A Review of Marine Viruses in Coral Ecosystem

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Abstract: Coral reefs are among the most biodiverse biological systems on earth. Corals are classified as marine invertebrates and filter the surrounding food and other particles in seawater, including pathogens such as viruses. Viruses act as both pathogen and symbiont for metazoans. Marine viruses that are abundant in the ocean are mostly single-, double stranded DNA and single-, double stranded RNA viruses. These discoveries were made via advanced identification methods which have detected their presence in coral reef ecosystems including PCR analyses, metagenomic analyses, transcriptomic analyses and electron microscopy. This review discusses the discovery of viruses in the marine environment and their hosts, viral diversity in corals, presence of virus in corallivorous fish communities in reef ecosystems, detection methods, and occurrence of marine viral communities in marine sponges.

Keywords: coral ecosystem; viral communities; corals; corallivorous fish; marine sponges; detection method

1. Coral Ecosystem

The earth is covered by an ocean that contains about 97% of the planet’s water [1]. Mora et al. [2] have estimated that about 2.2 ± 0.18 million species are found in the marine environment but only 91% of the ocean species have yet been discovered. The coral ecosystem consists of sponges, coral, corallivorous, crustaceans, molluscs and other organisms that live beneath the reef ecosystem. Sponges are among the oldest metazoans which can be divided into four classes: Hexactinellida, Calcarea, Demospongiae and Homoscleromorpha [3]. Sponges feed on plankton that include bacteria, algae, protozoa and microscopic animals which transfer carbon flow to higher trophic levels [4]. These sponges are also known to be food sources for organisms, for example, fish, crustaceans, sea urchins, star fish and molluscs [4]. Sponge’s morphology is very diverse with a colorful array ranging from amorphous types, to branching, with a great variety in length and size [5]. Moreover, sponges are plentiful and functionally essential for coral reef systems [6]. They play a crucial role in numerous ecosystems such as substrate accretion [7] and erosion [8,9]. As described by Aerts [10], out of 128 sponge species, 30 interact with corals in coral over-growth [9]. As reviewed by Bell [6], functional roles that are played by sponges in Caribbean coral include increasing coral survival by binding live corals to reef frame and preventing entry to their skeletons by excavating organisms, nutrient cycling, bioerosion reworking of solid carbonate, primary production via microbial symbionts, removing prokaryotic plankton at water column and providing food sources for organisms.

Corallivores are known as fishes that feed on live corals in reef ecosystems. These coral-feeding fishes have shown that almost 80% of their feeding is based on coral, which assumes that they are dependent on coral for their survival [11]. They can be classified as polyp-feeding, removing coral tissues. Persistent predation caused by coral fish aggravate...
the effects of coral disturbance and slow down reef recovery [11]. As reviewed by Cole [11], the corallivorous species can vary among habitats and geographic areas. Coral colonies as a food source for these corallivores need to find a balance between feeding severity and coral regeneration [11].

Meanwhile, coral reefs are among the most biodiverse biological systems on the planet, the persistence of which relies on the reef-building capacity of scleractinian corals. The reef-building corals accrue almost 250 million years with hundreds of scleractinian coral species that exhibit in multiple colony sizes, shapes and life spans, providing a wide assemblage of territory for molluscs, fish and crustaceans [12]. Corals are made up of networks of polyps and gastrovascular system that consist of tissue layers that contain numerous cell types such as epidermis mesoglea, gastrodermis, coelentron, gastrodermis mesoglea and calicoblastic epithelium [12]. According to Tresguerres and Barott [13], the corals’ oral ectoderm connects to the external environment and is involved in the production of the mucus layer which helps corals in capturing prey and guarding against nematocysts. Hence, corals filter the surrounding food particles and other particles in seawater including pathogens such as viruses.

Corals are either hermatypic (reef-building) or ahermatypic (non-reef-building). Hermatypic corals flourish in shallow waters which contain millions of zooxanthellae. *Symbiodinium* are colloquially known as zooxanthellae. Due to the complex beneficial interactions among coral hosts, unicellular algae and dinoflagellates *Symbiodinium* spp., and their different microbiomes, coral reefs flourish in oligotrophic tropical waters [14]. Coral beneficial interaction with *Symbiodinium* algae permits the coral to harness power from daylight (photosynthesis), as fixed natural carbon is moved to the host while the algae obtain inorganic supplements reprocessed from the host’s metabolism, for example ammonium and carbon dioxide [15]. These resources supply the coral with vitality for growth, reproduction and respiration [14]. Zooxanthellae conducts photosynthesis from sunlight as it captures and transfers 95% of the energy generated to the coral polyps. This relationship between zooxanthellae and corals supports both the reef and the zooxanthellae, sustained itself by nutrients such as inorganic substances and acquiring refuge in exchange. Global climate change can also stress the coral, collapsing the symbioses, which leads to bleaching (paling) or loss of zooxanthellae [14].

Cziesielski et al. [16] discovered the first mass coral bleaching in 1988 and over the past 4 years alone prominent coral reef ecosystems such as the Great Barrier Reef have lost about 50% of shallow-water corals [17]. Coral reefs depend on a differing consortium of free-living and host-related microorganisms for the capture, maintenance, and reuse of nutrients and minor components that permit these environments to flourish in the marine environment, which can be compared to a desert [18,19]. Climate change can trigger disruption of the natural microbiome which could lead to a state of dysbiosis with the exposure of opportunistic and probably pathogenic taxa, resulting in an inclining incidence of disease, bleaching, and host mortality [20,21]. It has been proposed that the microbiome could play a central role in coral reef reclamation, including marine viruses [21]. These changes in the microbial community cause the aggravations that could act as early warning signals, since these movements may anticipate visual indications of bleaching and tissue necrosis [22–25]. Coral reefs have endured uncommon losses and are critically threatened by continuous elevation in ocean surface water temperature and ocean acidification due to climate change, despite viral infection in corals and their worldwide significance [26,27].

According to Thurber et al. [28], the coral holo-biont contains diverse viral-like particles (VLPs) which were first observed in stony corals (cnidarians) and the sea anemone [29]. It is reported that larger viruses could infect dinoflagellate endosymbionts of the corals due to environmental factors. Virus-associated corals infect the coral tissues and the coral surface microlayers (CSM) [30–33]. Cram et al. [34] predicted that high viral infection is the source of marine bacterial mortality that affects shape together with structure of the microbial host community in the marine ecosystem and transfers genetic material between microorganisms, known as horizontal gene transfer (HGT) [35]. Viruses also
encode auxiliary metabolic genes (AMGs) that increase microbial host growth and fitness [36–38]. Viruses exist as both pathogen and symbiont of metazoans, controlled by the environmental factors and mutual relationship between the host and virus itself [39,40]. The ecological roles of the virus communities in health and disease in corals are still inadequately recognized despite the availability of advanced molecular technology. According to Thurber et al. [28], the stress-effect of viral infections damages the coral tissues that drive carbon from the benthos into the water column in the reef ecosystem. Marine bacterioplankton blooms trigger viral production in reef waters that releases more carbon and nitrogen into the environment. These occurrences induce viral production and mortality in corals and lead to coral reef decline [28]. Generally, corals are involved in the biogeochemical cycles in the reef ecosystems due to the release of dissolved organic carbon (DOC) [28]. The presence of DOC stimulates bacterial growth and it has been reported to enhance the DOC flux processes, and nutrients released from CSM have negative feedback on the coral reefs [41,42]. A shift in the relative abundances of eukaryotic viruses and phages has been reported by Correa et al. [43] (lab-stressed corals, Hawaii and Florida) and Soffer et al. [44] (bleached, disease and healthy corals, Caribbean reefs). The shifts in the relative abundance of virus families may also play a role in coral mortality and disease. For instance, the Circoviridae family is one of the most abundant viruses in corals that causes a disease known as the white plague [28].

According to Sweet et al. [45], viral agents may act in various manners, including critical infection, reactivation of inert disease, immune suppression (declining of the immune system of the host or weakening of the immune system due to natural aging), where it is able to destroy algae symbionts under environmental pressure and may participate in coral bleaching reactions. Nonetheless, some of these viruses are possibly host-specific to the symbiotic algae and may perform as primary pathogens in coral disease. In conjunction with these known groups, various viral sequences have been distinguished that cannot be appointed to any known families of viruses, demonstrating that the coral microbiome is a rich environment for novel viral revelations [45].

The bacteriophage-adhering-to-mucus (BAM) model had been hypothesized and named due to the observation of enrichment of phage in mucus occurring through interaction of mucin glycoproteins and Ig-like proteins that realm on phage capsids [45]. These BAM models assimilate a mechanism in supporting the specific relationship of mutualistic bacteria with host, and dispenses an evolutionary structure for a process of specific co-advancement of a phage-bacterial-host related microbiome. Therefore, evidence has demonstrated the role of viruses in the control of coral-related bacterial communities, where viral lysis rates rise in the surface mucus layer and complex associations are presented in the bacteriophage-adhering-to-mucus model. Viruses were also indirectly involved in controlling pathogenic bacterial populations and disease pervasiveness [45]. Wood-Charlson et al. [46] showed that diverse viral families had been detected from coral and symbiotic microbes by metagenomics. They reported that these viruses are likely to play numerous, commensal roles and are parasitic, regarding the health of coral reefs. Regardless of these assorted varieties, a number of taxonomic classifications are generally found in corals, including bacteriophages belonging to an order of the Caudovirales, and eukaryotic nucleocytoplasmic large DNA viruses (NCLDV) associated with families such as Phycodnaviridae, Mimiviridae, Poxviridae and Iridoviridae, as well as Polydnaviridae and Retroviridae [43,46]. Other than the families that affect unicellular algae, there are a few a number of coral-associated families known to infect plants and/or fungi and protists including Geminiiviridae, Nanoviridae, Tymoviridae, Potyviridae, Tombusviridae, Caulimoviridae, Alphaflexiviridae, Endornaviridae, Partitiviridae and Reoviridae [46].

2. Progress of Marine Virus Research

Marine viruses are found to be abundant in the ocean in many organisms as they play vital roles in global geochemical cycles [47]. Viruses are widely distributed in various
environments including extreme environments, such as hydrothermal vents, cold springs and hypoxic saline conditions. They exist widely in seawater [48] and sediment [49].

Spencer et al. [50] discovered the first bacteriophage from the marine environment. Viruses recycle nutrients together with organic matter via a process known as the viral shunt. The cellular materials released as particular or dissolved organic material are not directly available for utilization by organisms from higher trophic levels but are primarily utilized by predominantly heterotrophic bacteria, although some efforts have shown nutrients released in this manner are rapidly assimilated by eukaryotic plankton [51]. Spatio-temporal dynamics of these viruses accounted for 10% of phytoplankton mortality within the course of phytoplankton blooms and additionally stimulated recycling of nutrients, together with organic matter, via viral shunt [52–54]. Research advances in these environments have encountered marine viruses and their hosts and organisms including plankton and aquatic invertebrates.

The Kill the Winner (KtW) hypothesis proposed that viruses are sustained via host specific infection including plankton and lysis, the most abundant microorganisms in the environment [55]. Numerous efforts have been made to identify and isolate viruses from cultivated microorganisms and have increased understanding of genomic structure and the host range of marine viruses, especially from Cyanobacteria (such as Prochlorococcus and Synechococcus) [56–59]. The RNA-dependent RNA-polymerase (RdRp) gene is an essential protein encoded in the genomes of all RNA-containing viruses such as Picornavirus-like viruses and DNA containing viruses such as T4-like myoviruses (gene marker g23 and g20) have limited the research on viral diversity to genome fingerprinting [60–63]. Thereby, metagenomics studies were introduced, to overcome the bottleneck of cultivation and the lack of universal markers, in the early twenty-first century. Breitbart et al. [64] reported that both single-gene-based and genome-fingerprinting-based methods have revealed the temporal and spatial dynamics of marine viral communities.

Metagenomics-based studies have enabled scaling of the information on viral genomics and sequencing of the fragmented nucleic acid from seawater and marine sediments [65]. However, several important issues, despite the progress in the study of marine viruses, remain unexplored, for instance, the examination of specific-host interactions, expansion of spatio-temporal marine viral studies, linking the environmental viruses with their hosts and enhancement of knowledge particularly regarding deep-sea viral communities and viral auxiliary metabolic genes (AMGs) [38]. Advanced informatics and theoretical research have unveiled the biological basis of complex host range patterns and explicated largely unknown viral sequences in marine ecosystems [66,67]. Regarding this, the progress of marine viruses from marine sponges are recommended so that we know the abundance or presence of viral communities that have been detected, making it easier for other researchers to refer to.

3. Marine Viruses and Their Host

The major impact of viruses in the marine environment began when it was discovered that seawater contains around $10^{10}$ viruses per liter [68]. In the mid-1970s, viruses or virus-like particles (VLPs) were reported in numerous taxa of algae. In the 1980s, a group of large double stranded (ds) DNA-containing viruses (Chloroviruses) was discovered. These viruses infect and replicate in unicellular, eukaryotic, symbiotic, chlorella-like green algae known as Micratinium (formerly known as Zooclorella) (Chlorophyta). As described by Breitbart et al. [69], viral abundances are known to be tightly linked to their host and are generally more abundant in phytoplankton and Cyanobacteria than in any other microorganisms.

In the past, large-scale spatial investigations of viral dispersion in the Pacific and South Atlantic Oceans have utilized flow cytometry to reveal that viral abundance in 200 m of the water surface column is high in tropical and subtropical districts yet lower in Antarctic waters [70,71]. A virus “hot-spot” was recognized in the mid-scope region of the North Pacific supporting the hypothesis that large-scale distribution patterns of viruses
are influenced by host distributions and physical procedures [71]. Brum et al. [72] used cultivation-independent methods such as metagenomics and revealed that the Southern Ocean is dominated by lysogenic viruses, which are termed as “seasonal time bombs” since they can shift to a lytic cycle as their bacterial host production rises. Roux et al. [73] collected virome data that identified virally encoded AMGs (Auxiliary Metabolic Genes) in surface waters that appear to be involved in nitrogen and sulfur cycling.

The Pacific Ocean Virome (POV) [74] is another significantly important curated dsDNA virome dataset that comprises 32 quantitatively representative viromes collected from different depths and seasons in transects from coastal waters to open-ocean waters in the Pacific Ocean [74]. POV study revealed that the richness of viruses in the Pacific reduced from deeper to surface waters, from winter to summer, and, in surface layers, with distance from the shore. Other than that, data collected by the TARA ocean expedition were used to develop a global virome map of dsDNA viruses sampled in surface and deep-ocean waters [73], along with the genomic data from the Malaspina 2010–11 Circumnavigation Expedition, which has assessed pelagic processes along the Indian, Pacific, and Atlantic Oceans [75]. The authors found that 38 of 867 viral clusters were locally or globally abundant and represented almost 50% of the viral population in any given Global Ocean Virome (GOV). Such huge datasets are critical in developing our insights into marine viruses on a global scale and are important in divulging uncultivated novel viruses and initiating important marine ecosystem models.

Hence, the International Committee on Taxonomy Viruses (ICTV) have classified and named viruses according to their taxonomy and binomial species [76]. The key factors that are used for the identification and classification of viruses include the display of capsid protein and viral morphology via TEM [77]. Nineteen families of unassigned viruses were reported, whereas approximately 5000 marine viruses were assigned to 26 families according to ICTV [67].

Moreover, viruses can be grouped based on their hosts such as bacteria, animal, archaea, algae and plant viruses (Table 1). Authors have also discovered single stranded DNA (ssDNA) and double stranded RNA (dsRNA) viruses other than the double stranded DNA (dsDNA), abundant in the ocean with marine organisms as their hosts.
Table 1. Marine viruses and their hosts in the marine environment adapted from He et al. [67] and King et al. [78].

| Virus Genome | Order | Family | Morphology | Size (min Diameter) | Host Species | References |
|--------------|-------|--------|------------|---------------------|--------------|------------|
| Double stranded DNA (dsDNA) | Caudovirales | Myoviridae | Polygonal head (icosahedral) with contractile tail (helical) | 50–110 | Bacteria | [79–81] |
| | Caudovirales | Podoviridae | Icosahedral | 130–200 | Bacteria | |
| | Caudovirales | Siphoviridae | Icosahedral with noncontractile tail | 60 | Bacteria | |
| | Herpesvirales | Herpesviridae | Pleomorphic, icosahedral, enveloped | 150–200 | Fish, corals, mammals, mollusks, and bivalve | [82] |
| | Ligamenvirales | Lipothrixviridae | Thick rod with lipid coat | 400 | Archaea | [83] |
| | Unassigned | Baculoviridae | Enveloped rods, some with tails | 100 × 230–335 | Crustaceans | [84] |
| | Unassigned | Corticoviridae | Icosahedral with spike | 60–75 | Bacteria | [85] |
| | Unassigned | Indoviridae | Round, icosahedral | 190–200 | Fish, Mollusks | [86] |
| | Unassigned | Mimiviridae | Icosahedral with microtubule-like projections | 650 | Marine fish | [87] |
| | Unassigned | Nidoviridae | Enveloped, oval with tail-like appendage | 275 | Marine crustaceans | [88] |
| | Unassigned | Phycodnaviridae | Pleomorphic, icosahedral, enveloped | 130–200 | Algae | [89] |
| | Unassigned | Tectiviridae | Icosahedral, with noncontractile tail | 60 | Bacteria | [90] |
| | Unassigned | Totiviridae | Round, icosahedral | 30–45 | Protist | [91,92] |
| | | Anelloviridae | Icosahedral | 22 × 38 | Prokaryotes | |
| Single stranded DNA (ssDNA) | | Inoviridae | Genus Inoviruses: filamentous; plectroviruses: rod-shaped; inoviruses: 7 × 700–3500; plectroviruses: 15 × 200–400 | | Bacteria | [78] |
| | | Microviridae | Icosahedral | 25–27 | Bacteria | |
| | | Nanoviridae | Icosahedral | 18–20 | Prokaryotes | |
| | | Parvoviridae | Linear, icosahedral | 21–26 | Vertebrates, invertebrates | |
| | Bunyavirales | Peribunyaviridae | Round, enveloped | 80–120 | Crustaceans | [94] |
| Mononegavirales | | Paramyxoviridae | Various, mainly enveloped, icosahedral | 60–300 × 1000 | Mammals | [95] |
| | | Rhabdoviridae | Bullet-shaped with projections | 45–100 × 100–400 | Fish | [96] |
| Single stranded RNA (ssRNA) | | Nidovirales | Coronaviridae | Rod-shaped with projections | 200 × 42 | Crustaceans, fish, seabirds | [97,98] |
| | | Picornaviridae | Icosahedral | 30 | Crustaceans | |
| | | Picornaviridae | Icosahedral | 25 | Algae | [99–101] |
| | | Picornaviridae | Round, icosahedral | 27–30 | Algae, crustaceans, thraustochytrids, mammals | |
| | | Caliciviridae | Round, icosahedral | 35–40 | Fish, mammals | [102] |
| | | Leviviridae | Round, icosahedral | 26 | Bacteria | [103] |
| | | Microviridae | Icosahedral with spikes | 25–27 | Bacteria | [104] |
| | | Nodaviridae | Round, icosahedral | 50 | Fish | [105] |
| | | Orthomyxoviridae | Round, with spikes | 80–120 | Fish, mammals, seabirds | [106] |
| | | Togaviridae | Round, with outer fringe | 66 | Fish | [107] |
| | | Reoviridae | Icosahedral, thick outer layers, smaller electron-dense inner cores | 90–95 | Algae | [108–110] |
| Double stranded RNA (dsRNA) | | Birnaviridae | Round, icosahedral | 60 | Mollusks, fish | [111] |
| | | Cystoviridae | Icosahedral with lipid coat | 60–75 | Bacteria | [112] |
| | | Totiviridae | Round, icosahedral | 30–45 | Protist, shrimp | [113,114] |
The concentration of free virions decreases with depth in seawater [47] with a total abundance of more than $10^{3}$ [47], whereas the concentration of marine virio-plankton in surface seawater is typically billions per milliliter [54,114]. The published data on viral abundances in seawater are mostly found in freshwater, coastal water, open ocean, deep ocean and estuarine waters, but the discovery of marine viruses in Asia is still at an early stage.

Zhong et al. [115] have discovered four targeted viruses (e.g., Cyanomyovirus, T4-like myovirus, Cyanophage, Phycodnavirus) in Lake Annecy and Lake Bourget. Molecular detection such as PCR-denaturing gel gradient electrophoresis (DGGE) had been used to discover viruses in the lake water. DGGE banding pattern analysis revealed the different similarities of the viruses in both lakes. The results demonstrated the presence of 70% of mcp phycodnaviruses (Lake Bourget), 45% of polB phycodnaviruses (Lake Bourget) and 60% (Lake Annecy), respectively, 45% of psb A cyanophages (Lake Bourget and Lake Annecy), 45% of cyanomyo-viruses in Lake Bourget and 75% of T4-like myo-viruses in Lake Bourget. The total bands in common that showed the presence of the viruses in both lakes were as follows: mcp (85%), polB (54%), g20 cyanomyovirus (52%), psb A cyanophages (39%) and g23 of T4-like myo-viruses (75%), respectively. Previously, this method had focused on marine ecosystems where only a single gene marker was used typically to identify the presence of the viruses in the marine environment, g20 [116–118], polB [118,119] or mcp [120–122]. Parvathi et al. [123] demonstrated the dynamics of virus infection of autotrophic plankton in Lake Geneva over a 5-month period and the abundances were determined via flow cytometry and PCR-DGGE method identification. The viral signature genes used by Parvathi et al. [123] were similar to those used by Zhong et al. [115] to identify the viral abundances in surface water. Parvathi et al. [123] have discovered that the abundances of picocyanobacterial hosts was in concurrence with cyanophages, which were higher in late summer.

Luo et al. [124] discovered metagenome sequence data that yielded about 16787 virus populations, and 1352 of these were identified as putative temperate phages with temperate phage marker genes. Moreover, about 12 complete archaeal virus genomes and 25 genome fragments of eukaryotic viruses have been identified [124]. They discovered that the depth of ocean inferred the Virus:Cell ratio (VC) temporal variability where, as the depth of ocean decreased, there were more temperate phages present compared to other viruses. The temperate phage peaked at a photic zone in the ocean at about 150–250 m. This peak indicates increased temperate phage productivity relative to deeper waters, with slowly growing hosts. A high VC variability driven by temporal resource variability indicates phages with more episodic virus particle production [124]. Thus, this shows that the ecology and biogeochemistry of microbial communities were impacted by viruses across the ocean.

4. Coral Viruses

Reef-building corals lay the foundation for the structure and biodiversity of the coral reef ecosystem. These huge biological structures can be seen from space and are the culmination of complex developments. The interaction between coral micro-polyps and their unicellular symbiotic algae is closely related to microorganisms such as bacteria, archaea, fungi and viruses. Reef building corals have existed in various forms for more than 200 million years, and human-induced conditions have been reported to threaten their function and durability [12]. The coral reef ecosystem is at the forefront of people’s attention in the Anthropocene; for instances corals, the main species, are sensitive to human interference ranging from local activities (such as overfishing, coastal development and pollution) to worldwide phenomena (e.g., climate change and ocean acidification) [12].

Bacteria, Achaea and eukaryotic viruses are cosmopolitan and exist all over the world’s oceans [125]. According to Thurber and Correa, [126], a few published studies have directly evaluated VLPs associated with shallow-water scleractinian (stony) corals, the primary architects of the coral reef ecosystem. According to Paul et al. [127], VLPs
were detected in surface water, sediments and several invertebrate groups in tropical coral reefs and seagrass beds, and changes in terms of distance from coast, seasonality and salinity were recorded in the abundance of these particles. The first detection of a marine cnidarian-based VLP is based on the temperate plumose sea anemone, an old specimen of *Metridium senile* [127]. Since VLP is visualized in the tissues of the anemone, *Metridium senile* does not form symbioses with algal partners, and VLP may infect the anemone itself and/or organisms outside the anemone. Wilson et al. [128] studied the first characterisation of viruses associated with corals where VLPs were detected in both healthy and heat-stressed colonies, coral *Pavona danai*, *Acropora formosa* and *Stylophora pistillata*. Tail-less VLPs, hexagonal and about 40 to 50 nm in diameter, were present around the corals. A large number of VLPs were related to heat shock treatment, prompting a viral outbreak in these coral fragments. One of the most fascinating papers on coral-associated viruses in the study of VLPs was related to the coral surface microlayer of *Acropora muricata*, *Porites lobata* and *Porites australiensis* [129]. VLP were divided into five groups (tail phage, polyhedron/spherical, lemon-shaped, filamentous and unique VLP) and 17 subgroups based on the morphological similarity to the previous described viruses which have potential hosts existing in the coral surface microlayer, including algae, cyanobacteria, archaea, fungi and the coral animal.

A previous meta-analysis [46] found approximately 60 virus families in corals around the world as recognized by ICTV. A number of dsDNA ssDNA type viruses were identified from coral-holobiont sequence data sets and the coral transcriptomes generated from extracted holobiont RNA were dominated by 36–78% of RNA viruses that includes ssRNA viruses (1–13%) and dsRNA virus (2–31%). The analysis made by Wood-Charlson et al. [46] demonstrated that dsDNA viruses from the order Caudovirales were the only group of viruses that were dominant in all of the data sets (ICTV, 2012). Besides, most of the sequences from the coral-related viral metagenomes were dsDNA and ssDNA bacteriophages that show significant matches to the NCBI'S RefSeq Virus database.

Weynberg et al. [130] have identified that about 84% of the sequences belonged to dsDNA viruses and approximately 85.6% were ssRNA viruses from *Alternaria tenuis* (Fungi, Ascomycota). Most of the ssRNA viruses matched with the major capsid protein (MCP) gene from dinoflagellate-infecting ssRNA virus (HcRNAV) which supported the observation by Correa et al. [131] in *Montastrea cavernosa* (Animalia, Cnidaria). Studies which used approaches such as transmission electron microscopy and flow cytometry revealed the presence of VLPs associated with cultures of *Symbiodinium* (Miozoa, Dinophyceae) cells from corals. According to Thurber et al. [28], core coral viromes comprise 9–12 families in three viral lineages known as dsDNA group I, ssDNA group II and retrovirus group IV [43]. A typical virus related to the Herpesvirales order reported to be a member of the core coral virome showed 98% sequence similarities to the Herpesviridae virus [43]. Similar authors stated that only 10% of ssDNA (Circoviridae) and ssRNA (Caulimoviridae) were represented in the data set, probably due to the methodological differences among the studies. TEM-based studies identified VLP morphotypes that were comprised of enveloped, icosahedral capsids ranging between 120 to 150 nm in diameter from Kane‘ohe Bay in Hawaii in the United States, as well as in the corals that reside within a cellular vacuole alongside VLPs, and indicated its atypical herpes-like viral particles.

The morphological identification of VLPs was performed in the tissues of *Acropora muricata* colonies infected with healthy and white syndrome (WS) via TEM. This was the first study of cnidarians, which included temporal and spatial components. The characteristics of these dominant VLPs and their existence at multiple sampling time points led Patten et al. [30] to assume that the colony of the *Acropora muricata* is suffering from persistent infection of Phycodnaviridae and/or Iridoviridae. Buerger et al. [132] described the degradation of *Symbiodinium* cells and linked this to the abundance of VLPs in the coral. Table 2 shows the coral-related viruses reported in the reef ecosystem. As suggested in the case of virus-induced coral bleaching and yellow blotch disease, the virus itself causes the disease and therefore directly interacts with the coral itself, whereas the indirect
processes involve bacteriophages that interact with the prokaryotic community. Phages may go through the horizontal transfer of virulence genes, increasing the virulence of the infected bacterium, which then causes coral diseases. In addition, bacteriophages may infect and lyse pathogenic bacteria, reduce the impact of disease and become a part of the coral microbiome, or reduce the external influences from the overall organism of the coral, for instance, manual application in phage therapy [132].

Table 2. Coral-associated viruses in reef ecosystems, detection method and their host.

| Virus Family          | Size (nm in Diameter) | Host                        | Coral Species                  | Method of Detection                        | References |
|-----------------------|-----------------------|-----------------------------|---------------------------------|--------------------------------------------|------------|
| Closteroviridae       | 12                    | Marine algae                | Unclassified                    | Analytical fluocytometry, Transmission Electron Microscopy | [133]      |
| Flexiviridae, Potyviridae, HaRNAV | 200 nm–2 um           | Marine algae                | Unclassified                    | Unclassified                               | [134]      |
| Mimiviridae, Iridoviridae | 25                   | Marine Algae                | Montastraea cavernosa           | Pyrosequencing                             | [131]      |
| HcRNAV                | 30                    | Marine algae                | Unclassified                    | Transmission Electron Microscopy            | [136]      |
| Geminiviridae, Nanoviridae, Tymoviridae, Potyviridae, Tombusviridae | 18–20, 30, 30, 11–20, 28 | Protist, plants, invertebrate | Unclassified                    | Metagenome                                 | [46]       |
| Herpesviridae         | 120–150               | Terrestrial and aquatic animals | Montastraea annularis, Symbiodinium sp., Diploria strigosa | Transmission Electron Microscopy, Metagenome | [43,44,137,138] |
| Poxviridae            | 200                   | Insects, terrestrial invertebrates (humans and birds), whales, sea lions, dolphins | Acropora tenuis, Fungia fungites, Goniastria aspera, Galaxea fasicularis, Pocillopora acuta, Pocillopora damiicomis, Pocillopora verrucosa Galaxea fasicularis, Mycedium elephantotus, and Pachyseris selecta | Transmission Electron Microscopy | [28,139,140] |
| Mimiviridae, Retroviridae, Siphoviridae, Picobirnaviridae Retroviridae, Hepadnaviridae, Parvoviridae, Iridoviridae, Herpesviridae | 400, 100, 60 | Eukaryotes and bacteria | Pocillopora verrucosa Galaxea fasicularis, Mycedium elephantotus, and Pachyseris selecta | Metatranscriptome and metagenome | [141] |
| Herpesviridae         | 70–150                | Target vertebrates and invertebrates | Acanthastrea echinata, Diploastrea heliopora, Fungia sp., and Plerogyra sinuosa | Metatranscriptome and metagenome | |
| Podoviridae-like, Geminiviridae-like | 100       | Bivalves, protist, bacteria | Porites compressa | Metagenome                               | [142]      |
| Mimiviridae           | 40                    | Symbiodinium spp. cells      | Mussismilia braziliensis        | Transmission Electron Microscopy            | [143]      |
| Potyviridae           | 11–20 nm              | Symbiodinium spp. cells      | Unclassified                    | Transcriptome                               | [144]      |
Table 2. Cont.

| Virus Family       | Size (nm in Diameter) | Host               | Coral Species                        | Method of Detection                  | References |
|--------------------|-----------------------|--------------------|--------------------------------------|--------------------------------------|------------|
| Unclassified       | -                     | Symbiodinium spp.  | *Acropora tenuis*                    | Metagenomic analysis, Transmission   | [130]      |
| Herpesvirus-like   | 120–150               |                    | *Acropora aspera,* *Acropora millepora* | Electron Microscopy, Transmission    | [41]       |
| Viral-like particles | -                     |                    | *Acropora muricara,* *Porites spp.*  | Electron Microscopy                  | [129]      |
| Myoviridae,        | 47–65, 200            |                    | *Acropora millepora*                 | Transmission Electron Microscopy     | [20]       |
| Poxviridae,        |                       |                    |                                      |                                       |            |
| Microviridae        |                       |                    |                                      |                                       |            |
| Virus-like particles| -                     |                    | *Acropora muricata*                  | Transmission Electron Microscopy     | [30]       |
| Herpesviridae,     | 45–120                |                    | *Montastraea annularis*              | Transmission Electron Microscopy     | [44]       |
| Circoviridae,      |                       |                    |                                      |                                       |            |
| Nanoviridae        |                       |                    |                                      |                                       |            |
| Herpes-like viral  | 120                   |                    | *Montastraea annularis*              | Transmission Electron Microscopy     | [44]       |
| Dicorna-like virus | 30                    |                    | *Acropora tenuis,* *Fungia fungites,* *Galaxea fascicularis,* *Pocillopora damicornis* | PCR-Based Assay                     | [146]      |
| Bavuloviridae,     | 45–400                |                    | *Pocillopora spp.*                   | Metagenome                           | [147]      |
| Herpesviridae,     |                       |                    |                                      |                                       |            |
| Polynnaviridae,    |                       |                    |                                      |                                       |            |
| Retroviridae,      |                       |                    |                                      |                                       |            |
| Myoviridae,        |                       |                    |                                      |                                       |            |
| Myoviridae,        |                       |                    |                                      |                                       |            |
| Mimiviridae,       |                       |                    |                                      |                                       |            |
| Baculoviridae       |                       |                    |                                      |                                       |            |
| Siderastrea siderea| 60–400                |                    |                                      | Metagenome                           | [148]      |

Wood-Charlson et al. [46] have discovered Phycodnaviridae, Marnaviridae and Alvernaviridae, which were the best characterized group of algal viruses, via metagenomic studies [149,150]. Nanoviridae and Geminiviridae are common viruses that have been found in almost every coral-associated virus study. These viruses are usually linked with sewage, which may highlight the connection between certain types of virus and environmental degradation [44]. Therefore, the abundance of viruses in corals is proportional to the concentration of local inorganic nutrients and human population centers [135,151]. According to Futch et al. [148], certain “human-specific” viruses such as Adenovirus have also been shown to exist in coral surface mucus layer, possibly due to human pollution, including sources of fecal pollution such as boats and contaminated groundwater associated with septic systems and injection wells.

According to the metagenome studies conducted by Wang et al. [152], the top five viral families that have been found in *Siderastrea siderea* coral were Myoviridae (25.98%), Siphoviridae (9.26%), Mimiviridae (7.89%), Baculoviridae (7.61%) and Poxviridae (5.81%) whereas the overall mean number of viral abundances was about 1.14%. Moreover, similar studies have discovered thermal anomalies related to microbiome shifts, and the order Caudovirales has been found to be in high proportion in certain samplings in warmer months (July and August). Caudovirales have been found consistently in coral virome [28,46]. The member of the family known as Poxviridae is often found in marine coral viromes [140].
that infect marine invertebrates yet has been found in coral, *Siderastrea sidereal*, where thermal stress increased and coral health decreased [152].

A viral outbreak in both coral species, *Acropora aspera* and *Acropora millepora*, was caused by the Herpesvirales order which has been commonly identified in these coral species. These herpesvirus-like VLPs are composed of an enveloped and circular capsid that hosts on coral epidermal and gastro-dermal cells. Moreover, the second most common abundant eukaryotic virus annotations were the NCLDV (Nucleocytoplasmic Large DNA Viruses) including, Phycodnaviridae, Mimiviridae, Poxviridae, Iridoviridae, Marseillevirus and Ascoviridae. The phages that were found to dominate in the *Acropora aspera* virome were Sipho- and Myoviridae [43].

According to Cardenas et al. [141], the viral community composition in Red Sea corals detected via metagenomic study included 97 viral families, which were found across meta-transcriptomics. The most abundant viral families were Siphoviridae, Mimiviridae and Retroviridae (dsDNA viral families) found in eukaryotes and bacteria, whereas ss-RNA viral families such as Qiniviridae, Nyamiviridae and Soliviridae were present in meta-transcriptome studies. Parvoviridae was found to be highly abundant in stress-tolerant coral virome with massive growth in *Acanthastrea echinata*, Diploastrea heliopora, *Fungia* sp., and *Plerogyra sinuosa*. Dicistroviridae was observed in the outgroup samples of *Millepora platyphylla*, *Xenia* sp., and *Stylophora pistillata*. Similar studies have revealed the relative abundances of Picobirnaviridae and Siphoviridae that were most accounted for in viromes of *Galaxea fascicularis*, *Mycedium elephantotus*, and *Pachyseris speciosa* when compared to *Acropora cutherea*, *Pocillopora verrucosa*, and *Stylophora pistillata* [141].

5. Coral Fish Viruses

Coral disease outbreaks are the main cause of coral death and subsequent coral reef degradation [153]. It is reported that corals are susceptible to viral infections and the organisms involved mainly contribute to the HGT (Horizontal Gene Transfer) of viral particles to coral, for instance, fish, invertebrates and macroalgae [126]. Coral feeding fish (e.g., parrotfish and butterfly fish) and invertebrates [154–156] are another reasonable mechanism for the introduction of viruses into individual coral communities. According to Rotjan and Lewis [154], coral tissue mortality can be classified into two categories, where mortality of coral tissue occurred due to parrotfish grazing scars over the colony surface or mortality from unknown causes. Evidence provided by Bettarel et al. [157] that the grazing activity of the specific corallivorous gastropod *Drupella rugosa* damaged coral polyps were the result of predation on coral microbial associates is still obscure. Similar studies have revealed the presence of dsDNA virus from the coral *Acropora Formosa* which mainly belongs to uncultured Mediterranean phage uvMed, while others were Myoviridae, Podoviridae, Siphoviridae and Microviridae. The coral predators were suspected to assist in disease transmission either by acting as vectors or stressors on coral microbiota, while the presence of *Drupella rugosa* has corresponded to disease such as white syndrome, skeletal eroding band disease and black band disease [157].

Corallivorous fish act as vectors for disease transmission [158]. Aeby and Santavy [158] have determined that the coral-feeding butterflyfish, *Chaetodon capistratus* was involved in the colony transfer of black band disease. In aquaria, the presence of *Chaetodon acapistratus* increased the rate of spread from infected *Montastraea faveolata* to uninfected fragments. Both protected corals that were exposed to fish predation suffered from black band disease. Therefore, oral transmission of pathogens directly and/or via indirect fecal transmission may spread from colony to colony. This kind of direct feeding may actually be beneficial because it can reduce the extent and progression of the disease [158].

Thurber et al. [142] proposed that coral related viruses known as herpes-like viral were found to shift in response to abiotic factors when exposed to decreasing pH, elevated nutrients and thermal stress. Similar studies suggest that coral-related viruses target hosts such as protists, fungi, plants and metazoans. It is also found that invertebrates infecting
viruses were mostly Baculoviruses and Polydnaviruses that predominantly infect the arthropods [159,160].

According to the study by Cherif [161], the molecular detection of Lymphocystis Disease Viral partial genome (LCDV-Sa) in Tunisian gilthead sea bream (Sparus aurata) caused fatal, chronic, rare and slowly developing disease which affects more than 150 marine and freshwater fish [162–164]. The etiological agent of LCD (Lymphocystis Disease Virus) belongs to genus *Lymphocystivirus*, family Iridoviridae [165,166]. *Lymphocystivirus* have been known to affect marine species such as *Holacanthus* spp., wrasses *Halichoeres* spp., grunts *Haemulon* spp., pinfish *Lagodon rhomboides*, puffers *Canthigaster* and *Sphoeroides* spp., porcupine fish *Diodon hystrix*, and many more, as stated by Stoskopf., [167]. Another study revealed LCDV strains from clownfish, *Amphiprion percula* in Indonesia. Lymphocystis in Atlantic croaker *Micropogonias undulates* and sand seatrout *Cynoscion arenarius* have been reported in Mississippi estuaries from 1966–1969 [168]. According to Bowden et al. [169], lymphocystis was observed in red drum *Sciaenops ocellatus* and other species in the Gulf of Mexico. In addition, a rhabdoviral infection was first described in 1983 in gray angelfish (*Pomacanthus arcuatus*) and French angelfish (*Pomacanthus paru*) collected from the Florida Keys. Table 3 below shows the reef-associated fish that have been infected with the virus.

### Table 3. Lymphocystis disease virus (LCDV), detection method and its host in a coral ecosystem.

| Virus Type                  | Host                          | Size (nm in Diameter) | Detection Methods                      | References |
|-----------------------------|-------------------------------|-----------------------|----------------------------------------|------------|
| LCDV-Clownfish-Indonesia    | *Amphiprion percula*          | 120–350               | Polymerase Chain Reaction, LAMP        | [170]      |
| LCDV-Gilthead Sea Bream-Spain | *Sparus aurata*              | 120–350               | Next-Generation Sequencing             | [171]      |
| LCDV-Paradise Fish-China    | *Macropodus opercularis*      | 120–350               | Electron microscopy, Polymerase Chain Reaction | [162]      |
| LCDV-Sea Bream-Israel       | *Sparus aurata*              | 120–350               | Polymerase Chain Reaction              | [172]      |
| LCDV-Flounder-China         | *Paralichthys olivaceus*     | 120–350               | Whole-genome Shotgun Sequencing        | [173]      |
| LCDV-Largemouth Bass-USA    | *Micropteris salmoides*       | 120–350               | Nested Polymerase Chain Reaction       | [174]      |
| LCDV-Flounder-NorthSea      | *Platichthys flesus*          | 120–350               | Polymerase Chain Reaction              | [165]      |
| LCDV-Sa                     | *Sparus aurata*              | 120–350               | Nested Polymerase Chain Reaction       | [161]      |

6. Marine Sponge Viruses

Marine sponges (phylum *Porifera*) are metazoans and have been distributed all over the world in the aquatic environment since 600 million years ago [175,176]. Marine sponges are a rich source of biotechnologically potential compounds [177,178]. There is a lack of information regarding the role of sponge-related virus communities and the impact of the virus on sponge holo-biont is still unclear [179–183]. Sponge microbiome composition is shifted by environmental factors such as climate changes [184] and host sponge habitat [185] in nine sponge species [186,187]. Fan et al. [188] suggested that marine sponge symbionts lose their metabolic functional potential during the early stages of heat stress and hence destabilize the sponge holo-biont before visual signs of stress occur in the host animal. Global climate change has had a significant effect on the associated microbial communities. For example, the rise of temperature in the ocean controls the link between viruses and the cells they infect, where the growth rate of prokaryotes increases, the length of lytic cycle decreases and burst size increases, resulting in higher virus production rate [189–191]. Thus, changes in climate have direct and indirect effects on marine viruses, including impact of cascade on biogeochemical cycles, food webs and the metabolic balance of the ocean [191]. The main focus of increased studies in sponges is due to their abundance as a high source of biologically active secondary metabolites and a focal point for various aspects of research in organism origin and evolution [179,192,193].

Despite the fact that the diversity and importance of viruses in sponge-associated microorganisms are still largely unknown, a virus associated with the Lake Baikal sponge (*Lubomirskia baikalensis*) was part of the first study using cyanophage related marker gene (g20 gene) [194] and g23 gene for the detection of T4-like bacteriophage (Butina T.V.,
unpublished data). Table 4 represents marine sponge related viruses and types of method used to identify marine viruses.

Marine sponge related VLPs were investigated from the Great Barrier Reef (Carteriospongia foliascens, Stylissa carteri, Xestospongia sp., Lamellodysidea herbacea, Cymbastela marshae, Cinachyrella schulzei, Pipetella candelabrea and Echinocalina isacii) and Red Sea (Xestospongia testudinaria, Amphimedon ochracea, Hyrtios erectus, Crella (Grayel)a cyathophora, and Mycale sp.) [195]. Pascelli et al. [195] revealed various types of marine sponge-associated viruses via transmission electron microscopy (TEM). Almost fifty VLP morphotypes were found in sponge tissues and mucus or surface biofilm where the viruses possessed an icosahedral symmetry morphology with diameter ranging between 60–205 nm. Moreover, the same author confirmed the presence of bacteriophage in sponge species assigned to three Caudovirales families (based on capsid symmetry and tail shape). Virus families found from marine sponge tissue and mucus in the Great Barrier Reef were Podoviridae and Siphoviridae, including Myoviridae and Inoviridae from marine sponge meso-hyl, sponge tissues and sponge mucus in the Red Sea [195].

Fan et al. [196] observed the presence of cyanophage in high abundances in sponge Stylissa sp. 445, suggesting that the cyanobacteria may have a lysogenic relationship with their host [197]. A few double-stranded DNA (dsDNA) viruses were abundant in a diseased branch of endemic sponge Lubomirskia baikalensis, for instance, Siphoviridae, Myoviridae, Phycodnaviridae, Poxviridae, and Mimiviridae; while Podoviridae, Iridoviridae and Herpesviridae can be found in healthier Lubomirskia baikalensis sponge [198]. The order Caudovirales with tailed bacteriophages influenced all datasets, yet the distribution of these taxa varied between holo-bionts. Phycodnaviridae, Poxviridae, Mimiviridae, and Herpesviridae dominated all of the viromic datasets which comprised almost 98% of reads, with other unassigned viruses in Baikal sponge. Podoviridae viruses were more abundant in Lubomirskia baikalensis (Sv3h) healthy sponge and coral Acropora millepora. The presence of Herpesviridae comprised approximately 95–98% of metaviromic dataset in Rhopaloeides odorabile [198].

Batista et al. [199] recorded sponge Darwinella sp. and Dysidea etheria, with the highest abundances of Myoviridae virus detected from Arrarial do Cabo Bay site, South-Eastern Brazil, at low, upwelling and high anthropogenic influence. Laftty et al. [200] demonstrated that most dominant sponge-associated viruses detected were DNA-containing viruses, order Caudovirales. Butina et al. [201] presented virome datasets on Baikalospongia bacillifera species sponge in nine types of dsDNA virus families (Myoviridae, Phycodnaviridae, Siphoviridae, Poxviridae, Mimiviridae, Herpesviridae, Baculoviridae and Inridoviridae) which comprises more than 70% of the identified virome sequences. Potapov et al. [202] reported that 37 nucleotide sequences of g23 gene fragment (accession number MH576490-MH576574) were found in sponge from Lake Baikal. The data produced by Patapov et al. [202] revealed seven sequences included in Far T4 group that contains phages (Escherichia phage 121Q and RM378).

RNA viruses have been discovered in marine sponges, coastal water [203,204], benthic sediments [205], invertebrates [206] and vertebrates [207]. The dsRNA virus genome had been detected through advanced technology, for example, fragmented and primer-ligated dsRNA sequencing (FLDS), which obtained the full-length of the sequence of dsRNA [208–210]. Waldron et al. [211] revealed the presence of RNA virus families such as Narnaviridae, Dicistroviridae, Partitiviridae, Picobirnviridae, Picornaviridae, Tombusviridae, Nodaviridae and Herpesviridae via meta-transcriptome-FLDS analysis. Similarly, Urayama et al. [212] revealed the presence of RNA virus (Dicistroviridae) in the sponge, Hymeniacidon sp. Thus, they have acquired sequence encoding RdRp gene sequence, about 253 (2014) and 233 (2015), from Tokyo Bay which are related to nine dsRNA virus families. Of these sequences, about 78 were obtained from the sponge of Hymeniacidon sp. that were classified as an unassigned RNA family.
Table 4. Marine sponge associated viral communities and detection methods used to identify marine viruses.

| Detection Method       | Viruses                                      | Sponge Species                                      | References |
|------------------------|----------------------------------------------|------------------------------------------------------|------------|
| Transmission Electron  | Podoviridae, Siphoviridae, Inoviridae, Myoviridae | Carteriospongia foliascens, Stylissa carteri, Xestospongia sp., Lamellodysidea herbacea, Xestospongia testudinaria, Mycale sp. | [195]      |
| Microscopy             | Siphoviridae, Myoviridae                      |                                                      |            |
| Metagenome             | Podoviridae, Phycodnaviridae, Poxviridae, Mimiviridae | Lubomirskia baikalensis, Acropora millepora          | [198]      |
| Metagenome             | Myoviridae, Podoviridae                       | Dysidea etheria, Darwinella sp.                      | [199]      |
| Metagenome             | Polydnaviridae, Myoviridae, Siphoviridae      | Rhopaloeides odorabile                               | [200]      |
| Metavirome             | Myoviridae, Phycodnaviridae, Poxviridae, Podoviridae, Mimiviridae, Herpesviridae, Baculoviridae | Baikalospongia bacilifera                          | [201]      |
| Metagenome             | Herpes-like virus                             | Halichondria panicea                                 | [211]      |
| Metagenome             | Dicistoviridae                                | Hymeniaciadon sp.                                   | [212]      |

7. Detection Methods for Marine Viruses in Coral Ecosystem

Diverse approaches have been used to identify and describe viruses in various organisms including transmission electron microscopy (TEM) as described in Tables 2–4 [129,213], PCR-based analyses [214], DNA in situ hybridization [215], immune-histochemistry [216], flow cytometry [217], next generation sequencing (NGS) [218] and metagenomic analyses [138,142].

Weynberg et al. [130] investigated coral associated viruses via metagenomic analysis where studies clarified that the method is a relatively promising tool for characterizing coral related viral communities. Molecular detection is frequently used by researchers in coral ecosystem associated marine viruses, which includes the viral metagenomic method and transmission electron microscopy. Sequencing of environmental DNA samples (metagenome) and sequence of other plankton viruses have revealed an unanticipated abundance of large DNA viruses associated with the marine environment [219]. Metagenomic analysis is an important tool for describing viruses, because many viral hosts are not suitable for cultivation [64] and this method does not require any of the gene markers for virus identification. Metagenomic studies have pointed out challenges and cataloged a group of worldwide viruses in corals and their symbionts [45] and this approach has widened the diversity of viral communities [130].

Although the field of coral virology is still at its early stage, some researchers have applied microscopy and genomic methods to examine the diversity and role of viruses in coral organisms. Evidence from microscopy studies has shown that virus-like particles (VLP) are present in all of the corals [29,220]. VLPs observed are likely to have been produced throughout the lytic replication phase of endogenous infections of coral animals or their microbiota [30,129]. Lawrence et al. [221] reported that the TEM approach revealed structures within corals which are marine viruses in the coral ecosystem.

Advanced molecular approaches have shown that viruses disperse in all types of environment. Sequencing of 16SRNA techniques is not recommended because they lack the gene to identify viruses, when viruses do not share common genes which significantly fit as phylogenetic markers [222]. Traditional techniques have been used to identify viruses, for example filtration, tissue culture, electron microscopy and serology. Traditional methods and advanced molecular techniques have contributed to the exploration of more viruses [222]. Electron microscopy is considered to be an expensive tool with a paucity of sensitivity. Polymerase chain reaction (PCR) only focuses on certain genes that use markers of related viruses, but PCR analyses are unable to identify complete novel viruses. In conjunction with this, metagenomic analyses are recommended to track viruses whether they are known or unknown, and they are easily detected via this method. Metagenomic
study was first used in marine environmental research, where the analysis was done in San Diego [64,222], and depended upon cloning of double stranded DNA genomes. Implementing this method will discover many unidentified viruses and uncultured novel viruses which will benefit researchers in this field. Due to the difficulty of identifying some of the marine environmental viruses, especially in the ocean, a metagenomic approach would be a major breakthrough in discovering new viruses.

8. Conclusions

Marine viral communities play a crucial role in biogeochemical cycles in the ocean, indirectly and directly. These viral communities induce mortality and disease in the reef ecosystem through abiotic and biotic factors which causes the reduction in the symbiotic relationship between the coral and their surrounding hosts. This review emphasizes marine viruses from the ocean, coral-associated viruses, marine sponge and coral fish viruses in reef ecosystems, examining previous research via traditional methods to modern advanced approaches. The findings of this review have enhanced the understanding of coral-virus interactions and enriched our understanding of reef-associated virus interaction and the diversity of viral communities in marine environments.

Author Contributions: Conceptualization, S.C.Z. and S.I.; resources, L.A.; writing—original draft preparation, L.A., R.F. and E.H.S.; writing—review and editing, S.C.Z., S.I.; supervision, S.C.Z. and S.I.; funding acquisition, S.I. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by Fundamental Research Grant Scheme, Ministry of Higher Education, Malaysia (FRGS vot. no. 59535).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data presented in this study are available on request from the corresponding author. The data are not publicly available due to confidentiality.

Acknowledgments: The authors would like to thank Faculty of Fisheries and Food Sciences, Universiti Malaysia Terengganu for their immense support. The authors also would like to thank the anonymous reviewers and editors for their helpful and constructive comments.

Conflicts of Interest: The authors declare no conflict of interest.

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