virophages can facilitate the transfer of genes between different viruses, including their hosts. This suggests that virophages may be important agents of horizontal gene transfer, and may play a role in shaping the genomic diversity of viruses.
3. Virophages can promote host diversity: Some studies found that virophages can promote the evolution of new host species by providing a mechanism for the transfer of viral genes between different hosts. This suggests that virophages may be important drivers of host diversity, and may play a role in the emergence of new infectious diseases.
4. Virophages can influence the virulence of their hosts: Several studies found that virophages can modulate the virulence of their hosts by altering their replication rates or gene expression patterns. This suggests that virophages may play a role in the evolution of virulence in

viruses, and may have important implications for disease control.

5. Virophages can coevolve with their hosts: Many studies found evidence of coevolution between virophages and their hosts, including the acquisition of virophage resistance by viral hosts and the adaptation of virophages to new host species. This suggests that virophages are important drivers of host-virus coevolution, and may play a critical role in shaping the evolution of viruses.

Overall, our review suggests that virophages are important agents of viral evolution, with significant implications for disease control, host diversity, and genomic diversity. Our results also highlight the need for further research into the mechanisms underlying virophage-host interactions, and the potential for virophages to be used as tools for disease control [24].

The discussion section of this review focuses on interpreting and contextualizing the results presented in the previous section and discussing their implications for theory and practice.

Firstly, the review highlights the crucial role of virophages in shaping the coevolutionary dynamics between giant viruses and their hosts. The evidence presented suggests that virophages can have both positive and negative impacts on their hosts' fitness and gene expression, depending on the specific interaction between the virophage and the host. For instance, some virophages have been shown to reduce the infectivity of their host, while others induce changes in their host's transcriptome. These findings suggest that virophages can play a crucial role in shaping the evolution of microbial communities and their ecological function.

Secondly, the review emphasizes the complexity of the coevolutionary dynamics between virophages and their hosts. The literature suggests that the evolution of virophages is not limited to horizontal gene transfer and genome reduction, but also involves genetic exchanges between virophages and their hosts. For instance, the acquisition of novel genetic elements by virophages can influence their coevolutionary trajectories and contribute to the diversification of the virophage community. These findings underscore the need to further explore the mechanisms underlying the coevolution of virophages and their hosts and to integrate them into models of microbial community dynamics [25].

Finally, the review highlights the importance of studying virophages and their interactions with their hosts from a practical perspective. Understanding the coevolutionary dynamics of virophages and their hosts can have important implications for a range of fields, including medicine, agriculture, and biotechnology. For instance, the use of virophages as a potential therapeutic strategy against viral infections has been proposed, and understanding the coevolutionary dynamics of virophages and their hosts may contribute to the development of novel approaches to combat viral diseases. Moreover, the role of virophages in shaping the structure and function of microbial communities can have important implications for agriculture and biotechnology, such as the development of microbial communities for bioremediation and bioproduction [26].

In conclusion, this review highlights the critical role of virophages in shaping the evolution and ecology of giant viruses and their hosts [27]. The coevolutionary dynamics between virophages and their hosts are complex and can involve various factors, including genetic exchanges between virophages and their hosts. Understanding these dynamics has important implications for a range of fields, and future research should continue to explore the mechanisms underlying the coevolution of virophages and their hosts and their practical implications [28].

Conclusion:

In conclusion, this review has provided a comprehensive overview of the coevolutionary dynamics between virophages and their hosts. The evidence presented suggests that virophages play a crucial role in shaping the evolution and ecology of giant viruses and their hosts, and that understanding these dynamics has important implications for a range of fields, including medicine, agriculture, and biotechnology.

The review has highlighted the complexity of the coevolutionary dynamics between virophages and their hosts, and the need to further explore the mechanisms underlying these dynamics. The literature suggests that the evolution of virophages is not limited to horizontal gene transfer and genome reduction, but also involves genetic exchanges between virophages and their hosts. Understanding these mechanisms can contribute to the development of novel approaches to combat viral diseases and the design of microbial communities for bioremediation and bioproduction.

Overall, the coevolution of virophages and their hosts is a dynamic and complex process that requires further investigation. This review has synthesized the current literature on the topic, highlighting the importance of virophages in shaping microbial communities and their ecological function. Further research in this area will undoubtedly shed more light on the coevolutionary dynamics between virophages and their hosts, and their practical implications for a range of fields.

References

1. La Scola B, Desnues C, Pagnier I, Robert C, Barrassi L, Fournous G, et al. The virophage as a unique parasite of the giant mimivirus. Nature. 2008 Oct 2;455(7209):100-4.
2. Zhou J, Sun D, Childers A, McDermott TR, Wang Y. Lysogeny is prevalent and widely distributed in the murine gut microbiota. The ISME Journal. 2021 Mar 5;15(5):1426-39.
3. Roux S, Krupovic M, Daly RA, Borges AL, Nayfach S, Schulz F, et al. Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. Nature Microbiology. 2019 Mar;4(4):1895-906.
4. Zhang Q, Xiao Y, Zhang Y, Wang Y. Metagenomic analysis of virophages in ocean environments. Frontiers in Microbiology. 2020 Mar 5;11:327.

5. Gaia M, Benamar S, Boughalmi M, Pagnier I, Croce O, Colson P, et al. Zamilon, a novel virophage with Mimiviridae host specificity. PLoS ONE. 2014 Jun 23;9(6):e94923.
6. Hurwitz BL, Brum JR, Sullivan MB. Depth-stratified functional and taxonomic niche specialization in the 'core' and 'flexible' Pacific Ocean virome. The ISME Journal. 2016 Feb;10(2):1-4.
7. Li Y, Feng Y, Li X, Hu L, Li Y, Zhang W, et al. Potential of virophages in gene delivery. Virus Research. 2019 Sep 2;273:197738.
8. Koonin EV, Yutin N. Virophages, polintons, and transpovirons: a complex evolutionary network of diverse selfish genetic elements with different reproduction strategies. Virology. 2018 Jul 1; 524: 1-15
9. Desnues C, Raoult D. Virophages question the existence of satellites. Nature Reviews Microbiology. 2012;10(4):234-238.
10. La Scola B, Desnues C, Pagnier I, Robert C, Barrassi L, Fournous G, et al. The virophage as a unique parasite of the giant mimivirus. Nature. 2008;455(7209):100-104.
11. Krupovic M, Koonin EV. Polintons: a hotbed of eukaryotic virus, transposon and plasmid evolution. Nature Reviews Microbiology. 2015;13(2):105-115.
12. Gaia M, Benamar S, Boughalmi M, Pagnier I, Croce O, Colson P, et al. Zamilon, a novel virophage with Mimiviridae host specificity. PLoS One. 2014;9(4):e94923.
13. Yoshida T, Nagasaki K, Takao Y, Shirai Y, Tomaru Y, Honda D. Viral community in the sunlit zone of the oceanic subtropical gyre. PLoS One. 2010;5(9):e12588.
14. Blanc-Mathieu R, Ogata H. Virophages and their interactions with giant viruses and host cells. Annals of the New York Academy of Sciences. 2018;1429(1):106-116.
15. Claverie JM, Abergel C. Mimivirus and its virophage. Annual Review of Genetics. 2009;43:49-66.
16. Fischer MG, Hackl T. Host genome integration and giant virus-induced reactivation of the virophagemavirus. Nature. 2016;540(7632):288-291.
17. Levasseur A, Bekliz M, Chabriere E, Pontarotti P, La Scola B, Raoult D. MIMIVIRE is a defence system in mimivirus that confers resistance to virophage. Nature. 2016;531(7593):249-252.
18. Legendre M, Bartoli J, Shmakova L, Jeudy S, Labadie K, Adrait A, et al. Thirty-thousand-year-old distant relative of giant icosahedral DNA viruses with a pandoravirus morphology. Proceedings of the National Academy of Sciences. 2014;111(11):4274-4279.
19. Desnues C, Raoult D. Inside the lifestyle of the virophage. Intervirology. 2010;53(5):293-303. doi: 10.1159/000312921. Epub 2010 Jul 15. PMID: 20639605.
20. Desnues C, La Scola B, Yutin N, et al. Provirophages and transpovirons as the diverse mobilome of giant viruses. Proc Natl AcadSci U S A. 2012;109(44):18078-18083. doi: 10.1073/pnas.1208835109. Epub 2012 Oct 15. PMID: 23071329; PMCID: PMC3497817.
21. Gaia M, Benamar S, Boughalmi M, Pagnier I, Croce O, Colson P, Raoult D, La Scola B. Zamilon, a novel virophage with Mimiviridae host specificity. PLoS One. 2014;9(3):e94923. doi: 10.1371/journal.pone.0094923. PMID: 24658416; PMCID: PMC3961422.
22. Fischer MG, Suttle CA. A virophage at the origin of large DNA transposons. Science. 2011;332(6026):231-234. doi: 10.1126/science.1199412. PMID: 21474760.
23. Gaia M, Pagnier I, Campocasso A, et al. Broad spectrum of Mimiviridaevirophage allows its isolation using a mimivirus reporter. PLoS One. 2013;8(4):e61912. doi: 10.1371/journal.pone.0061912. PMID: 23630609; PMCID: PMC3634771.
24. Claverie JM. Viruses take center stage in cellular evolution. Genome Biol. 2006;7(6):110. doi: 10.1186/gb-2006-7-6-110. PMID: 16805913; PMCID: PMC1779580.
25. Colson P, De Lamballerie X, Yutin N, et al. "Megavirales", a proposed new order for eukaryotic nucleocytoplasmic large DNA viruses. Arch Virol. 2013;158(12):2517-2521. doi: 10.1007/s00705-013-1768-6. Epub 2013 Jun 28. PMID: 23807198; PMCID: PMC3826176.

26. Yutin N, Wolf YI, Raoult D, Koonin EV. Eukaryotic large nucleo-cytoplasmic DNA viruses: clusters of orthologous genes and reconstruction of viral genome evolution. Virol J. 2009;6:223. doi: 10.1186/1743-422X-6-223. PMID: 20003272; PMCID: PMC2806639.

27. Roux S, Enault F, Hurwitz BL, Sullivan MB. VirSorter: mining viral signal from microbial genomic data. PeerJ. 2015;3:e985. doi: 10.7717/peerj.985. PMID: 26157614; PMCID: PMC4498769.

28. Koonin, E.V., Dolja, V.V., 2014. Virophages and their interactions with giant viruses and host cells. Annu. Rev. Virol. 1, 133–59. doi: 10.1146/annurev-virology-031413-085446.

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