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Structure and function of proteins from an algal bloom-regulating virus

Diatoms are a type of plankton found almost everywhere there is water. They play crucial roles in Earth's ecosystems, firstly because they form the basis of the food web and thus provide food for animals, and secondly because they drive the biological pump that converts carbon dioxide from the atmosphere into oxygen (*1*). However, some diatoms create harmful blooms that lead to economic losses for the fishing industry due to toxin release or physical harm to marine organisms. Maintaining a balance among diatom populations is essential for ecological stability. One of the factors that contribute to this balance is host-specific diatom viruses (*2*). To understand the growth behaviour of diatoms, how their growth is affected by various external factors, and how growth can be controlled in cases where harmful blooms occur, we also need to study their viruses.

This project focuses on studying the bloom-regulating virus *Chaetoceros tenuissimus* DNA virus type II (CtenDNAV-II), a ssDNA virus of the family *Bacilladnaviridae*. This virus encodes for three viral proteins (VPs): VP1, VP2 and VP3. Based on sequence and structural analysis, VP1 appears to function as a lipase, potentially involved in disrupting endosomal membranes during replication. VP2 is the capsid protein, and VP3 is the replication initiation protein (Rep) (*2*). We have previously determined an atomic structure of the capsid (see figure, left) and a low-resolution model of the capsid interior (*3*). Our current objective is to deepen our understanding of the virus's replication cycle, including viral genome release, replication and virion assembly. To achieve this, we aim to conduct functional and structural studies of the individual viral proteins VP1-3.

The student project can be adapted to the student's interests. It may involve cloning, expression, and purification of one or a few viral proteins, cryo-EM, crystallography, bioinformatic analysis and biochemical/biophysical characterisation.

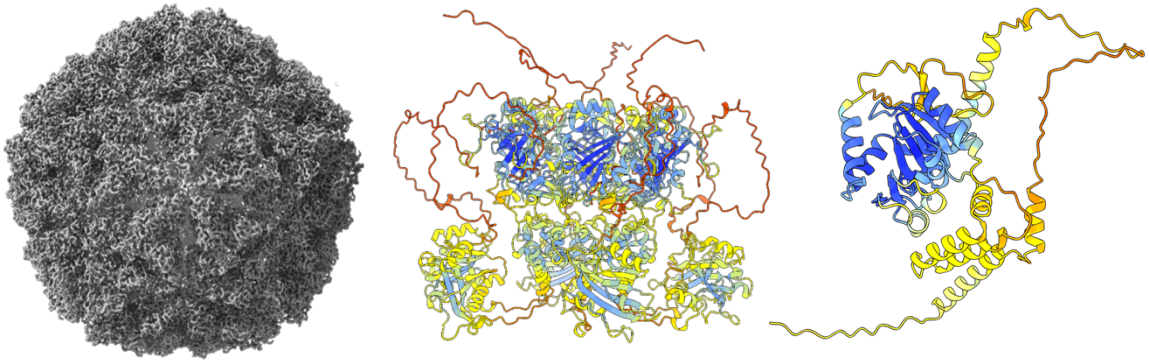

Figure: The capsid reconstruction (*3*) and AlphaFold models of a hexameric Rep and the putative lipase are shown from left to right.

References

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3. A. Munke, K. Kimura, Y. Tomaru, H. Wang, K. Yoshida, S. Mito, Y. Hongo, K. Okamoto, Primordial Capsid and Spooled ssDNA Genome Structures Unravel Ancestral Events of Eukaryotic Viruses. *mBio* **13**, e00156-22 (2022).