

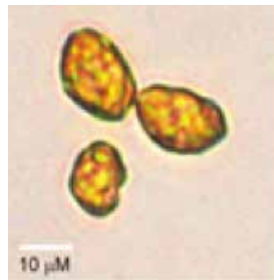


Assoc. Prof.
UEKI Shoko



Study on dynamics of Phytoplankton in environment

Our group focuses on the study of *Heterosigma akashiwo*, a unicellular alga that forms harmful algal bloom (commonly termed 'red tide'). Algal bloom is typically caused by aberrant propagation of a single species, resulting in its predomination in the local population. While environmental factors including temperature and eutrophication are linked to bloom, the precise mechanism of its formation process is still obscure. We isolated a bacterial strain, *Altererythrobacter ishigakiensis*, a member of the class *Alphaproteobacteria*, that promotes growth of *Heterosigma akashiwo*. This is the first example of selective growth promotion of *H. akashiwo* by a marine bacterium, and may exemplify importance of symbiotic bacterium on algal bloom forming process in general.



A bloom causative phytoplankton,
Heterosigma akashiwo

Study on interaction between a giant double-stranded DNA virus and its host



HaV infect and lyse its host, *Heterosigma akashiwo*. The virus was identified as a bloom terminating factor.

H. akashiwo bloom is known to be terminated by algicidal bacteria and viruses. *Heterosigma akashiwo* virus (*HaV*) was identified as one of such bloom-terminating factors. We completed the sequencing of its genomes. The viral genome was characterized to be a linear double stranded DNA (dsDNA), with an estimated size of ~290 kbp. It is a member of *Phycodnaviridae*, one of the viral families regarded as "giant dsDNA viruses" that possess genomes larger than several hundred-kbp in size.

We are particularly interested in studying about the infection mechanism of *HaV* at cellular and molecular level. The study will provide insights into infection strategies of a giant dsDNA virus, and the molecular mechanism of a major environmental phenomenon, bloom termination.