

Assessing the genetic diversity of zooxanthellae associated with host coral species in Perhentian Island

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Reef corals are hosts to a group of exceptionally diverse dinoflagellate symbionts in the family Symbiodiniaceae, consisted of numerous genetic “clades” that are now partitioned into a total of nine genera. These symbionts are critical components of the coral reef ecosystem. Loss of these symbionts in their coral hosts during the stress-related bleaching events can lead to mass mortality of the coral hosts and collapse of the coral reef ecosystem. It is therefore essential to characterize the partnership between the coral hosts and the zooxanthellae genetic clades under elevated SST. In this study, 14 genera coral fragments were collected from Perhentian Islands Marine Park, Terengganu, Malaysia. Here, we applied next generation sequencing of the nuclear-encoded ribosomal RNA gene in the second internal transcribed spacer (ITS2) region to elucidate the genetic diversity of this dinoflagellate endosymbionts. Our results revealed that Clade C (*Cladocopium*) were predominant, but with exception in some specimens. Clade D *Durusdinium*, a stress-tolerant symbiont, was also found to be dominant in some coral species such as *Diploastrea* and *Pocillopora*. While the findings are not generalizable beyond the samples examined in this study, it provides a baseline data on the diversity of endosymbionts and the host coral species in Perhentian Island, and further our understanding of their potential adaptive capabilities in tropical coral reef system.

Expansion of emerging HABs in Asian waters--opportunity for more cooperation between China and ASEAN countries

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Understanding how environmental change affect the marine ecosystem has become a key issue worldwide. Phytoplankton accounts for approximately 50% of the total photosynthesis on Earth and provides food for higher trophic levels. These photosynthetic micro-algae contribute to the removal of CO₂. The distribution of organisms is a particularly sensitive indicator of environmental change. The frequency of harmful algal blooms (HABs) caused by different micro-algal groups have been increasing especially for dinoflagellates. The scale of HABs in the last decade becomes much more extensive and toxic species have been recorded more frequently than ever before. Climate change together with human activities are considered as main responsible cause for inducing the phytoplankton change in the ocean which would quite likely result in changes of the structure and function of the marine ecosystem. Therefore, more regional cooperation and long-term monitoring on marine ecosystem particularly toxic phytoplankton in the ocean should be intensified.

Hypoxia-inducing microalgal blooms in the coastal ecosystem of Malaysia

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Coastal ecosystems are subjected to disturbance from land-derived or other coastal anthropogenic activities that lead to deterioration of water quality, nutrient enrichment, and development of microalgal blooms. In this study, two algal blooms induced hypoxic-anoxic events were confirmed for the first time in the Malaysian coastal waters, *viz.* Teluk Bahang, Penang and Johor Strait, Johor. High biomass algal blooms were observed in Teluk Bahang in August 2019. The diatom assemblages comprised *Proboscia* sp., *Rhizosolenia* sp., *Chaetoceros* sp., *Guinardia* sp., *Coscinodiscus* sp., and *Leptocylidrus* sp. The event caused serious economic damage to the mariculture industries with over 50 tonnes of cultured fishes. The dissolved oxygen (DO) levels in Teluk Bahang changed drastically over diurnal cycle; ranged from 8 during the day to 1.93 mg/L at dawn, owing to the high consumption of DO by respiration of algal biomass. In the innermost of the Johor Strait, the supersaturated DO and hypoxia conditions were observed, with >10mg DO/L during daytime while extremely low DO levels of 0.19–1.7 mg/L at deeper layers. Our findings based on the molecular investigation using metabarcoding approaches revealed the dynamics of algal communities at the innermost of the strait. The occurrence of high biomass microalgae has induced the formation of hypoxia-anoxia in the water due to over-consumed DO either through respiration or/and by microorganism decomposition. The spatial-temporal changes of the algal bloom-induced hypoxia events in Malaysian coastal waters required further investigations for better understanding of the potential socio-economic impacts as well as its adverse effects to the benthic organisms and the ecosystem health.

Hypoxia in Thai waters: A Case Study of the Upper Gulf of Thailand

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The coastal ecosystems, especially those adjacent to dense population regions are highly susceptible to eutrophication which often results in oxygen depletion, or hypoxia, and ocean acidification. Here we examined the hypoxic condition in the Upper Gulf of Thailand based on an extensive biogeochemical database generated via the collaboration of the Thai-China Joint Laboratory for Climate and Marine Ecosystem. We found that emerging hypoxia in the Tha Chin Estuary and the Chao Phraya Estuary, where DO concentrations were below 3 mg L^{-1} since 2008, primarily caused by increased nutrients loading from rivers (?) and local sewage discharged from the large Delta regions of the Chao Phraya. The hypoxia development was strongly correlated with southwest monsoon when abundant runoff discharges flow in the estuarine zone. In the coastal zone off the estuaries, phytoplankton bloom assimilated dissolved inorganic carbon (DIC) ($\sim 223 \text{ } \mu\text{mol kg}^{-1}$), raised $\sim 247.5 \%$ of DO saturation, and the partial pressure of carbon dioxide drawdown to $112.2 \text{ } \mu\text{atm}$ at sea surface water, whilst oxygen-depleted and DIC release occurred at the bottom water during November 2019.

Morphological study of Carukiidae (Cubozoa), Pelagiidae and Lobonemidae (Scyphozoa), and Physaliidae (Hydrozoa) from the coastal along the Andaman Sea and the Gulf of Thailand

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Jellyfish materials of Family Carukiidae (Cubozoa), Pelagiidae and Lobonemidae (Scyphozoa), and Physaliidae (Hydrozoa) were collected from coastal waters of the Andaman Sea and the Gulf of Thailand, during the period 2008–2020. The diagnosis of the Carukiidae as *Morbakka virulenta* were based on their thick and very long, ribbon-like tentacles, broad and long pedalia, and pear-shaped rhopalia niches. 929 Pelagiidae specimens were identified as *Chrysaora chinensis* by shape of their umbrellas, number or marginal lappets and tentacles, type and size of their tentacular nematocysts, while the other 353 were diagnosed as *Pelagia panopyra* based on shape of their cnidocyst warts, number, colouration and length of the tentacles. The type of intra-circular anastomosing canal network connections indicated that specimens of Lobonemidae belong to two separate species: *Lobonema smithii* and *Lobonemoides robustus*. Specimens of the Physaliidae, although unanimously placed in genus *Physalia*, exhibited four different morphologies distinguished by number of the fishing tentacles and length of the crest, i.e., *Physalis utriculus*, *Physalia* sp.1, *Physalia* sp.2 and *Physalia* sp.3.

Incidentally, this is the first description of *M. virulenta* from Thai water. According to the result of this study, the distribution range of *Pelagia panopyra* has also been extended from the center of the Indian Ocean (southwest of Chagos) to the Andaman Sea. The identities of the four *Physalia* species, however, still need further investigations.

Genetic diversity of the venomous jellyfish in Thai waters

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Surveys on venomous jellyfish in Thai waters suggested high species diversity, including approximately 11 species of 6 families in both Scyphozoa and Cubozoa. Explicitly identifying these venomous jellyfish, however, is difficult due to morphology plasticity, complicated life cycles and fragile tissues etc. And the unstable taxonomy in many jellyfish genera further confounded the species designation of the jellyfish, especially those morphologically divergent with the known species. In this joint program, we are going to study the genetic diversity of the venomous jellyfish observed in Thai waters, and evaluate the feasibility of DNA barcoding these jellyfish using the common genetic markers. The major objective of this project was to assist the taxonomy, and further facilitate the research on ecology, life cycle and toxicity of the venomous jellyfish in Thai waters. The initial data suggested capable of distinguishing these jellyfish using these markers. Whereas species designation of a number of samples remained unclear due to un-resolved taxonomy, highly scattered and incomplete genetic database across the various genera in Scyphozoa and Cubozoa. Therefore, it is necessary to conduct systematic study on the venomous jellyfish combining both morphology and molecular data.

DESCRIPTION OF THE MARINE FOOD WEBS IN BRUNEI BAY AS INDICATED BY STABLE ISOTOPES ANALYSIS ($\delta^{13}\text{C}$ AND $\delta^{15}\text{N}$)

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The application of stable isotope analysis (SIA) in studying the trophic dynamics of marine food webs is becoming more popular due to its convenience and advantages as compared to the conventional approaches such as gut content analysis, as it only provides recent dietary information of the organisms but do not reveal their long-term diet. The stable isotopes $\delta^{13}\text{C}$ values indicate the type of diet and the $\delta^{15}\text{N}$ values indicate the trophic levels in the food web. This study was conducted within the Brunei Bay waters, a sheltered bay that is important nursery, feeding and transient ground for dugongs, turtles, dolphins, and seabirds. The traditional fishing gear known as “Kabat” was used to collect the fish samples from two sites namely Bukit Sari and Awat-Awat. Circa 1 – 2 cm³ of muscle tissues were cut from each specimen and prepared for SIA. The mean values of $\delta^{13}\text{C}$ ranged from -15.62 ‰ to -23.11 ‰ in the food web components from Bukit Sari (BS), and from -17.06 ‰ to -23.72 ‰ in Awat-Awat (AA). Meanwhile, the $\delta^{15}\text{N}$ values ranged from 2.62 ‰ to 10.64 ‰ and 4.37 ‰ to 15.74 ‰ in BS and AA respectively. The highest trophic level in BS and AA were occupied by *Scomberoides commersonianus* (Talang Queenfish) from the Family Carangidae, and *Harpadon nehereus* (Bombay Duck) from the Family Synodontidae respectively. In general, higher trophic level was observed in AA as compared to BS, mainly due to the resource partitioning from the both sites. This study suggested that the food web of BS and AA relied on the benthic and planktonic resources respectively.

Effect of dietary lipid levels on replacing fish meal with soy protein concentrate in golden pompano *Trachinotus ovatus* diet

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A 7-week feeding trial was conducted to examine the effects of dietary lipid levels on replacing fish meal with soy protein concentrate (SPC) in diets for golden pompano *Trachinotus ovatus*. Eight isonitrogenous (465 g/kg crude protein) diets containing four lipid levels (65, 85, 105 and 125 g/kg) and two fish meal levels (diet C contained 280 g/kg fish meal, and 50% of the fish meal in diet C was replaced by SPC) were designed. In fish fed diets C (C6, C8, C10) and S (S6, S8, S10), the weight gain and NRE increased, while feed intake, FCR and nitrogen waste decreased with the increase of dietary lipid level. At the same dietary level, no significant differences were found in weight gain, feed intake, FCR, NRE, condition factor, hepatosomatic index, body contents of crude protein and ash, and nitrogen waste between fish fed with different fish meal inclusion diets (C6 vs. S6; C8 vs. S8; C10 vs. S10; C12 vs. S12). This study reveals that the suitable dietary lipid level and fish meal level for golden pompano reared in inshore net pens should be 105 g/kg and 140 g/kg, respectively, and increasing dietary lipid level could improve fish meal replacement by SPC.

Genetic diversity of dugong (*Dugong dugon*) along the sea coasts of Thailand

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Dugong (*Dugong dugon*) populations have been shrinking globally, due in large part to habitat fragmentation, degradation and ocean pollution. Determining genetic diversity in the remaining populations is essential for conservation planning and protection. In this work, measures of inter-simple sequence repeat (ISSR) markers, mtDNA D-loop and microsatellite markers were used to evaluate the genetic diversity of 118 dugongs from skin samples of deceased dugongs collected in Thai waters over a 29-year period. Thirteen ISSR primers revealed that dugongs from the Andaman Sea and Gulf of Thailand exhibited more genetic variation in the first 12 years of the study (1990-2002) compared to the last decade (2009-2019). Populations in Trang, Satun and some areas of Krabi had highest diversity compared to other regions of Thailand. The dugongs from the Andaman Sea were genetically distinct, with a separate haplotype belonging to two clades found only in Thai waters that separated from other groups around 1.2 million years ago. The dugong populations in the Sea of Thailand are experiencing some levels of inbreeding, and so may warrant special protections. Genetic diversity of dugongs in present times was less than that of past decades, likely due to increased population fragmentation. We need to improv *in situ* conservation actions to sustain genetically healthy wild populations.

Solving Mysteries of Sea Turtle Life History in the South China Sea

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Despite being charismatic animals that cross oceans around the globe, sea turtles begin their life in underground nest. Upon hatched, sea turtle hatchlings must dig out to escape the nest and consumes a large amount of the residual yolk. Over 50 years ago, scientists suggested that ‘social facilitation’ within the nest played an important role in conserving energy of hatchlings in nest escaping. However, empirical evidence for the existence of mutual benefits to individual hatchlings during nest escape has been limited. Our study provides new insight into sea turtle hatchling synchronous activity during nest escape, and how it influences the energetic cost of nest escape. This study now entered the new niche research area by incorporating animal energetics data into simulation modelling software to predict oceanic dispersal of our hatchlings in the South China Sea. We modelled the dispersal range of green turtle hatchling from Redang Island, Malaysia in various monsoon season using the particle-tracking program Ichthyop v3.2 and ocean surface current output from HYCOM (Hybrid Coordinate Ocean Model). The simulated hatchlings are distributed north into the Gulf of Thailand during the Southwest monsoon, while during the Northeast monsoon, the simulated hatchlings travel south into the Java Sea. By quantifying hatchlings potential energy, they can swim 116 km and can last up to seven days

Bryde's Whales (*Balaenopter edeni*) in The Upper Gulf of Thailand and The Beibu Gulf, Photo ID comparison

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Bryde's whales (*Balaenopter edeni*) as an important marine mammal in marine ecosystems, generate income for local communities and countries an important research and learning area. Bryde's whales were found in Thai coastal areas, in the Gulf of Thailand coast and in the Andaman sea coast. Bryde's whales is marine mammal migratory species or wind free home rang. The Bryde's whales population assessment requires cooperation from countries in the region to effectively collect population data. In 2017, there were reported of encountering Bryde's whales in the Beibu Gulf of China. Bryde's whales population in the Beibu Gulf was identify with Photo identification to compare the population of Bruda whales found in the upper Gulf of Thailand. Under the Department of Marine and Coastal Resources and Guangxi Academy of Science, China collaboration.

Photo identification technique was used to compare between Bryde's whales population in the Upper Gulf of Thailand and in the Beibu Gulf of China during 2017-2021. The technique provide identification of each Bryde's whale through specific characters such as shape of dorsal fins, Scar on mounts bodies or dorsal fins, mark on lips or black stripes or black spots or black stipes on palates, the result has distinguished 61 individual whales in the Upper Gulf of Thailand and 40 individual whales in the Beibu Gulf of China. The comparison between the two populations. Therefore, it can be concluded that the population of Bryde's whale in the Upper Gulf of Thailand and the population of Bryde's whales in the Beibu Gulf of China are the different ones.

Smart Perception of the Marine Ecosystem

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The complexity of marine ecosystem requests humans to obtain and analysis of big data in order to gain effective perception. The seas in Southeast Asia, connecting the Indian and Pacific Oceans, accommodate rich marine mammal species that lie on apex of the trophic levels and signal healthy ocean. There are also diverse coral reefs that support local communities' welfare. Notwithunderstanding, we are short of methods and knowledge on them and this has been limiting relevant science advances and supporting of society development. To overcome the problem, we propose smart perception methods including the WALA perception framework including unmanned sailboat etc. for marine mammals, and a real-time remote monitoring system for coral reef biodiversity and bleaching. The proposal is laid on the foundation of our recent research and cooperation. We expect to develop our partnership on smart perception of the marine ecosystem and contribute to the UN Decade of Marine Science for Sustainable Development.

The 1st microplastic survey in offshore of Andaman coastal of Thailand

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Department of Marine and Coastal Resources (DMCR) have monitored microplastic in seawater, sandy beach, and in marine organisms for several years. Most of the study sites are located in the coastal area. Then this study aim to determine density and types of microplastic in offshore area, during 1-5 March 2021, a cruise was conducted to the Andaman Sea in the project Ocean Forecasting and Marine Disaster Mitigation System of Southeast Asia Seas, which is under collaboration between Thailand and China. During the cruise, Samples were collected from five stations one of which is located as far as 150 nautical miles from PhangNga coast. To collect the samples, Manta net was towed for 10 minutes each time and then repeated thrice for each station. Results show that the density is between 0.12 and 0.50 piece/m³, and the average is 0.27 ± 0.18 piece/m³ (average \pm standard deviation). Dominant types are Polypropylene (46.2%), Polyethylene (26.3%), and Polystyrene (24.8%). Dominant shapes are fragment (73.7%), foam (22.9%), and fibres (3.4%). Polypropylene fragment are the most dominant, followed by Polystyrene foam. Meanwhile, fiber from textile and fishing gear are very rare. In addition, visual observation of floating marine debris was also conducted to examine micro and macro debris distribution in the offshore area in the Andaman Sea.

Microplastic Research in the South China Sea and Importance of Protocol Standardization

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Marine plastic pollution is a global, transboundary problem. It poses a growing threat to the marine ecosystem and potentially to human health. The South China Sea (SCS) is a hot spot for plastic pollution study. As an important part of plastic pollution, microplastic pollution remains under-studied. These small pieces of plastics which are usually smaller than 5 mm in the longest dimension have far more impact on the marine ecosystem. Understanding the current microplastic pollution status is important for countries in the region to assess potential marine environmental threat. Studies on the input, transfer, accumulation and sink of microplastic in the SCS will help us to fill the information gap and find ways to deal with the problem. However, recognizing the large variation in data acquired from different research groups needs special attention. A review on the microplastic research done in the SCS will be presented. At the same time, sources of data variation will be discussed to better understand the importance of using standardized sampling and analytical methods.