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Viral impacts on algal blooms: quantitative and qualitative effects

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Recently, an increasing number of viruses infectious to bloom-forming microalgae are isolated and characterized. In this paper, significance of their ecological roles is mainly introduced. HcRNAV is a polyhedral virus infecting the bivalve-killing dinoflagellate *Heterocapsa circularisquama*, which harbors a linear 4.4-kb ssRNA genome. In the RdRp sequence tree, this virus fell into a phylogenetic clade which is distant from any other virus ever reported so far; just recently approved as the typical species of a new genus "Dinornavirus" by the International Committee on Taxonomy of Viruses (ICTV). Based on a field survey for more than six years in Ago Bay, Japan, an intimate ecological relationship between the host and the virus was elucidated. HcRNAV population is composed of multiple types which differ in intraspecies host specificity; i.e., differing in strain-specific infectivity among them; on the other hand, the host is composed of distinctive types differing in virus sensitivity spectra. Thus, virus infection can change clonal composition of the host population. Results of genome comparison supported the hypothesis that the nanostructural difference on the viral surface among these types is crucial for determining the specificity. We assume that the type variations of *H. circularisquama* and its viruses are more complicated than we suspect in natural environments. The host algal population dynamics is apparently affected by HcRNAV infection; viral impact on the algal population is considered to be not only quantitative (on biomass) but also qualitative (on clonal composition).

Keywords: virus, microalgae, algal bloom, aquatic ecology