

Structure of a novel virus infecting the marine diatom *Chaetoceros tenuissimus*

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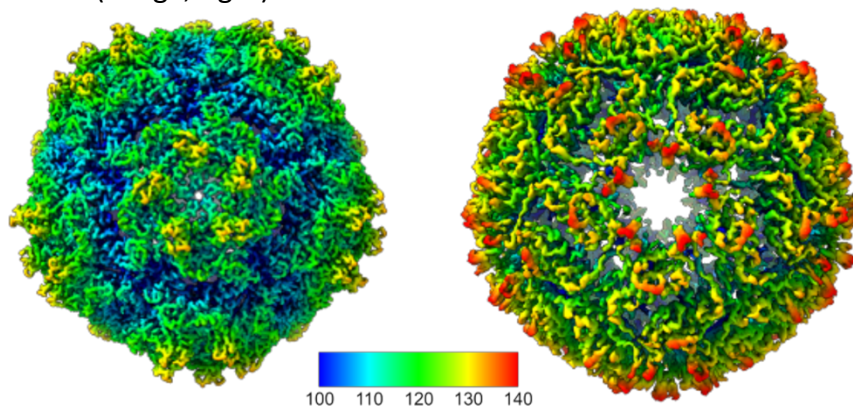
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Diatoms, a type of unicellular eukaryotic algae, are of great importance in oceanic ecosystems, constituting about 40% of primary marine production and influencing global biogeochemical cycles. Nonetheless, some diatoms can cause Harmful Algal Blooms as they release toxins or cause mechanical damage to fish. One such diatom species is *Chaetoceros tenuissimus*, a cosmopolitan species that occurs along the coastal lines around North America and Europe, including the Baltic Sea, and often causes blooms on the west coast of Japan.

Studying the factors that regulate diatom growth dynamics is essential for understanding global ecosystems. While environmental factors like temperature, light, and nutrient availability are widely recognized as key regulators of diatom growth, research over the past two decades has increasingly emphasized the significance of viral infections in this process. To this day, a few tens of diatom viruses have been isolated. These are either of (+)ssRNA or ssDNA type, phylogenetically clustered in the families *Marnaviridae* and *Bacilladnaviridae*, respectively.

In our previous studies, we have determined the structures of a *C. tenuissimus* marnavirus and bacilladnavirus. The capsid proteins of these viruses contain the common viral jelly-roll fold. Marnaviruses, classified within the order *Picornavirales*, share the same overall structure with capsid proteins of other viruses within the order, such as picornaviruses, however, with some host adaptations (Munke et al 2020). Surprisingly, the capsid protein of the bacilladnavirus showed greater resemblance to capsid proteins of ssRNA viruses, including nodaviruses, rather than those of other ssDNA viruses, hinting at a potential evolutionary horizontal gene transfer event (Munke et al., 2022).

Here, we present a new *C. tenuissimus* virus structure from a novel ssDNA virus. As for the other two viruses, the capsid protein has a jelly-roll fold, but it is unique and does not resemble any other known viruses. We have reconstructed two particle types: a smaller, more compact genome-containing type to 2.3 Å (image, left), and a slightly expanded, more heterogenous empty type to 3.8 Å (image, right).



References: Munke et al J Virol 94 2022, DOI: 10.1128/jvi.01855-19, Munke et al mBio 13, DOI: 10.1128/mbio.00156-22