

Application of Novel technologies developed in the CREST program for the preservation and regeneration of marine biodiversity to the Fisheries fields

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The CREST Program of “Establishment of core technology for the preservation and regeneration of marine biodiversity and ecosystems (Research supervisor: Isao Koike (Professor Emeritus, The University of Tokyo)) was launched in 2011. In the total, 16 projects were adopted, and many novel technologies for observation and monitoring and prediction models have been developed for the better understanding of biodiversity and ecosystems. On the other hand, some of them are expected to become powerful tools for sustainable use for fisheries resources. Decline of various fisheries resources is one of the major problems for the fisheries industries. As increasing in the demand of fisheries products in the world, even the small pelagic fish resources such as saury mackerel and Pacific common squids off the Pacific coast of the North east Japan have been incorporated in the framework of international fisheries management based on the scientific basis. As a result, importance of monitoring to examine where and how the fisheries resources as well as other marine livings are distributed has been increased. This presentation will show the prospects and expectation for applying the technologies developed in this program to the fisheries fields.

Keywords: marine biodiversity, CREST, Fisheries field

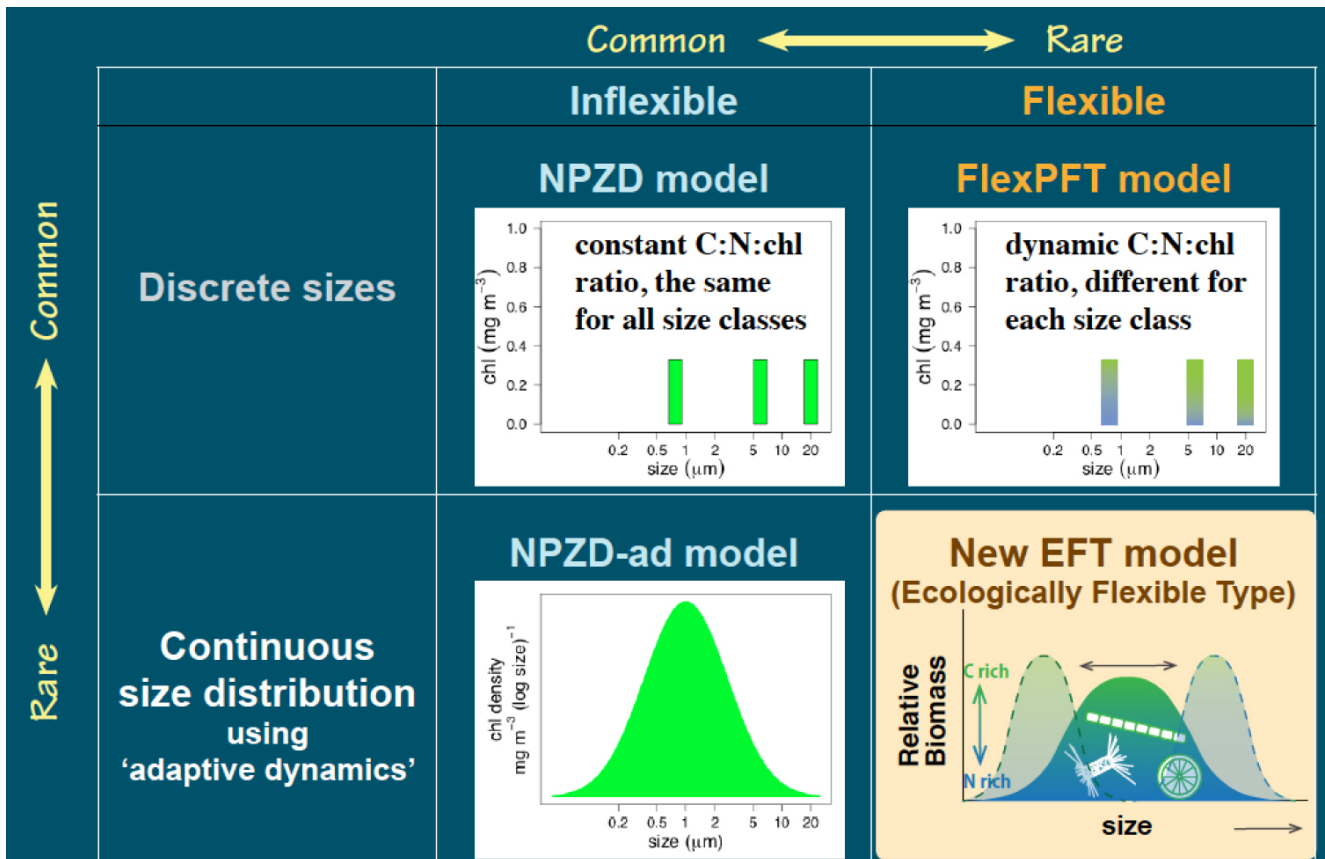
Untangling the effects of individual-level acclimation and inter-specific competition on the modeled dynamics of phytoplankton community size structure

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A variety of ecosystem models have been developed that resolve the size distribution of phytoplankton using multiple (now up to hundreds of) discrete size classes. Although such models have proven useful as research tools, they require a great many calculations for large-scale and long term modeling studies. As an alternative, continuous size-distribution models, which require many fewer calculations, could in principle be used for faster large-scale simulations. However, few such models even exist, and their ability to reproduce observations has not been well tested. This study compares the discrete and continuous approaches, and furthermore aims to clarify the relative importance of acclimation (at the individual or species level) and competition between multiple size-classes (or species) for the dynamics of size-based phytoplankton communities. We compare the performance of discrete and continuous size-distribution models, each formulated with and without flexible physiological response (acclimation) for each size class. All four models were implemented in a 0-D (box) model of the oceanic mixed layer and fitted to data from two contrasting time-series observation stations in the North Pacific, including size fractionated chlorophyll observations. Unexpectedly, the continuous size distribution model with acclimation reproduces the observations better than the corresponding discrete model. However, accounting for acclimation response makes more difference for model results than does the choice of discrete or continuous size representation. Finally we compare modeled relationships to observed patterns of size-fractionated chlorophyll vs. total chlorophyll, to clarify how the acclimation response and inter-specific competition impact the dynamic size structure of phytoplankton communities.

Keywords: ecosystem model, biodiversity, adaptive dynamics, chlorophyll



Radiocarbon value as an indicator of carbon sources during breeding of Japanese chum salmon (*Oncorhynchus keta*)

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There has been increasing interest in understanding the responses of Pacific salmon to marine climate variation. Chum salmon (*Oncorhynchus keta*) is the second most abundant salmonid in the North Pacific Ocean, and important for the fisheries in the northern Japan (especially Hokkaido and Iwate). For migrating animals like salmon, breeding strategy would be one of key factors for their sensitivity to changing environments. Do they prepare their eggs from recently ingested nutrients during/after migration to Japan ('income' breeders) or from body stores which are mainly produced in the Bering Sea ('capital' breeders)? Here, to address this important ecological question, we propose radiocarbon analysis as a new useful method to locate oceanic regions where Japanese chum salmon obtained their carbon resource. To our knowledge, this study is the first study to utilize radiocarbon ($\Delta^{14}\text{C}$) value as an indicator of salmon ecology in the ocean. We determined bulk $\Delta^{14}\text{C}$, $\delta^{13}\text{C}$, and $\delta^{15}\text{N}$ values of muscle and gonad (eggs) samples from female chum salmon collected during October-December 2015 at Otsuchi Bay, Japan. We also analyzed bulk $\Delta^{14}\text{C}$ values of plankton net samples collected in the Bering Sea, to constrain the $\Delta^{14}\text{C}$ values of salmon's diets in the Bering Sea. The gonad samples generally showed lower $\Delta^{14}\text{C}$ values, which overlap with the range of the plankton net samples in the Bering Sea. On the other hand, the muscle samples generally showed higher $\Delta^{14}\text{C}$ values, which overlap with the range of fishes collected around Sanriku area, Japan. These results suggest that Japanese chum salmon (at least individuals from Otsuchi Bay) produce eggs mainly using the carbon resource obtained in the Bering Sea before migration to Japan (i.e., capital breeders), while their muscle tissues are affected by feeding around Japan.

Keywords: Radiocarbon, Isotopic Analysis, Marine Ecology, Salmon, Bering Sea, Otsuchi Bay

Ecological study of Whale and Marine mammals using radiocarbon

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North Western Pacific including off Japan is rich in biodiversity due to high productivities induced by ocean currents such as Oyashio and Kuroshio. Marine mammals are living in this part of ocean and their ecology have been gradually revealed because of advances in technology such as GPS tagged logging devices. In Hokkaido, stranding of marine mammals are reported occasionally and *The Stranding Network Hokkaido* have been conducted their activity documenting species to better understand their ecology. However ecological information of stranded individuals had not been able to disclose as is an critical data to preserve the marine ecological systems.

Radiocarbon is produced in upper atmosphere and distributed around the world via carbon cycles. North Pacific ocean waters have distinct radiocarbon values because of global ocean circulation. Namely radiocarbon depleted water is existed in Oyashio region due to the influence from upwelled deep Pacific water, whereas higher radiocarbon is characterized in the Kuroshio region.

A single stage accelerator mass spectrometry was installed at Atmosphere and Ocean Research Institute, the University of Tokyo since 2013 and radiocarbon measurements for large number of samples now can be achieved. We have been applying radiocarbon based ecological study for marine organisms including stranded marine mammals. The results show clear picture where they have been migrated as well as their dietary information and we introduce several recent results using this techniques.

Keywords: Ecology, Radiocarbon, Whale

Migration history of sardine reconstructed from carbon-14 as a tracer

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Radiocarbon concentration of DIC in seawater can be varied depending on the location due to the global ocean circulation. Since it takes around 1,000 years to travel around the world the area that is influenced from upwelling water is depleted in radiocarbon owing to the decay since the last contact with the atmosphere. Oyashio water is such location thus the large difference between Kuroshio water is existed. Fish captures these signals during their lifetime via the marine food web hence it is possible to identify their ecological information including migration histories.

We applied this concept using improved radiocarbon techniques using Single Stage Accelerator Mass Spectrometry installed at the Atmosphere and Ocean Research Institute, University of Tokyo (Yokoyama et al., 2016 PNAS). Groups of sardine captured off Japan were used and clearly identified two different types namely the one that was born in Kuroshio region from winter to spring and traveled to the north where Oyashio water is dominant, whereas the other group remained entire time before captured by fisherman. This is the first time to distinguish individual life history of sardine in quantitative manner and shows strong promise of radiocarbon based ecological studies of fish migration.

Keywords: Radiocarbon, Isotopic Analysis, Marine Ecology, Sardine

Biology of a picoeukaryotic phytoplankton, Parmales, a sister group of diatoms

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Parmales is a group of pico-sized eukaryotic marine phytoplankton with cells surrounded by several silica plates. Parmales has been found widely in the world's oceans, from polar to subtropical regions, and is frequently abundant in polar and subarctic regions. Based on similarities in cell wall structure, Parmales has been proposed as a close relative to diatoms, which are the most successful phytoplankton group in modern oceans. However, there was very little biological information on Parmales, because no cultures were available for laboratory study. Recently, we successfully established the first ever culture of Parmales isolated using a fluorescent silicon tracer PDMPO from the Oyashio water in the Western Subarctic Pacific. SEM and TEM observations, molecular phylogenetics and photosynthetic pigments analyses of this culture indicated that Parmales belongs to Heterokonta and is positioned within a sister group of diatoms, Bolidophyceae, which are pico-sized autotrophic naked flagellates mainly living in subtropical waters. It can be hypothesized that parmalean and bolidophycean algae (or their common ancestor) have a life cycle that switches between silicified non-flagellated and naked flagellate stages. This hypothetical life cycle has similarities to centric diatoms, which are an ancient lineage that has a vegetative stage that switches to production of naked flagellated male gametes (spermatozoa) for sexual reproduction. Because the origin of the silica cell wall and the early evolution of diatoms are not yet fully understood, Parmales may play a key role in answering these questions. We present an overview of our current study of the biology of Parmales to explore the evolutionary link between Parmales, Bolidophyceae and diatoms using ecological, physiological, genomic, metagenomic and biogeochemical approaches.

Keywords: Ocean, Phytoplankton , Diatom, Evolution, Ecology

Selection of ecologically or biologically significant marine areas for kelp forest ecosystem in northern Japan through assessment and future prediction of species distribution

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The present study aimed to carry out quantitative estimation of biodiversity in kelp forest ecosystems in Japan, along with future prediction of their changes with different IPCC scenarios of climate change, and selection of the ecologically or biologically significant marine areas (EBSAs), based on the combination of biodiversity database analyses, species distribution and future projection models. We first constructed a database of the distribution of algal species in Japan which contained a total of 28,358 data, and used them to estimate the distribution of each kelp species over the coastline of Japan by species distribution models. Species diversity of kelps was the highest in northern and eastern Hokkaido. Variation in water temperature is the most influential factor responsible for the estimated distribution patterns. Based on the obtained statistical relationship between the distribution and multiple environmental factors, we then forecasted future distribution of major kelp species with different scenarios of climate changes by IPCC. Distribution of kelp species was predicted to move northward and cold-current species would disappear from coasts of Japan by 2100. As a result, kelp species diversity in Japan was predicted to decrease greatly with ongoing climate changes. Finally, we selected EBSAs for kelp forest ecosystems along the whole coastline of Japan, by developing protocols to combine different multiple criteria based on scientific information. EBSAs selected based on current kelp distributions included coastal areas in Hokkaido, Sanriku, Izu Peninsula, eastern Kii Peninsula, and northwestern Kyushu. We also developed an additional EBSA selection method incorporating the future shift of species distribution with climate change, which revealed that kelp forests in eastern and southern Japan would not be selected as EBSAs. We expect that the obtained results would contribute to planning long-term conservation and management strategies, as well as adaptation programs of kelp forests in Japan.

Keywords: Biodiversity, Coastal ecosystem, Water temperature rise, Scenario analyses, EBSAs

Predicting potential fish distributions in the western North Pacific: an attempt to construct species distribution models using commercial fisheries data

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Understanding the effects of ocean conditions on distributions of commercial fish is critical for elucidating potential distributions of fish and forecasting where they will be in the future. Species distribution modellings (SDMs) enable estimation of habitat suitability for each species at a site as a function of environment factors. Traditionally modelling of species distribution has been applied to species data surveyed through standardized methods that could collect both presence and absence records, but was incapable for using presence-only data, such as those collected from fisheries or citizen monitoring schemes. Maximum entropy (MaxEnt) model provides high predictability using a presence and pseudo-absence data, which relatively fewer studies applied it to marine areas than terrestrial fields. We developed MaxEnt model to relate the occurrence records from fisheries data obtained in the western North Pacific with environment condition such as annual sea temperature and salinity from Four-dimensional Variational Ocean ReAnalysis for the Western North Pacific (FORA-WNP30), and topology. Our model indicated *Sebastolobus macrochir*, for instance, was influenced by both ocean conditions and topology, and would potentially distribute in the area where was no catch record. MaxEnt models will contribute to infer the probability of species using data of which detection was imperfect.

Keywords: ecological niche modelling, habitat suitability, sampling bias, fisheries data, mapping

Development of habitat suitability index models of demersal fishes off the eastern coast of Japan

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An accurate estimation of a potential habitat of fish species enables us not only to understand the response of species to environmental changes but also to utilize it for an efficient use of fish resources. Habitat suitability index (HSI) model is widely used as tool in ecological impact assessments, ecological restoration studies, and practical exploration of potential fishing zone. It describes the relationships between fish abundance and ocean environmental variables and then estimates the level of habitat suitability as an HSI score representing “poor” to “good” habitat qualities. In this study, we developed the HSI models for several species of demersal fishes off the eastern coast of Japan by applying several machine learning algorithm to Japanese commercial fishery dataset compiled by Tohoku National Fisheries Research Institute, Japan Fisheries Research and Education Agency, that includes trawling catch data of more than 30 species of demersal fishes. In addition, we used an ocean reanalysis dataset FORA (4-dimensional variational Ocean Re-Analysis)-WNP30 produced by JAMSTEC/CEIST and MRI-JMA. The horizontal resolution is 0.1*0.1 degree of latitude and longitude with 54 vertical levels, which can provide realistic fields of 3-dimensional ocean circulation and environmental structures including ocean bottom layers up to 1500m depth. We investigated the HSI response of several species to ocean environmental changes occurring off the eastern coast of Japan. The results indicated that the habitat distributions of *Pseudopleuronectes yokohamae* and *Mlicrostomus achne* could be influenced by the Oyashio intrusion occurred in 2012 winter.

Keywords: habitat suitability index model, demersal fish, FORA

Global and local activities to collect and share marine biodiversity information

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In response to the concerns to marine environment issues, information on marine biodiversity has become more important. Ocean Biogeographic Information system (OBIS; <http://www.iobis.org/>), a project under the International Oceanographic Data and Information Exchange programme, is currently recognized as one of the global framework to integrate information on marine biodiversity. Since the establishment of OBIS, oceanic area of interest which requires biodiversity information has been largely changed from time to time: coastal area in the discussion of setting marine protected area, arctic area in the discussion of global warming, or deep sea in the discussion of the areas beyond national jurisdiction. For such interests or discussions, OBIS contributes by providing reliable scientific information which covers from tropical to arctic area, from coastal to offshore area, and from surface to bottom layer.

Information in OBIS is an aggregation of datasets provided from local nodes. Japanese OBIS node was launched in 2012, and provides data obtained from Japanese research activities through an information system of BISMAL (<http://www.godac.jamstec.go.jp/bismal/j/>). The data from Japanese node is characterized by its high quality and its wide spatio-temporal coverage. For example, “JODC Dataset” : a large dataset on plankton which cover the western Pacific in 1971-2006; “Asia-Pacific Dataset” : marine organism occurrence data of the Asia-Pacific region extracted from literature in 1820-2014; “Marine Biological Sample Database” : a catalog of specimen collected from deep sea in 1982-2016. In addition, ecosystem-specific datasets such as seagrass, coral and kelp species around Japan are also being established in BISMAL. BISMAL currently published total 445,993 occurrence records with 5,992 marine species. This means BISMAL have information on 20% of all known marine species around Japan (marine species is estimated at about 33,000 species).

As a recent challenge in OBIS activities, OBIS started to collect a different type of information related to marine biodiversity. OBIS has basically collected occurrence records of marine species which compose of “Scientific name” , “Event date” , “Latitude” , and “Longitude” . However, to answer recent scientific needs, OBIS adopted a new data format that allow handling more complex data structure including both occurrence record and occurrence related environmental data. It is expected that an accumulation of such data enables to conduct combined analysis with biological and environment variables in global scale.

Keywords: marine biodiversity, database, OBIS