

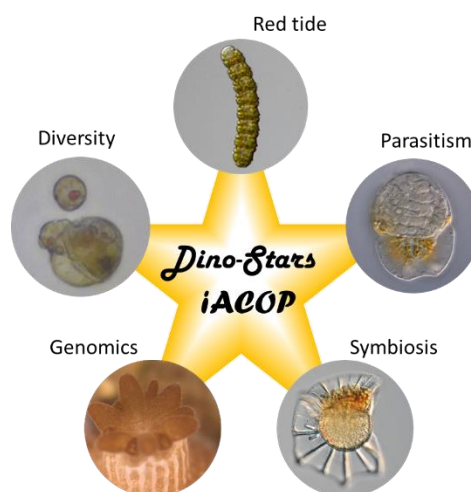
Symposium 6

Ecology and evolution of dinoflagellates in the genomics era

Organizers: Hwan Su Yoon (Sungkyunkwan University, Korea) and Cheong Xin Chan (University of Queensland, Australia)

Synopsis: Dinoflagellates are protists that are ubiquitous in marine and fresh waters. They critically sustain global aquatic ecosystems via primary production and cycling of organic carbon and nitrogen. Estimated at ca. 2,500 species, dinoflagellates are highly diverse, covering a broad spectrum of trophism (heterotrophy, photoautotrophy, and/or mixotrophy), environment (tropics, temperate, or polar), and lifestyle (free-living, symbiotic, or parasitic). Bloom-forming species may cause “red tides”, which produce toxins that pose serious human health risks. Symbiotic species of family Symbiodiniaceae are crucial symbionts in corals and other coral reef organisms. Parasitic species can cause death in economically important crustaceans such as crabs and lobsters.

Although dinoflagellates are ecologically and economically important, they pose many challenges in modern research. Their taxonomy can be confounded by subtly different morphology, ecology may involve distinct modes of symbiosis and multiple interacting species in a complex ecosystem, chromosomes are permanently condensed in crystalline structure, nuclear genomes are large (up to 70-fold larger than a human genome), and organellar genomes are atypical of eukaryotes. Their evolutionary history is also highly intricate; some photosynthetic lineages harbor tertiary plastids derived from haptophyte, diatom and/or green algal sources. In this symposium, we will discuss current understanding of dinoflagellate ecology and evolution, with perspectives of taxonomy/diversity, red tide, parasitism, symbiosis, and genomics, and how we can use this knowledge to drive future research.



S6-1

Morphological and physiological diversity of dinoflagellates

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Dinoflagellates are primarily unicellular flagellates having two distinctive flagella. However, the types of dinoflagellate are various such as a single cell without flagellum or cells in a chain-form. The dinoflagellates cell surface is covered by thecal plates, which are major morphological features that have been widely used in taxonomy. The numbers, sizes, and shapes of thecal plates vary in the genera and species of dinoflagellates. Also, some intercellular structures of dinoflagellate are often used in taxonomy. Physiologically, dinoflagellates have diverse trophic modes such as phototrophic, mixotrophic, and heterotrophic. Such a variety of trophic modes may allow dinoflagellates to play an essential role in the marine environment and inhabit a wide range of environments. Dinoflagellates are found in both low-nutrient pelagic and highly eutrophic waters and benthic habitats as well. Complex cellular structure and physiological features help to explain the essential ecological roles of dinoflagellates and their adaptation in a wide variety of environments. I will discuss the diversity in the morphological and physiological features of dinoflagellates, and it might provide an insight into dinoflagellate ecology.

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S6-2

Effect of marine heatwaves on bloom formation of the harmful dinoflagellate *Cochlodinium polykrikoides*

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In 2018, the bloom of harmful dinoflagellate *Cochlodinium polykrikoides* occurred under abnormally high water temperature (WT) conditions caused by heatwaves in Korean coastal water (KCW). To better understand *C. polykrikoides* bloom at high WTs in 2018, we conducted field survey and physiological and genetic experiments in laboratory using two different strain of CP2013 and CP2018. The heatwave increased the WT from 24.1°C to 29.2°C for two weeks, leading to strong stratification even in mid-July ($p < 0.01$, Chi square = 94.656, Kruskal–Wallis test). Under early stratification conditions, patch blooms formed more earlier than the average outbreak in the last 17 years in KCW, despite high WT reaching 30°C. In laboratory experiments, although there were no genetic differences in the LSU rDNA, both strains showed a significant different growth response to high WTs; above 28°C, CP2013 did not survive, but CP2018 was able to grow, suggesting that CP2018 had potential growth capacity at high WTs. However, the growth rate of CP2018 was low at 30°C. In addition, the blooms of *C. polykrikoides* in 2018 lasted only 3 weeks, an exceptionally short compared to average duration of past 20 years. The negative correlation between the average WT and duration of *C. polykrikoides* bloom in previous 17 years ($R^2=0.52$, $p<0.01$) supports that high WT approaching 30°C is not favorable for *C. polykrikoides* in KCW. Thus, in relation to heatwaves, our findings indicated that early stratification condition plays a critical role in developing *C. polykrikoides* blooms, but maintaining bloom are negatively affected under high WT conditions.

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S6-3

Diversity and distribution of marine parasitic dinoflagellates

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Approximately 150 species (35 genera) of dinoflagellates are known as parasites of a variety of marine organisms including protists, larvaceans, crustaceans, annelids, and fish. Many of these species are parasitoids, which kill the hosts to complete their life cycle. Thus, epidemics by parasitic dinoflagellates causing host mortality could influence host population dynamics and cause significant loss to fisheries. A majority of literatures for infections of parasitic dinoflagellates have been mainly recorded from temperate coastal habitats. During the past decade, molecular studies exploring in marine picoeukaryote diversity using a high-throughput sequencing discovered the novel eukaryotic lineages (i.e. Marine AVLeolate; MALV). These enigmatic new lineages represent up to 50% of sequences retrieved in all marine environments, from temperate coastal waters to polar regions, to anoxic environments, even to deep hydrothermal vents. Now, the MALV sequences are believed to be attributed to parasitic dinoflagellate Syndiniales, a group of composed of obligate parasites. Evidences for the great diversity and widespread distribution of syndiniales parasites suggest that these parasites could have an important role in host population regulation and further studies are required to better evaluate the functional role of these parasites and their contribution to carbon flow in marine food webs.

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S6-4

Diversity of symbiotic cyanobacteria seen in pelagic dinoflagellates

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Symbiosis is one of the most important topics among the diverse phenomena exhibited by dinoflagellates. While some dinoflagellates are widely known to live in the bodies or cells of other organisms as symbionts, some of them are also known to host a variety of unicellular organisms in

their cells. The symbioses hosted by dinoflagellates have attracted attention as a key to understanding symbiotic evolution, yet the details of many of these relationships remain to be explored. Pelagic species of Dinophysiales have long been known to host cyanobacteria as symbionts. These dinoflagellate species possess an extracellular chamber per cell and cyanobacterial symbionts are residing in the specialized space. Despite the existence of the symbionts being first recorded over 100 years ago, detailed characteristics of the cyanobacteria as well as the nature of the symbiosis had remained poorly understood. In the presentation, I will introduce features of symbiotic cyanobacteria isolated from two Dinophysiales species, *Ornithocercus magnificus* and *Histioneis depressa*, revealed by single-cell genomic analysis. The genome information suggested contrasting natures between two symbionts from the different hosts. The cyanobacterial symbiont from *O. magnificus* was unveiled to be of lineage lacking nitrogen-fixing ability and its genome has been reduced compared to genomes of close relatives. In addition, a metagenomic analysis suggested an obligate symbiotic relationship between the cyanobacteria and dinoflagellates. On the other hand, all the genes necessary for nitrogen fixation were identified in the genome of *H. depressa* symbiont, indicating that the symbiont has nitrogen-fixing ability in addition to photosynthetic ability. Furthermore, the estimated distribution pattern in the environment suggests that the symbiosis between *H. depressa* and the cyanobacterium would be facultative. These results illuminate the diversity of symbiotic relationships seen in Dinophysiales, in terms of the lineage and roles of the symbionts, as well as the strength of the relationship.

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S6-5

Dinoflagellates in the genomic era: what do genomes tell us about their ecology and evolution?

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Dinoflagellates range from free-living, parasitic to symbiotic species in a broad spectrum of trophism. Genome data from dinoflagellates offer clues to how molecular and evolutionary mechanisms contributed to their diversification to occupy distinct ecological niches. Genomes of dinoflagellates are large (some over 200 Gbp), complex and exhibit idiosyncratic features compared to other eukaryote genomes. They had long been out of reach of academic researchers until recently, due in part to the time and cost of generating high-quality assemblies. Dinoflagellate research is entering a new genomic era, with the recent availability of chromosome-level genome assemblies, and more genome data from more-broadly sampled taxa are expected. To date, we have generated genome data from 14 taxa of dinoflagellates: 12 from family Symbiodiniaceae (known for their symbiotic associations with corals and other marine organisms), two from the sister lineage *Polarella*. Our comparative genomic analyses thus far have uncovered extensive genomic divergence among Symbiodiniaceae, reflecting the rapid evolution of these dinoflagellates and their phylogenetic diversity hidden behind subtly different morphology. Our results also reveal conserved gene functions related to symbiosis and meiosis, tendency of genes encoded in unidirectional clusters, and tandemly repeated single-exon genes in the genomes. In this presentation, I will discuss how our knowledge of genomes is elucidating the molecular and evolutionary mechanisms that underpin the ecological and genetic diversity of dinoflagellates and their adaptation to changing environments, and how other genomic technologies can help address key question of how dinoflagellates evolved to become some of the most ecologically successful organisms.

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