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THE ECOLOGICAL SIGNIFICANCE OF VIRUSES IN AQUATIC ECOSYSTEMS: A COMPREHENSIVE ANALYSIS

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ABSTRACT

It is widely acknowledged that viruses are essential elements of the aquatic Environment, contributing significantly to various ecological processes and altering the dynamics of aquatic ecosystems. The variety of viruses in aquatic habitats, including freshwater and marine ecosystems, is enormous. Numerous different types of organisms, such as bacteria, algae, protozoa, and even multicellular organisms, are susceptible to these viral interactions, and these organisms have a significant impact on the design and operation of aquatic ecosystems. In aquatic ecosystems, viral-mediated mortality facilitates the recycling of nutrients and energy by influencing the composition of microbial populations. Additionally, viruses participate in genetic transfer procedures and are essential for horizontal gene transfer. They also serve as genetic material carriers, allowing the transfer of genes between various organisms. This phenomenon affects the ecological balance in the aquatic Environment and the evolution and adaption of microbial communities. Viruses can be used as instruments to investigate microbial ecology, comprehend host-virus interactions, and create fresh antiviral tactics. Viruses are essential to the health and stability of aquatic environments. Aquatic viruses have attracted attention because of their potential utility in various sectors, including biotechnology and medical research; they are essential elements of the aquatic environment due to their capacity to control microbial populations, reduce toxic algal blooms, and offer insights into microbial ecology. Our comprehension of these complex interactions and their larger implications for environmental health and management will be improved by additional study and investigation of viral dynamics and interactions within aquatic ecosystems. This review attempts to present an overview of the significance of viruses in aquatic ecosystems by highlighting their variety of roles and interactions.

Keywords: aquatic ecosystem, bio-symbionts, host-virus interaction, marine viruses, microbial control

INTRODUCTION

The oceanic realm, often perceived as a vast expanse of serene waters, harbors a concealed tapestry of genetic diversity primarily orchestrated by an inconspicuous yet influential agent-viruses (Jansson *et al.,* 2023). These miniscule entities, which vastly outnumber cellular life, epitomize the enigma that underlies the intricate web of marine biodiversity. In a remarkable testament to their ubiquity, if the length of all oceanic viruses were extended, they would effortlessly traverse the span between sixty neighboring galaxies. Emerging research is unraveling the cryptic yet crucial role of these 'lifeforms' that dictate the fate of marine ecosystems (Li *et al.,* 2023). These viruses, comprised of proteinaceous capsids encasing genetic cargo, are characterized by profound genomic variability. Their dimensions, ranging from 20 to 200 nanometers, encapsulate the extraordinary diversity that is harbored within their genetic blueprints.

The revelation that viral densities in oceanic expanses may reach up to 108 per milliliter rekindles the scientific fervor to comprehend the intricate dynamics of marine viral communities (Wang *et al.,* 2023). Advancements in detection and quantification methodologies amplify the scope to probe the abundance and variety of these marine entities. Notably, these microorganisms orchestrate pivotal ecological shifts, orchestrating the intricate interplay between bacterial and algal populations on a microscopic scale. Simultaneously, their impacts resonate on a macroscopic level, echoing through biogeochemical cycles and governing

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*Corresponding author: anwaariftikhar33@gmail.com oceanic productivity (Santiago-Rodriguez *et al.,* 2023). The emergence of molecular biology tools, underscored by DNA sequencing techniques, ushers in an era where viral genetic variation and intricate virus-host interactions take center stage (Yang *et al.,* 2022). Yet, these enigmatic agents remain elusive to conventional light microscopy, necessitating specialized methods for their extraction from the saline milieu. The intricate tapestry of these invisible architects emerges under the magnification of transmission electron microscopy (TEM), shedding light on their profound influence (Al-Hazmi *et al.,* 2022).

Meticulous refinement of methodologies, such as ultracentrifugation coupled with TEM visualization, advances our comprehension of marine viruses and prokaryotes (Hill *et al.,* 2023). These endeavors, spanning decades, have hastened the revelation of numerous viruses and prokaryotes concealed within aquatic ecosystems. In a transformative shift, biological oceanography and limnology pivot towards a microbiological vantage, transforming the landscape of research.

The ebbs and flows of viral populations are intrinsically intertwined with ecological events, such as algal blooms, reshaping the intricate balance of marine habitats (Liang *et al.,* 2023). These viruses, reliant on host metabolisms, function as parasitic entities, prompting a paradigm shift in understanding evolution, ocean biogeochemistry, and even human health. A mesmerizing panorama unfolds as viruses, harboring the ability to infect an array of cellular organisms, transcend taxonomic boundaries. These entities, which depend on interactions with cellular components, lay claim to an astonishing numerical dominance, surpassing the combined abundance of bacteria, archaea, and eukarya in seawater (Owen *et al.,* 2022). The oceanic tapestry, woven by these viral architects, is underscored by virion concentrations that span the vastness of open ocean waters, resonating even in sediments that have aged across millennia (Köstlbacher *et al.,* 2022).

The microplankton, encompassing an orchestra of viral actors, weaves intricate melodies in the aquatic milieu, shaping the marine plankton and sedimentary realms (D'Adamo *et al.,* 2022). The finesse of nature's arrangement resonates within these dimensions, encompassing pico-plankton and femto-plankton categories, where viruses orchestrate the unseen choreography of aquatic life (Haridevamuthu *et al.,* 2023). Kau As the oceanic stage unfolds, the profound interplay between animal families and the aquatic milieu is mirrored by the intricate viral landscapes that pervade marine ecosystems (Krishna *et al.,* 2023). Viruses stand as architects, sculpting the intricate balance that reverberates through biogeochemical cycles, underscoring their indispensability (Jiang *et al.,* 2023).

Inquisitive minds traverse beyond the surface, delving into coral reefs, sediments, freshwater realms, and the uncharted frontiers of the deep biosphere. These endeavors paint a vivid mosaic, illustrating that every aquatic expanse is a haven for these enigmatic entities, while also unearthing ancestral lineages that bridge the gap between microscopic and macroscopic realms (Ahmed *et al.,* 2022). In the symphony of aquatic life, the significance of understanding the nexus between viral forces and their impacts on health, biodiversity, and biogeochemical cascades takes center stage. As scientific inquiries pierce the veil, the burgeoning field of aquatic virology paves the way for holistic comprehension, casting light upon a realm that shapes the very essence of our planet's oceans.

Aquatic biosphere and environmental variability

Aquatic ecosystems, spanning a vast expanse of Earth's surface, stand as intricate hubs of ecological equilibrium with profound implications for global stability (Han *et al.* 2022). Comprising diverse realms such as coral reefs, lakes, oceans, wetlands, and rivers, these watery domains provide vital services-ranging from water purification to carbon sequestration and nutrient cycling-all essential for sustaining life. With a myriad of organisms adapting to aquatic habitats (Pongpakdeesakul *et al.,* 2023), these dynamic ecosystems fuel intricate interactions that cascade through the aquatic food web. At the heart of this intricate dance lie microorganisms like bacteria and algae, orchestrating the nutrient cycles and primary production that underpin aquatic ecosystems (Gisele *et al.,* 2023). These microorganisms form the foundation of the aquatic food web, sustaining larger organisms like zooplankton, microscopic fish, and invertebrates, thus shaping the balance of life within these aqueous realms. Meanwhile, seagrasses and macroalgae serve as architectural keystones, providing refuge, sustenance, and oxygen for a multitude of marine creatures while bolstering sediment stability and shoreline resilience (Ribeiro Prist *et al.,* 2022). Amidst the fluidity of aquatic existence, organisms confront the rhythmic flux of ever-changing environmental conditions (Zayed *et al.,* 2022). Yet, as global changes amplify the complexity of these fluctuations, the scientific community is prompted to reassess our predictive capacity. Conventional models and static studies falter in capturing the intricate ecological responses to dynamic variations. Within aquatic ecosystems, a gap exists in harnessing temporal environmental variability for experimental designs (Trubl *et al.,* 2023). Anthropogenic pressures introduce novel stressors, exacerbating ecosystem patterns and inducing consequences across various temporal and spatial scales, permeating through individual organisms to entire ecosystems (Takuissu *et al.,* 2023).

Navigating this ever-shifting tapestry unveils differing reactions from organisms dwelling in inherently volatile or comparatively stable habitats, particularly in the face of continuous disturbances induced by human activities. Fluctuations in temperature, for instance, might elicit more pronounced impacts on organismal performance than steady warming scenarios (Du *et al.,* 2023). Similarly, the intricate interplay between ocean pH and the vitality of corals and coralline algae yields multifaceted outcomes contingent on the ocean acidification context, underscoring the importance of exploring diverse factors and embracing the nuances of natural variability when forecasting biotic responses to global shifts (Farooq *et al.,* 2022g).

The tableau of aquatic life intricately interweaves an array of environmental parameters-temperature, light quality and intensity, oxygen levels, salinity, PCO_2/pH, and hydrodynamics-each shaping organisms both directly and indirectly by molding their interactions (Arun *et al.,* 2023). The hierarchy of these influencers varies, echoing the uniqueness of each system, whether nestled within a pond, lake, river, or marine expanse (Zhao *et al.,* 2022). This dynamic interplay forms the fabric of aquatic existence, resonating through its intricate ecosystems and yielding insights that extend beyond the surface, enriching our comprehension of nature's enigmatic fluidity.

Diversity and pathogenicity of marine viruses (Table 1)

Phytoplankton viruses, pervasive inhabitants of the world's oceans and rivers, have emerged as influential orchestrators of aquatic ecosystems (Wicaksono *et al.,* 2023). Beyond their role in enhancing aquatic ecosystem productivity, they catalyze organic matter recycling, thereby contributing to the intricate balance of these dynamic habitats (Popovic *et al.,* 2022).

Estimates reveal that aquatic systems teem with millions of viruses per milliliter of seawater, underscoring their prevalence (Kaushik *et al.,* 2023). Among their versatile prey are bacteria, phytoplankton, protozoa, and even fish, accentuating their diverse ecological impact (Kieft *et al.,* 2020).

The global expansion of aquaculture has unveiled a new facet of the viral impact, with viral infections emerging as significant causes of mortality in farmed species (Kaushik *et al.,* 2023). One such virus, the piscine orthoreovirus (PRV), stands as the catalyst behind muscular inflammation in Atlantic salmon, echoing the intricate interplay between viruses and aquaculture (Farooq *et al.,* 2023). This complex interaction comes into focus as viruses and bacteria ratios across marine settings demonstrate marked divergence, highlighting the nuanced microbial tapestry within these ecosystems (da Silva *et al.,* 2022).

Deciphering the dynamics of viral-bacterial interactions unearths a web woven with environmental intricacies, where inorganic nutrient concentrations emerge as pivotal regulators of the viral-host nexus (Malits, *et al.,* 2023). This intricate relationship ushers in a cascade of consequences, echoing across spatial and temporal dimensions. Environmental stability is paramount, as disturbances to microbial interactions can ripple through the intricate fabric of virus, prokaryote, and host communities (Dominguez-Huerta *et al.,* 2022). Temporal oscillations in viral populations mirror the seasonal variations in host diversity, underscoring the intricate interplay within the aquatic realm (Chen *et al.,* 2022).

Remarkable adaptations come to the forefront with viruses responding to environmental changes, as highlighted by shifts in the composition and diversity of Emiliania huxleyi viruses (EhV) in the wake of elevated PCO2 levels (Li *et al.,* 2022). The ever-pervasive Arctic landscape echoes these adaptations, as warming propels the emergence of novel viral genotypes that coincide with accelerated Micromonas growth rates (Li *et al.,* 2022). The landscape of viral diversity mirrors this complexity, with only a fraction of dsDNA viral populations linked to cultured counterparts, highlighting the vastness of uncharted viral realms (Wang *et al.,* 2019). Intricacies abound within the intricate web of marine viruses, urging the acceleration of genome-sequencing and characterization efforts across eukaryotes like *Prymnesium parvum* and bacteria such as *Shewanella, Vibrio anguillarum*, and *Dinoroseobacter shibae* (Carlson *et al.,* 2022). The exploration of viral gene flow within the marine milieu unravels localized diversities, uncovering the unending exchanges shaping these viral cohorts (La Rosa *et al.,* 2020).

As we traverse this realm, it's evident that the dissemination of viruses is far-reaching and capable of echoing through the marine environment, underpinning the intricate balance of these aquatic ecosystems (La Rosa *et al.,* 2020). Amidst this complexity, the diverse world of nucleocytoplasmic large DNA viruses (NCLDV) emerges, impacting photosynthetic protists, reshaping their survival strategies, evolution, and contributions to the aquatic landscape (Zayed, *et al.,* 2022). Prasinoviruses and viruses targeting haptophytes accentuate the manifold interactions within this viral world, unveiling the delicate symphony of life within the realm of aquatic ecosystems (V *et al.,* 2021).

Unique Methods to study aquatic viruses

Reckoning with viruses' extraordinary variety, genetics, and evolution is essential for comprehending how they shape life (Eckstrand *et al.,* 2023). No universally common gene exists in viruses despite all known cellular creatures having a genome of ds-DNA and key metabolic genes. It has been confirmed that the 195,728 viral populations found in the extended global ocean DNA virome dataset, which now includes the Arctic Ocean cluster into distinct genotypic groups (Li *et al.,* 2023).

Table 1. Shows the diversity of viruses in the marine environment

Virus Name	**Taxonomy**	**Hosts**	**Impact/Function**	**References**
T4-like Phages	Family: Myoviridae	Bacteria	Predation on bacterial hosts	(Zayed *et al.,* 2022)
Mimivirus	Family: Mimiviridae	Amoebae, others	Large DNA virus, a potential pathogen	**(**Kolundžija *et al.,* 2022)
Prochlorococcus Virus	Family: Podoviridae	*Prochlorococcus*	Affects marine cyanobacteria	(Jiang *et al.,* 2023
Coccolithoviruses	Family: Phycodnaviridae	*Emiliania huxleyi*	Affects coccolithophores	(Khalil *et al.,* 2022)
Phaeocystis globosa Virus	Family: Phycodnaviridae	*Phaeocystis globosa*	Affects microalgae	(Cruz-Pulido *et al.,* 2023)
White Spot Syndrome Virus	Family: Nimaviridae	Shrimp	Pathogenic to crustaceans	(Channappanavar, *et al.,* 2022).
Heterosigma akashiwo Virus	Family: Phycodnaviridae	*Heterosigma akashiwo*	Affects harmful algal blooms	(Gack *et al.,* 2022).

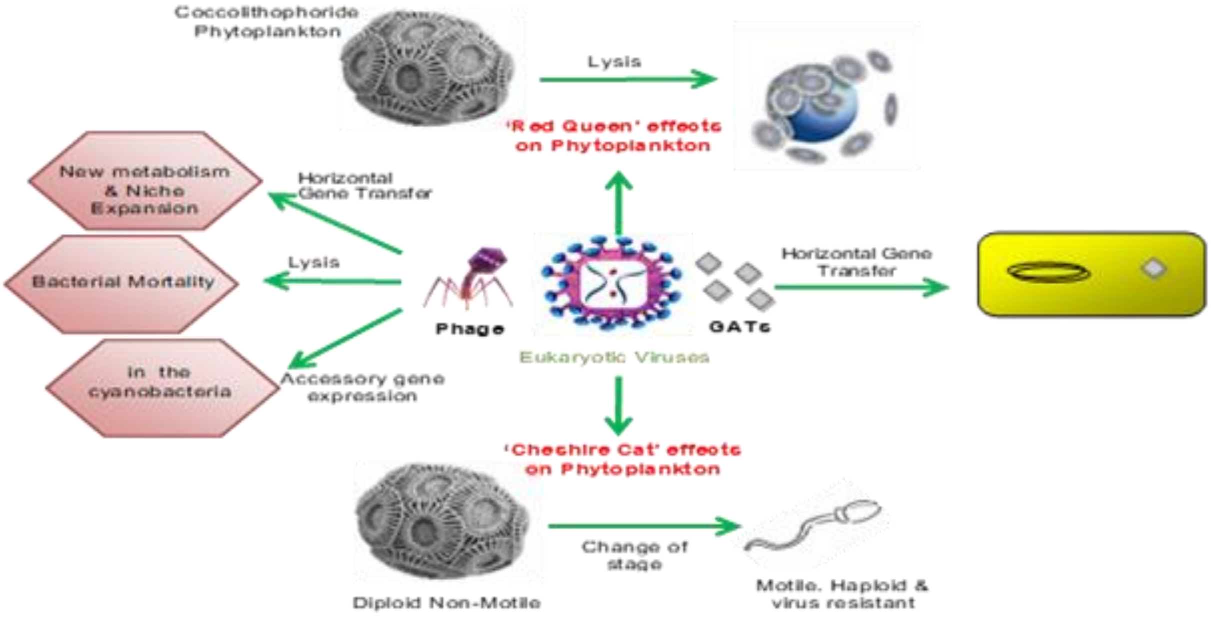

Figure 1. Shows the relationship of host -virus in the marine environment

However, creative approaches to data analysis are required because of the vast quantity and variety of information at our fingertips. For complicated aquatic environmental viral samples, qualitative and quantitative examination of the viruses is a daunting undertaking (Mannion *et al.,* 2020). While certain techniques (such as polymerase chain reaction (PCR) or the polony method may reliably quantify virus isolates, no such technique exists for environmental samples. New sequencing methods have greatly simplified the processes of viral delimitation and discovery (Cobbin *et al.,* 2021). In addition, virosphere comprehension and monitoring can benefit from genomic data exploration. Therefore, only new technologies will allow for a deeper comprehension of the ecological and evolutionary interactions between aquatic viruses, paving the way for creating a more balanced and productive aquatic environment (Jiang *et al.,* 2023). Aquatic virus research may benefit from several recently established or soon-to-be-used technological techniques. PCR-amplification and sequencing can target conserved genes to study environmental viral diversity. PCR and metagenomics have revolutionized microbiology by providing an assessment independent of culture and exploiting viral and microbial communities (Jansson *et al.,* 2023). Metagenomic research of viruses has uncovered unique patterns of evolution, altered previous theories about the viral world's makeup, and identified new groupings of viruses and virus-like entities. Without growing the virus in a lab, a single viral particle can now be isolated and its whole genome sequenced via single-virus genomics (SVGs) (Li *et al.,* 2022). The sequencing of even a single virus has led to exciting discoveries in the field of viral ecology and paved the way for isolating *hitherto* uncultured viruses. SVGs dominate both reported metagenome-assembled genomes of viruses and isolated viruses in global ocean virome data sets (Bi *et al.,* 2021). Over the last several years, over 750,000 novel viral genomes have been discovered in metagenome and metatranscriptome databases.

Individual study of plaque-forming units of viruses on solid media may generate Plaque mass spectrometry imaging (MSI) maps connecting metabolic states of the host and virus to infection states of the virus (Kim *et al.,* 2023. Cellular absorption of a biorthogonal synthetic amino acid is used in biorthogonal non-canonical amino-acid tagging (BONCAT) (Abedin *et al.,* 2022), which then incorporates the synthetic amino acid into de novo peptides. BONCAT may be used to observe and evaluate translation in microorganisms. The rapid and inexpensive detection of viruses in water is made possible by biosensors, a measuring device for detecting analytes that combines an element of biology with a physiological detector (Zhang *et al.,* 2023). (Volpe *et al.,* 2023). RMAN is a residual combined attention system that uses channel attention and a residual architecture to eliminate manual Annotation in viral classification from electron microscope pictures. Detection of viruses in water involves adsorption elution, ultra filtration, eco-physiological techniques (Khalil *et al.,* 2022), VIBRANT(Virus Identification By iterative Annotation), and FISH (Fluorescence in situ hybridization). VirION (Viral, long-read metagenomics) sequencing is a high-throughput DNA sequencing and bioinformatics process for improving metagenomics assemblies of viruses (Kumar *et al.,* 2022).

The effects of host-virus interactions on the aquatic bio-sphere

The effect that rising global temperatures have on the relationships between marine hosts and viruses is largely unknown (González *et al.,* 2023). Many environmental conditions, such as temperature and salinity, affect virus-host interactions and, by extension, the biosphere. Indirect and direct effects of marine viruses on global warming are possible. Most climate change models also leave viruses out since assessing the full scope of these effects is difficult. For marine scientists, especially virologists, the world's seas and other bodies of water will always be a source of novel knowledge (Wang *et al.,* 2023). Virus-host interactions in the deep biosphere may be just as nuanced and dynamic as those at the cellular level. Due to their parasitic nature, viruses were formerly considered natural enemies of bacteria. It is now known, however, that the viruses are not certainly damaging and that certain viral infections may even be 'helpful' to their hosts as part of well-orchestrated infection schemes (Cruz-Pulido *et al.,* 2023). There are three main methods through which viruses may spread. In the first kind of infection, a lytic infection, after binding the virus to a host cell, viruses inject their genetic material into the cell's cytoplasm, which dictates the host to make multiple copies of the virus. These copies are released when the cell breaks fatally, allowing the cycle to begin again (McMillan *et al.,* 2023). When offspring viral discharge is not lethal but rather happens through extrusion or budding from the host cell throughout several generations, the infection is said to be persistent. The third kind of genetic exchange between viruses and cells is called lysogeny and involves merging the viral genome into the host DNA and subsequent replication as a prophage or provirus (Tenthorey *et al.,* 2022). Here, an inducing factor like host stress may switch the virus to a lytic mode of operation. This kind of virus-host interaction is poorly understood, in which the virus's genome may live within the host cell for a long time and pass from generation to generation before the cell is killed by lysis (Sharma *et al.,* 2023). In a state of host hunger, the virus enters a dormant stage called pseudo lysogeny because it lacks the energy to trigger viral gene expression. A polysaccharide depolymerase released by infected cells may be responsible for the transient immunological response known as pseudo lysogeny, which helps maintain viral and host cohabitation (Ahmed *et al.,* 2021). Viruses and virus-like particles have been shown to kill cells in methods that do not need viral replication. Lytic viruses are considered murderers that work against their hosts. An often-cited example of an antagonistic interaction is the ongoing battle for supremacy between viruses and their host organisms, an evolutionary arms race (Delima *et al.,* 2023), which ends up in constantly developing antiviral techniques and responses by viruses. A lineage-level time series investigation of CRISPR spacers in hosts and protospacers in viruses verified this relationship in samples from deep terrestrial hydraulically damaged wells (Channappanavar *et al.,* 2022).

The relative abundance of *Halanaerobium* associated viruses, which are probably the sole 'predators' of *Halanaerobium* in this Environment, declined in parallel with the fall of *Halanaerobium* populations in hydraulically fractured shales, according to this long-term research (Su *et al.,* 2023). Furthermore, metagenome-assembled of a Halanaerobium genome exhibited 43 spacers, 20 of which were linked to the same viral gene, suggesting that active viral infection plays a vital role in promoting the establishment of microbial communities. Lysogenic and chronic viruses have traditionally been considered more cooperative with their hosts (Kumar *et al.,* 2023). Evidence from several research suggests that prophages help hosts survive in stressful circumstances by producing positive changes in the host's physiology and suppressing superfluous metabolic activity. Superinfection exclusion also occurs with moderate viruses, making their hosts resistant to subsequent infection (Chofong *et al.,* 2021). Recently, a great example of viral-host mutualism was discovered: cells of the archaeon *Sulfolobus islandicus* that were persistently infected with the virus were able to produce a toxic protein that showed resistanceagainstinfectedcells by viruses and therefore killed the cells resistant to viruses in the population (Molteni *et al.,* 2023). This method ensured the virus would survive in the face of widespread immunization by eliminating competing cells in the host population. Superinfection exclusion benefits viruses because it reduces interhost virus-virus rivalry and promotes sustained vertical transmission (Gack *et al.,* 2022). Being intracellular may also provide viruses a leg up in the face of the unfavorable circumstances typical of the deep biosphere, including a lack of susceptible hosts, limited host activity, and high temperature. The implications of viruses' ecological significance in the ecosystem of deep habitats may be better understood with knowledge of host-virus interactions in relevant situations from the biosphere in deep marine (del Arco *et al.,* 2023). From its discovery through the intricate interplays between virus and host and the interactions with ecologically significant environmental factors, eukaryotic and prokaryotic viruses are the focus of the contributions in this special issue (Lüscher *et al.,* 2022). The interesting realm of marine viruses is exemplified by the discovery of novel viruses and new processes governing viral dispersion and variety. The oceans play a crucial role in maintaining Earth's habitable temperature, storing 1.37 billion km^3 of salt water and producing 50% of the world's oxygen (Murthy *et al.,* 2022). Understanding how viruses impact biodiversity, host population dynamics, ecosystem, and biogeochemical cycling efficiency is crucial when sea life is under growing stress (acidification, global warming, economic usage, pollution). Figure 1 shows the Host-Virus relationship in the marine Environment.

quatic Viruses: A Molecular Analysis

Given the extraordinary variety of viruses and their rapid evolution, it is hard to establish a phylogenetic tree of their collective ancestry (Eckstrand *et al.,* 2023). Even though scientists believe there are more than a million different virus species, there are already more than 8,000 reference genome sequences. To optimize their number of progenies, replication rate, and other characteristics that promote their infectivity (Fan *et al.,* 2023), most known viruses have genomes that encode just a small number of proteins; they also have near-optimal genomic packing and data compression. Proteins acquire their intricate three-dimensional forms via folding (Oliveira *et al.,* 2020). Researchers may piece together the histories of protein fold on a historical basis and genomes of species, which code them by comparative analysis of structures of fold across various branches of the tree of life. Due to the high similarity between viral and cellular protein folds coded by genomes of viruses, they have been thought to be living beings (Perez-Lemus *et al.,* 2022). There is mounting evidence that phages, notably cyanophages, promote microbial community adaptability and evolution. Random mutation, recombination, reassortment, and the amplification or decrease of genes are all factors that contribute to the development of viruses. Many distinct virus families can infect various aquatic hosts (Abd Elfatah *et al.,* 2021). Virus-host interactions are far more nuanced than previously believed. An aquatic virus's DNA or RNA genome may be delivered into a host cell, duplicated, and expressed. Some viruses can insert themselves into the host's DNA (Dai *et al.,* 2023). Gene and genetic association studies may shed light on the diversity, distribution, and evolutionary history of viruses that have made aquatic ecosystems their home. Several typical viruses found in aquatic animals, including Rana viruses, Herpesviruses, Nima viruses, Reoviruses, and Rhabdoviruses, have recently had their genes, proteins, or genomes investigated and discoveries made (Ganeshalingam *et al.,* 2023). Recent studies have shown that at least 30 proteins of the virus and six proteins of the host make up the Rana virus replication and transcription machinery. Disentangling the complicated web of interactions and correlations between parts of the transcription complex and replisome (Menéndez *et al.,* 2020), including identifying the Ranavirus ssDNA binding protein (SSB), makes a major accomplishment. Up to 22 Rana viruses have had their whole genomes sequenced.

High death rates and acute hemorrhages of the gills in infected crucian carp (Carassius auratus) are caused by fish herpesvirus CaHV (Rahmati-Holasoo *et al.,* 2023). CaHV-138L was found to be the membrane protein of herpesvirus with an immunoglobulin C-2 Type (IGc^2) domain and TM domains, and deletion mutants of the TM domains had a major impact on the subcellular localization of CaHV-138L. The FoF1-ATPase, a mitochondrial protein, may serve as a source of energy for viral replication since CaHV-138L can target Cha first anguillid herpesvirus (Booranathawornsom *et al.,* 2022), or AngHV-1, belongs to the family *Alloherpesviridae* and the genus *Cyprinivirus*. Compared to other cypriniviruses, AngHV-1 has a lower alternative rate and low positive selection based on analyses of three key genes conserved across all herpesviruses (Zhang *et al.,* 2022). An extremely fatal whispovirus (WSSV-Cc) was identified from a naturally infected population of freshwater crayfish (*Cambarus clarkii*). A complete genome phylogenetic study revealed associations between genome size and evolutionary relatedness. From the WSSV-Cc genome, we found 20 low-similarity genes and three variable areas (Lim *et al.,* 2023). The entire genome size of aqua reoviruses is anywhere from 18.2 to 30.5 kb, and it is composed of 11 segments of the dsRNA genome in size range from 0.8 to 4.0 kb.

Viral community's impact on the environment

Environmental viruses are now understood to serve as genetic storage facilities for terrestrial ecosystems (Xu *et al.,* 2023). Viruses may support terrestrial ecosystems during natural revegetation by enhancing host competitiveness, stress tolerance, and nutrient cycles. (Qin *et al.,* 2023). More than a third of all ocean microorganisms are lysed daily by marine viruses, releasing large quantities of carbon and nutrients. Research has shown that viruses can transport auxiliary metabolic genes, which are thought to serve crucial functions in the metabolism of their prokaryotic host. Phages may lyse bacteria, allowing plant-derived carbon to be redistributed into the rhizosphere environment (Zou *et al.,* 2020). This indicates that viruses may provide novel insights into the mechanisms of ecosystem function and natural revegetation in arid environments. Different aspects of the marine environment influence the composition and possible roles of the viral community there (Elgendy *et al.,* 2022). The makeup and organization of the marine viral population are affected by environmental variables such as temperature, salinity, nutrient availability, and the amount of sunlight that reaches the ocean floor. Seasonal changes in climate, biological output (Udayantha *et al.,* 2021), and host populations may profoundly affect the marine viral community, which determines the community's composition and diversity. The structure and functionality of marine viral communities are susceptible to change due to human activities, including pollution, eutrophication, and climate change (Chen *et al.,* 2023). Algal blooms, which in turn impact viral dynamics in the ecosystem, may be triggered by increased nutrient inputs from agricultural runoff or wastewater discharge. Climate change-related increases in water temperature and ocean acidity may affect viral-host interactions and community composition (Hutson *et al.,* 2023).

Driving entire aquatic ecosystems

Viruses are responsible for the daily deaths of almost 20% of all microorganisms in the water. By releasing their contents, the viruses that infect these bacteria and algae also enrich the water column with dissolved organic and inorganic nutrients (Debat *et al.,* 2023). In the food chain, dissolved materials are recycled via the growth of microbes, which are then consumed by bigger animals like zooplankton and fish, which sharks, whales, and humans consume. This is how viruses at the molecular level recycle the building blocks of life (Ter Horst *et al.,* 2021). Since the oceans make up more than half of the planet's surface, they significantly impact most of Earth's biota. This indicates that viral lysis is the primary source of mortality that regulates microbial population size and turnover in deep underground sediments (Bi *et al.,* 2021). Predation by viruses may strengthen ecosystems by preventing the proliferation of overpopulated host species and preserving genetic diversity. It is believed that in the hydraulic damaging Environment, a temporary community shift on the genotype level of *Halanaerobium* encourages the expansion of the remaining community members via nutrient regeneration and the release of ecological niches produced by viral lysis (Ibarbalz *et al.,* 2019). Therefore, lytic viruses may play the role of top-down controllers by eliminating the victor and, perhaps, influencing the host community's variety. Turnover durations of prokaryotes produced by viral lysis were estimated to be between 2.3 and 16.2 days after quantifying the viral infection in the Baltic Sea sediment (Cai *et al.,* 2023). These values are similar to what has been found in surface sediments of deep-sea (2-67 days). Still, they are substantially less than the tens to hundreds of years reported for cell turnover durations using other techniques, such as the metabolic rate of specific cells and amino acid racemization (Ji *et al.,* 2023). Collectively, the actions of many viruses in active infection in the deep virosphere would have enormous ecological consequences. However, suppose hosts fail to be infected by viruses due to processes such as adsorption, which may be prevalent in the deep biospherefor viruses (Neale *et al.,* 2023). In that case, the viruses' influence on microbial communities will be anticipated from surface systems and may be restricted in the deep biosphere.

Furthermore, viral lysates might act as a bottom-up regulator for host community establishment by promoting the development of non-infected bacteria and archaea (Cissell *et al.,* 2021). Figure 3 shows the advantages of marine viruses, possibly due to a constant feedback loop between viral bottom-up and top-down effects, Heterotrophs may get nutrients and energy from the new offspring virions and, after infection, from empty capsids outside of the host cell. It has been demonstrated that in deep-sea sediments with the activity of extracellular enzymes (Dominguez-Huerta *et al.,* 2022), viral particles undergo rapid breakdown and contribute significantly to carbon, phosphate, and nitrogen pools. In deep ecology, viral particles may be digested and utilized by heterotrophic microorganisms for development despite the lack of information about the breakdown of viral products and their accessibility (Che *et al.,* 2022). The 'viral shunt' in the ocean refers to the partitioning and distribution of organic and inorganic components caused by the viral lysis of host cells. In the deep tropical and subtropical seas, viruses are responsible for the yearly diversion of an estimated 145 gigatons of carbon, 4.6 gigatons of phosphate, and 27.6 gigatons of nitrogen (Rodríguez-Flórez *et al.,* 2023). There is insufficient information for a quantitative evaluation of the function of viruses in the carbon and other elements cycling in the biosphere of deep seas. Carbon released by possible viral lysis in the deep sediments of the Baltic Sea was estimated between 0.03 and 0.81

g cm^{-3} d1 (0.01-0.30 1018 gigatons cm^{-3} year) (Ferreira *et al.,* 2023). Viral lysates often demonstrated better bioavailability than the recalcitrant organic matter that is not readily used by bacteria after long-term sedimentation, as this reflects a very tiny and likely overstated quantity compared to the overall amount of organic matter (Gao *et al.,* 2022). According to their calculations, it is concluded that in relatively young sediments (10,000 years), the oxidation of a single dead cell every year produces sufficient electricity to meet the maintenance needs of dozens to thousands of cells (Zhang *et al.,* 2022). Therefore, in the low-energy deep biosphere, organic carbon recycled by viruses may fulfill the maintenance needs of uninfected organisms. Figure 2a, 2b of the article' Metabolic and bio-geochemical consequences of viral infection in aquatic eco-systems'(Vincent *et al.*, 2023).

Functionality in filter feeding organisms

Despite being vital species of coastal eco-systems, oysters are bivalves feeding on filters with extremely high feeding populations and species cohabitation; therefore, it is unclear which function they serve in the spread of marine viruses and the control of the coastal microbiome (Cissell *et al.,* 2022). Thousands more viruses associated with oysters are now identified. Molluscan bivalves, such as mussels, oysters, scallops, and clams, are significant marine animal species essential to marine ecosystems' health (Kang *et al.,* 2023). In addition to serving as models for research on biomineralization, ocean acidification, and adaptability to coastal settings under climate changes, they are also significant fisheries and aquaculture species. In addition to serving as models for research on ocean acidification, biomineralization (Eshaghi Gorji *et al.,* 2022), and adaptability to coastal settings under climate change, oysters and mussels are significant fisheries and aquaculture species. Filter-feeding organisms, like oysters and mussels, can pull water via gills to 5 liters per hour, which concentrates suspended particles and microorganisms by a factor of 1,000 to 100,000 times compared to concentrations in saltwater (Radhakrishnan *et al.,* 2023). Oysters lack body segmentation and have a partially open circulatory system.

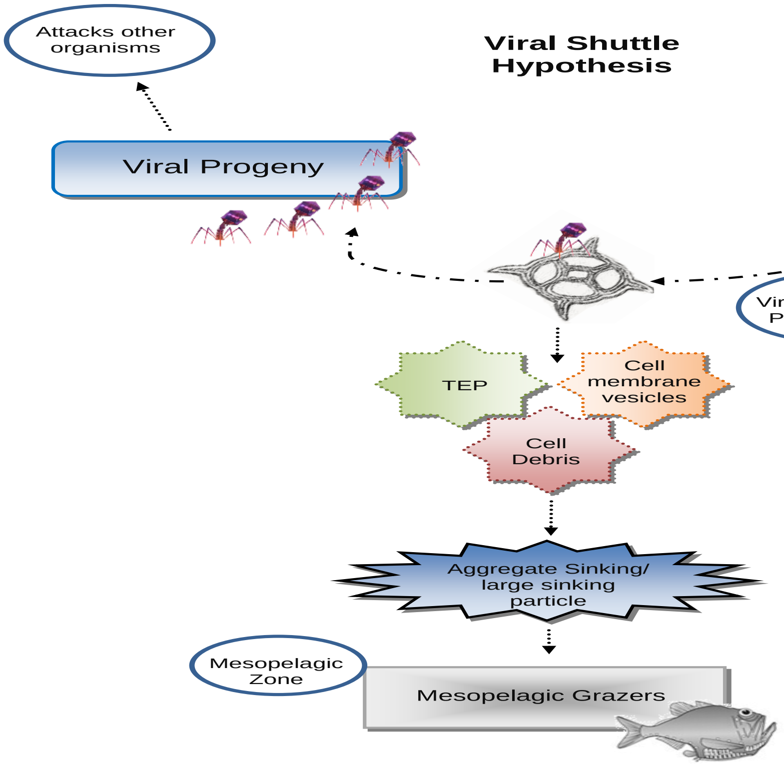

Figure 2a. Metabolic and biogeochemical consequences of viral infection in aquatic ecosystems

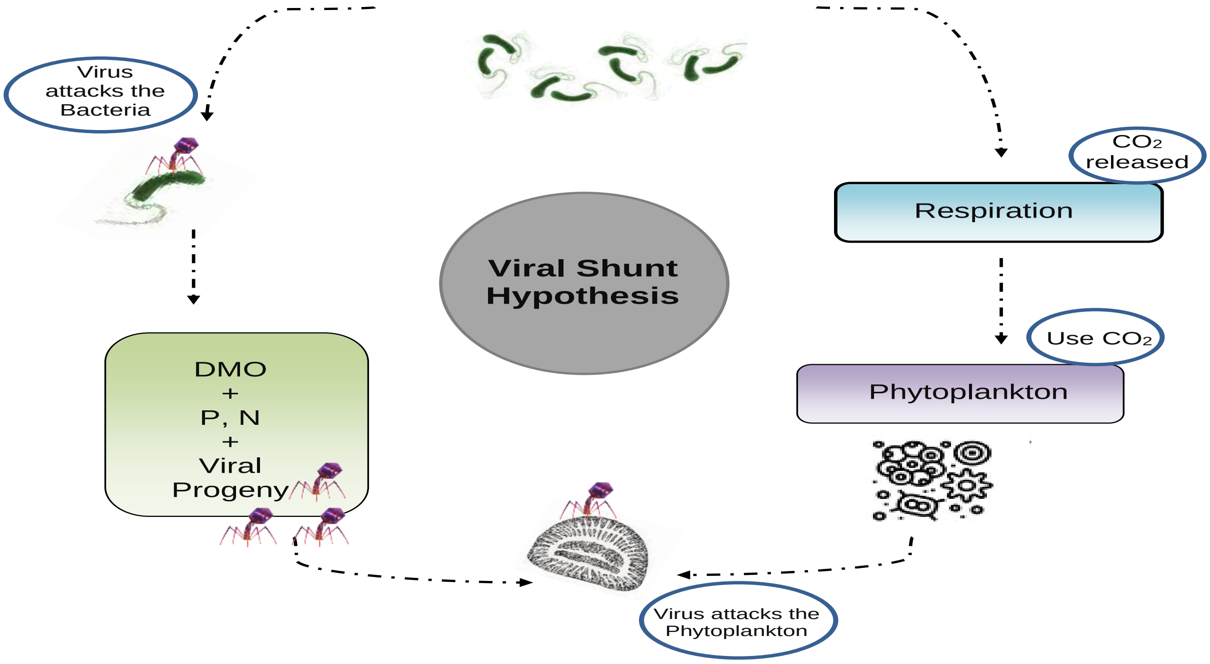

Figure 2b. Metabolic and biogeochemical consequences of viral infection in aquatic ecosystems

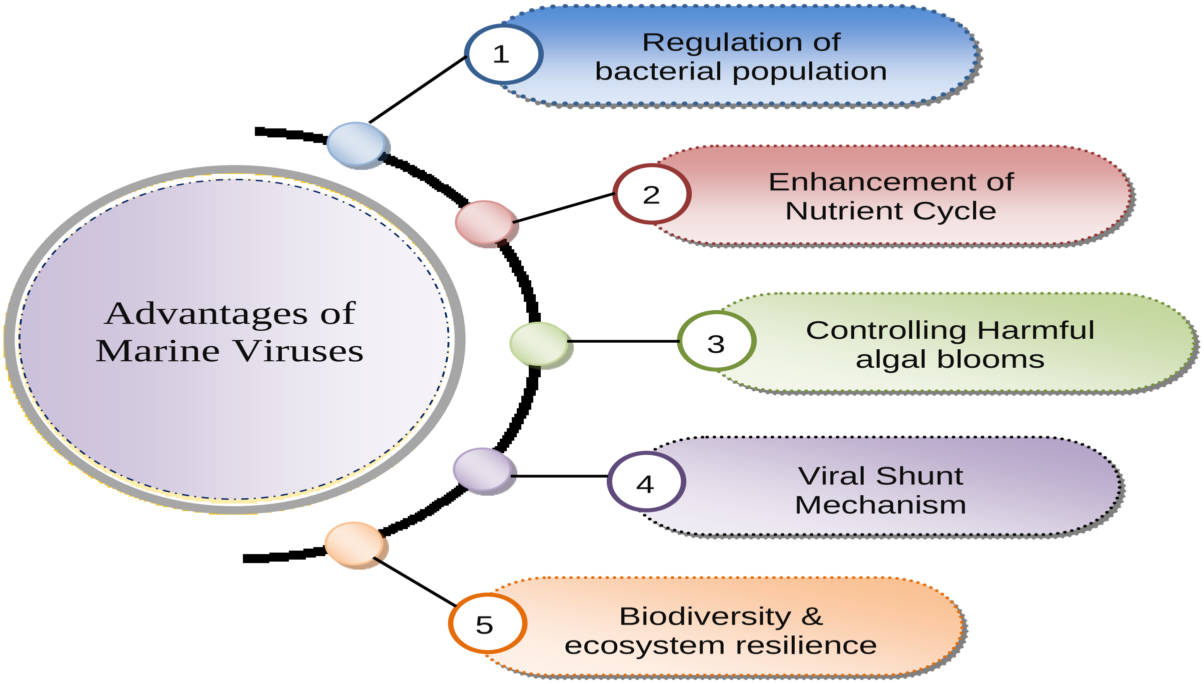

Figure 3. Shows various advantages of marine viruses

It is proposed that oysters provide a special environment distinct from saltwater and emphasize the significance of filter-feeding aquatic organisms for the study of marine viruses as well as their crucial but underappreciated functions in the control of marine ecosystems (Gökalp *et al.,* 2021). The dataset of oyster virome allows for the first thorough examination of both the RNA and DNA of viral populations in the oyster *Crassostrea hongkongensis*. It comprises 3473 high-quality viral genomes and 728,784 nonrepeat viral operational taxonomic unit contigs (800 bp) (Meng *et al.,* 2022). New viruses that inhabit this oyster exhibit enormous diversity, employing various techniques, such as read recruitment, high-quality virus genomes, and viral operational taxonomic units. Viruses are highly distinct compared to viruses found in other environments or the ocean (Gaïa *et al.,* 2023). The abundance of newly discovered circoviruses in the oysters suggests they might be hotspots. The viruses abundantly present in oysters are not haphazardly distributed but rather are well-formed communities that can adapt to stress in the host's and environment's health on both a compositional and functional level (Okeke *et al.,* 2022).

Effects on the geochemical balance of marine systems

Numerous environmental services are provided by microbes found in aquatic environments (Lei *et al.,* 2023). These microbes include viruses, microbial eukaryotes, bacteria, fungi, protozoa, and archaea. Planktonic microalgal-bacterial complexes aid in the decomposition of organic materials and the cleaning of aquatic habitats, while harmful microbial traps are another kind of microbial coalition (Ebert *et al.,* 2023). By participating in processes including nitrogen fixation, oxygen production, nutrient and mineral cycling, and methanogenesis, they make major contributions to the biogeochemical cycle. Water quality is enhanced due to the decomposition of environmental pollutants (Boratto *et al.,* 2022), and they also contribute to the flow of energy in aquatic environments. Through bioremediation, microbes offer a significant role in the cleanup of contaminated water by converting dangerous toxic chemicals to less toxic and desirable end products. It's a cheaper technique that can crank the same (Espinoza *et al.,* 2022). The sequestration of substances in bacteria, viruses, and matter that dissolves may result in improved nutrient retention in the zone of euphotic activity. Decreased viral activity may result in more material in bigger organisms, allowing inorganic nutrients and carbon to be transported from the zone of euphotic activity to the deep sea (Bhatt *et al.,* 2020). Viruses may also shape global climate by releasing a gas dimethyl sulfide (DMS) that impacts cloud nucleation. Experiments reveal that infection allows *M. pusilla* to discharge all of its internal dimethyl sulfide precursor (DMSP) and infects important DMSP-containing bloom species, including *E. huxleyi* 79 and *P. pouchetii* (Casertano *et al.,* 2020). Complex interactions throughout the food chain decide whether significant amounts of DMS may be released into the atmosphere or converted and digested predominantly by bacteria or animals in the water. Viral infection is assumed to be density-dependent and species-specific because unusual hosts are less sensitive to virus spread than more frequent hosts (Patterson *et al.,* 2022). Models of the possible variables affecting microbial biomass and species composition reveal that viruses influence the bacterial community's steady-state diversity (V *et al.,* 2021). Marine cyanobacteria are resistant to viral infection; however, the rapid rate of viral generation in some marine environments appears incompatible with a population dominated by virus-resistant species (Olive *et al.,* 2022). There are no obvious explanations for why viral resistance isn't a major concern, although laboratory studies show that inexpensive or no-cost resistance is feasible. The explanation for resistance to viral infection will likely lie outside the realm of simplified theoretical or laboratory systems (White *et al.,* 2021). In an oligotrophic (typical) marine ecosystem, unsuccessful viral infection to the host organisms of significant nutritional advantage, as the viral DNA injection is enriched of P, C, and N. System models show that Viral infection benefits heterotrophic bacteria tremendously because it increases their productivity and helps to keep nutrients in the illuminated surface waters (Shilky *et al.,* 2023). Individuals might profit from not developing resistance, according to group-selection theory. Lysogeny has been proposed as a virus survival strategy that offers advantages to the host, such as protection from infection by associated viruses and the emergence of new activities programmed by the viral genome (WM Hassan *et al.,* 2020). Lysogens are common in seawater and lake water, with variable abundances ranging from unidentified to almost 40% entire bacteria. However, lysogen induction is uncommon, and the incredible percentage of viruses found in seawater is most likely the consequence of sequential lytic infection (Grande-Tovar *et al.,* 2022). Marine viruses play an important role in the exchange of genetic material among microbes, which can have direct effects such as transduction and nonspecific horizontal gene transfer. Additionally, viral lysis can cause the discharge of DNA from the host cell, which can be transferred to another organism through natural transformation (Rodríguez-Ramos *et al.,* 2021). These activities have the potential to significantly impact the genetic structure and development of the worldwide population of marine bacteria, as well as the spread of genetically altered microbial genes or antibiotic resistance caused by extensive fish farming.

Crucial involvement in carbon cycling, metabolism, and biosynthesis.

Viruses' impacts on the system as a whole are the most crucial information included in this article (Zhang *et al.,* 2022). The lytic infection transforms cells into cellular debris and viruses, consisting of dissolved molecules (monomers, oligomers, and polymers), colloids, and pieces of cell membranes and nuclei. There is a good chance that bacteria will be able to use this material, notwithstanding the possibility that heterotrophic flagellates may graze on a tiny piece of it (Raven *et al.,* 2023). If the cell that is being lysed is a bacterial cell, then the presence of the products of the lysed bacteria indicates a half-closed trophic loop. In this scenario, the biomass of lysed bacteria is eaten mostly by other bacterial cells. This loop receives its input from the outside in the dissolved organic compounds released by phytoplankton and grazing animals (Dar *et al.,* 2020). The result of this loop is the oxidation of organic matter and the regeneration of inorganic nutrients. Furthermore, the materials consumption by bacteria that originated from other bacteria have the fascinating virtue of stealing produced food from the remaining part of the food web and seizing the production of biomass and activity into the most dissolved and minute particle forms (Yuan *et al.,* 2023). This may be considered a "robbing production from the rest of the food web". The viral lysis of phytoplankton would deprive bigger grazers of their food source and shift the material into microscopic forms (Wieczynski *et al.,* 2023). Studies show that when compared to a virus-free system, an identical food web with 50% bacterial death from viruses has a further 27% increase in bacterial respiration and production and 37% fewer bacteria foraging by protozoa, resulting in a decrease of 7% in microzooplankton generation. As a variation of the constant-state model2 that includes a small quantity of viral infection of phytoplankton (7% loss) and 3% virus grazing by flagellates (Yuan *et al.,* 2023) output has nearly the same net impact of boosting bacterial respiration and production (by 33%) and lowering animal and protist production. This increase in respiration and production of bacteria is due to increased bacterial production (Brahim Belhaouari *et al.,* 2022). In virus-infected systems, the material sequestered in bacteria, viruses, and dissolved substances may contribute to an increase in the amount of nutrients retained in the euphotic zone. A decline in viral activity would cause bigger organisms to accumulate more material, which might cause them to sink either by themselves or as detritus (Allen *et al.,* 2022). Other possible geochemical impacts, such as the sinking and aggregation of material from the euphotic activity zone, may be caused by the lysis of organisms and the release of the contents of their cells into the water (Wang *et al.,* 2022). Because they trigger the production of a gas known as DMS, vital in cloud nucleation, viruses may also play a significant role in climate change. Complex interactions within the food web dictate whether or not significant amounts of DMS can be released into the atmosphere (Sahoo *et al.,* 2023) or whether or not it is predominantly converted and destroyed by microorganisms or water living animals.

CONCLUSION

The hunt for pathogens has been the primary focus of research on marine viruses until now, but this will need to change if we are to understand the myriad of ways viruses affect life on Earth (Wieczynski *et al.,* 2023). This article reviews recent developments in the field of aquatic virology. It introduces a new framework for the classification of aquatic environments' living viruses, including viruses of aquatic animals (iridovirus, rhabdovirus), cyanophages, viruses of archaea (ampulla virus) (Huang *et al.,* 2023), giant viruses (mimivirus, tupan virus, andpithovirus), virophages, and pollinations. These viruses can replicate in eukaryotic, bacterial, and archaeal cells via gigantic viruses. Novel methods for researching viruses are discussed (Vincent *et al.,* 2023), along with a summary of the key molecular features and genetic development of aquatic viruses, virus-host interactions, the functions that viruses play in aquatic ecosystems, and more (Liao *et al.,* 2022. Since the discovery of new-type viruses, the distinction between the viral and cellular worlds has been increasingly blurred, even though aquatic viruses remain Earth's most varied, prolific, and pervasive living entities. Virus-cell interactions in aquatic environments have been crucial to biological evolution and global biogeochemical processes (Grossart *et al.,* 2021). Future research on marine viruses should focus on three primary areas of inquiry: finding and studying viruses that infect marine archaeal species, research into how viruses influence the function structure of communities of zooplankton, and research into tripartite symbioses involving bacteria, phages, and insects (Su *et al.,* 2020). Studies conducted in culture have shown that viruses may play a role in the boom-and-bust cycles that occur in many metazoans. Still, no one has investigated how the top-down pushing of metazoans caused by viral infections would affect zooplankton populations (Fenibo *et al.,* 2022). Finally, research in entomology has uncovered several fascinating examples of tripartite symbioses involving bacteria, phages, and insects. There is a lot of fascinating biology out there waiting to be found (Miah *et al.,* 2023).

AUTHOR’S CONTRIBUION

A. Iftikhar: Collection of papers and analysis
Hafsa: Literature reviewed
R. Farooq: Technical write up
F. Abdullah: Help in analysis
M. Ali: Proof reading

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