

DYNAMICS OF *CHAETOCEROS TENUISSIMUS* AND ITS VIRUSES IN HIROSHIMA BAY, JAPAN

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Since the findings of diatom viruses, it has been suggested that the viral agents are important for diatom dynamics in nature as well as traditional environmental factors, such as e.g. water temperature, salinity, light, nutrients, and water movement. Their relationships in nature, while, are not well understood, because the data based on field research are rarely accumulated. So far, over ten diatom virus species are isolated and characterized. They were divided into two groups based on genome type, single-stranded DNA and single-stranded ssRNA. Among them, CtenDNAV and CtenRNAV share a same host species, *Chaetoceros tenuissimus* Meunier (Bacillariophyceae, Centrales). In this study, we conducted a field survey to analyze the relationship between dynamics of *C. tenuissimus* and its viruses in Hiroshima Bay, Japan, from April 2010 to Dec 2011 and tried to identify the species of viruses detected during the research.

C. tenuissimus cell numbers were measured by real-time PCR methods, and viral abundances were determined by MPN method using two different host strains, *C. tenuissimus* strain 2-10 and 2-6. These strains have different viral susceptibilities, i.e. the former is susceptible to both CtenRNAV and CtenDNAV, but the later only to CtenDNAV. Viral isolates were established from each MPN culture plate.

Blooms of *C. tenuissimus* were observed from July to September every year and the maximum were as high as $\sim 10^4$ cells ml⁻¹. Specific increases of the viruses detected using the two different host strains were also observed during those bloom periods, which indicated the viruses affected the dynamics of the bloom population. Each of the viruses, however, showed individual dynamic patterns during the bloom periods. For example in 2001, the increases of the viruses detected with the host strain 2-10 (2-10 type viruses) were observed simultaneously at the temporal decreasing of the host cell numbers during the early and mid bloom periods. The viruses detected with the host strain 2-6 (2-6 type viruses) were gradually increased from mid bloom periods and reached the maximum at just before the host bloom disintegrations. Preliminary analysis revealed that the genome type of the most 2-10 type viruses seemed to be RNA and that of the 2-6 type viruses were DNA. Then, our hypothesis is as following; in early- to mid-bloom periods, the host strains susceptible to RNA viruses were dominant in the host population, and they were attacked by their infective viruses. The strains which are resistant to RNA viruses but susceptible to DNA viruses were gradually increased among the population from the mid bloom periods, which are caused the increases of the DNA viruses from mid to late bloom periods.