

DIATOM VIRUSES ISOLATED FROM JAPANESE COASTAL WATERS

Yuji Tomaru¹, Kensuke Toyoda^{1,2}, Kei Kimura¹ & Yoshitake Takao³

¹National Research Institute of Fisheries and Environment of Inland Sea, Fisheries Research Agency

²Department of Biology, Keio University

³Department of Marine Bioscience, Fukui Prefectural University

Since the first reports of large numbers of virus-like particles in natural seawater, the aquatic viruses have been intensively studied. Currently the viruses are regarded as one of the major biological factors that regulate carbon cycling, microbial biomass and the genetic diversity of protists and algae. Most of the virus particles in aquatic environments are considered to be bacteriophages and the viruses infecting eukaryotic phytoplankton may rank second in abundance. The roles of viruses in natural environments are considered to be important from the viewpoint of the ecological dynamics of microalgal host populations. Although the significances of diatoms as key players in the oceanic carbon cycle have been recognized, the existences of diatom viruses are scarcely known until recently. The first diatom virus was reported in 2004, a virus infecting *Rhizosolenia*. After the initial discovery, several *Chaetoceros* viruses have been isolated and characterized. Furthermore, just recently pennate diatom viruses have been successfully isolated. These viruses are grouped into two categories based on genomic features, single-stranded (ss) RNA and ssDNA. The members for ssRNA diatom viruses are RsetRNAV, CtenRNAV, CsfRNAV, Csp03RNAV and AglaRNAV which infect *R. setigera*, *C. tenuissimus*, *C. socialis* f. *radians*, *Chaetoceros* sp. strain SS08-C03 and *Asterionellopsis glacialis*, respectively. They harbor ca. 9kb ssRNA genome with two open reading frames encoding putative replication-related proteins and capsid proteins. Phylogenetic analysis based on the deduced amino acid sequence of the RNA-dependent RNA polymerase domains strongly supported the monophyly of these viruses with a bootstrap value of 99%. The ssDNA diatom virus group includes CsaDNAV, CtenDNAV, Csp05DNAV, ClorDNAV, CsetDNAV and TnitDNAV, infecting *C. salsugineum*, *C. tenuissimus*, *Chaetoceros* sp strain TG07-C28, *C. lorenzianus*, *C. setoensis* and *Thalassionema nitzschioides*, respectively. Their genomes are composed of covalently-closed circular ssDNA (ca. 6kb). The genome of CdebDNAV infecting *C. debilis* is also ssDNA (ca. 7kb) but its structure is unrevealed. These diatom viruses are all lytic to their respective host diatoms; and their infection is strain-specific rather than species-specific. These discoveries are important to understand diatom ecology, the carbon cycles related to diatom production and their evolution.