

Marine Viruses in Coral Reef Ecosystem

メタデータ	<p>言語: en</p> <p>出版者: Shizuoka University</p> <p>公開日: 2015-12-17</p> <p>キーワード (Ja):</p> <p>キーワード (En):</p> <p>作成者: Chitra, Ramphul</p> <p>メールアドレス:</p> <p>所属:</p>
URL	<p>https://doi.org/10.14945/00009284</p>

(課程博士・様式7) (Doctoral qualification by coursework, Form 7)

学 位 論 文 要 旨

Abstract of Doctoral Thesis

専攻:

氏名:

Course : Environment and Energy Systems

Name : RAMPHUL Chitra

論文題目: サンゴ礁生態系における海洋性ウイルス

Title of Thesis : Marine Viruses in Coral Reef Ecosystem

論文要旨:

Abstract :

Five marine phages were successfully isolated from shallow coral reef seawater of Bise and Sesoko, Okinawa, Japan (26°42'N, 127°52'E; 26°39'N, 127°51'E). Only one phage denoted as Vibrio phage RYC (VCPH RYC) infected the pathogenic bacteria, *V. coralliilyticus* (AB 490821, Japan) and the rest infected *V. coralliilyticus* P1 (LMG 23696, Australia). Most of the phages isolated from *V. coralliilyticus* P1 regardless of their sampling sites displayed phages with head-tail structures belonging to Myoviridae family. The size of the capsids and tails varied slightly from 57.65–58.33 nm and 95.38–105.88 nm, respectively. However, the phage isolated with the host *V. coralliilyticus* (Japan) exhibited no tails and non-enveloped structures with a diameter of 84.45 nm, which could not be classified morphologically. All the phages were chloroform resistant. The latent phases for phages lysing *V. coralliilyticus* P1 and *V. coralliilyticus* (Japan) were 45 and 60 min, respectively. The five isolated phages showed high host specificity. The genome of the phages was sequenced through the next generation sequencing technique. The genome of Myoviridae-type viruses was 48 kb and 35 kb, whereas VCPH RYC had a genome size of 158 kb. Cluster analysis of the isolated Myoviridae-type viruses revealed that they were closely related to *Vibrio parahaemolyticus* phage VP16T and VP16C based on partial sequencing. However, cluster analysis of VCPH RYC based on DNA polymerase showed that it was relatively close to Shewanella sp. Phage, though this finding could be limited owing to the lack of viral sequenced data. As a result, VCPH RYC could be considered a novel phage infecting *V. coralliilyticus*. Phages were also screened in healthy coral tissues (*Montipora digitata*) and lagoon sediments at the two sampling sites. Nonetheless, only seawater exhibited the presence of phages.

Virus-like particles (VLPs) are very important for their ecological roles, particularly in biogeochemical cycles and shaping marine communities in both oceans and coral ecosystem. Previous studies focused more on enumeration and functions of VLPs in deep sea/open ocean ecosystem rather than coral reef ecosystem. Hence, this study emphasized on coastal coral reef ecosystem, where Bise and Sesoko reef lagoons were opted as sampling sites. In order to determine the abundance of VLPs and prokaryotes, three sub-environments were chosen in the coral ecosystem: seawater, lagoon sediments and healthy coral tissues (*M. digitata*). Samplings were done during August 2013. Epifluorescence

microscopy was used to determine the abundance of the VLPs and prokaryotes. Seawater was found to have the highest abundance of VLPs among lagoon sediments and coral tissues. However, the VLPs density differed only in lagoon sediments neither in seawater nor in coral tissues. The abundance of bacteria was highest in seawater followed by lagoon sediments and coral tissues. The prokaryotes abundance showed no variation in coral tissues in regards to its location. A strong positive relationship was only found between the abundance of VLPs and bacteria in Bise seawater. Nevertheless, some relationships were found in lagoon sediments and coral tissues at both sampling sites, but none were significant. Hence, the abundance of VLPs differed significantly in lagoon sediments but not in seawater and coral tissues, indicating that local locations showed the least influential effect on the VLPs abundance in seawater and coral tissues.

VLPs can infect all types of marine organisms, where they play important roles in regulating the marine food web, controlling microbial loop, particularly the dynamics of phytoplankton and prokaryote communities. Thus, the links between phytoplankton, the abundance of microorganisms (VLPs, bacteria, and coccoid cyanobacteria) and different hydrographic factors (temperature, salinity, dissolved oxygen and pH), as well as nutrient availability (nitrates, nitrites, ammonium, total dissolved nitrogen, dissolved organic nitrogen, dissolved organic phosphorus and total dissolved phosphorus) were studied in coastal shallow reef seawater within 5 m depth at Bise (BE, Okinawa, Japan) and Tang Kheng Bay (TKB, Phuket, Thailand). VLPs density was more abundant than prokaryotes. Phytoplankton carbon biomass was significantly higher in TKB than BE, but BE showed more planktonic diversity than TKB. VLPs abundance was strongly linked to phytoplankton, bacteria and inorganic nutrients. Nevertheless, the ratio of virus:plankton and virus:bacteria differed between TKB and BE. The abundance of VLPs was linked to nutrient availability rather than hydrographical parameters. Multiple regression analysis showed that ammonium had greater influence on the abundance of VLPs.

Thus, it was shown that phages were most abundant in seawater and a novel possible phage VCPH RYC infecting *V. coralliilyticus* (Japan) was isolated. This study showed that the abundance of VLPs was high in seawater of Bise, Sesoko and Tang Kheng Bay. Nonetheless, within a similar local environment the viral density of VLPs in seawater did not show any variation, but it did differ between geographical areas: TKB and BE. This variation is attributed to the nutrients contents, especially ammonium concentration in seawater. Thus, marine viruses in coastal coral areas fulfill their ecological roles mostly in accordance with the prevailing nutrient availability.

Keywords: *V. coralliilyticus*, Virbio phage, genomic size, nutrients, prokaryotes