11.4

Center for Condensed Matter Sciences, NTU

11.5-6

Howard Civil Service International House

2019 4th ASIAN MARINE BIOLOGY SYMPOSIUM

Symposium Program

2019 4th ASIAN MARINE BIOLOGY SYMPOSIUM

Contents

Welcome Messages

On behalf of the local organizing committee of The Fourth Asian Marine Biology Symposium (AMBS), I would like to welcome all of you to the Fourth Asian Marine Biology Symposium to be held in Taipei, Taiwan, between November 4 and 6, 2019.

Because surrounded by ocean, Taiwan has fruitful marine resources and strong aquacultural industries. Recently, the ecology and ecosystem services at both marine and coastal areas has drawn increasingly attentions. Thanks to the help of previous AMBS organizing committees, especially Dr. Hiroaki Tsutsumi and Dr. Suriyan Tunkijjanukij, it is very pleased for us to have AMBS in Taipei to not only promote the interactions and collaboration among the communities of marine biologists and ecologists in Asian regions, but also to enhance the friendships between scholars in Taiwan and Asian countries.

I am looking forward to seeing you all in Taipei for a scientifically stimulating and socially enjoyable meeting.

Professor Hwa-Lung Yu
Chairman, the 4th AMBS organizing committee
Director, Ecological Engineering Research Center,
Department of Bioenvironmental Systems Engineering,
College of Bioresources and Agriculture, National Taiwan University

More Welcomes and Greetings from Previous AMBS Chairmans

Professor Hiroaki Tsutsumi
The chairman of the 3rd AMBS organizing committee
Faculty of Environmental and Symbiotic Sciences,
Prefectural University of Kumamoto,
Kumamoto, Japan

In Phuket, Thailand, in December 2013, Asian Marine Biology Symposium started to promote the exchange of information of the most recent achievements on the research in the fields of biological studies of marine and coastal areas in the Asian countries.

Very fortunately, due to the big efforts and cooperation of various researchers in various countries, this symposium has been held regularly (The 2nd in Jeju, Korea, in October 2014, The 3rd in Kumamoto, Japan, in November 2017). It is a great pleasure that we are able to have the fourth symposium in Taipei, Republic of China (Taiwan), between November 4 and 6, 2019. I would like to appreciate deeply to the efforts for preparation and management for the symposium held in Taipei by the members of the local committee of the symposium and the staff of Taiwan National University.

One of the most important things for us to meet each other regularly, and talk and discuss about the most interesting issues on the research of each other with the participants that we cannot meet to meet frequently. We are able to learn many things from the people with different sense, knowledges, experiences, techniques, and ways of thinking in research. I hope that all of the participants enjoy to get the latest information of various studies related to the biological studies in marine, coastal seas, estuaries, and related aquatic environment in Asian countries through this symposium in Taipei.

I am looking forward to seeing all of you soon at the symposium and having an exciting time to talk.

Professor Emeritus Jae-Sang Hong
Department of the Ocean Sciences,
College of Natural Science, Inha University
Incheon 22212, Republic of Kore

The Asian Marine Biology Symposium were dedicated to promoting researches in various topics in the field of marine biology and ecology and facilitating communications especially among the Asian marine biologists to protect, and ensure the sustainable use of our regional seas. These goals were possible by convening conferences to discuss a variety of issues and share ideas through the research collaboration and information exchanges on the regional and global issues in our coastal regions.

In fact, the past three Asian Marine Biology Symposia (The 1st in Phuket, Thailand, in 2012, The 2nd in Jeju, Korea, in 2014, and The 3rdin Kumamoto, Japan, in 2017) served as a source of current issues on coastal matters by addressing not only the local and regional marine biological phenomena, but also the global issues such as biological invasion, tsunami, hypoxia, and ocean acidification etc…

To me, as one of the international organizing committee (Scientific Committee) members, it is really a great pleasure for the 4th AMBS to be continued, and held in Taipei, Republic of China (Taiwan). I sincerely congratulate the meeting, and hope many Asian marine biologists participate in this event and it will be a great success.

I would like to express my appreciation to the supports and efforts for preparation of the 4th AMBS by the members of Local Organizing Committee of the symposium and the staff of Taiwan National University.

I would like to express my appreciation to the supports and efforts for preparation of the 4th AMBS by the members of Local Organizing Committee of the symposium and the staff of Taiwan National University.

I am looking forward to seeing all the participants at the symposium, and enjoying a talk with you.

Assistant Professor Suriyan Tunkijjanukij
The chairman of the 1st AMBS organizing committee
Faculty of Fisheries, Kasetsart University
Bangkok, Thailan

Since the first Asian Marine Biology Symposium (AMBS) in Phuket, Thailand, in December 2012, followed by the second one in Jeju, South Korea, in October 2014, and the third one in Kumamoto, Japan, in November 2017, this symposium has gained many fruitful achievement for promotion of the exchange of scientific information, discussion on various approaches to the future studies and collaboration in research among marine biologists and marine environmental scientists in Asian countries.

I then hope that the fourth symposium in Taipei, Republic of China (Taiwan), between November 4 and 6, 2019 could provide more chance of further active exchange of the researchers studying various issues including basic research fields of marine biology, application fields of marine fisheries, and environmental issues in the coastal seas, among the Asian countries.

I believe that the efforts to continue AMBS will strengthen our academic society, and encourage collaboration among the researchers in these fields in the Asian region as well as those in the European and American regions.

In future, I hope that the symposium will grow fast and regularly catch the attention of many marine biologists and marine environmental scientists not only of Asian countries but also all over the world. Such activity will strengthen our academic society to have an efficient exchange of research information and will encourage collaboration among marine biologists working in a wide range of issues in marine biology in both regional and global scales.

I believe that the efforts to continue AMBS, especially the coming one this year in Taipei will strengthen our academic society, and encourage collaboration among the researchers in these fields, not only in the Asian region, but also in other region worldwide. I would like to meet and welcome all of you again to the Fourth Asian Marine Biology Symposium to be held in Taipei, Republic of China (Taiwan) between November 4 and 6, 2019. I look forward to seeing all of you soon at the symposium.

Symposium Schedule

Symposium venue

Day 1 (Nov. 4): Center for Condensed Matter Sciences, National Taiwan University
Day 2 (Nov. 5) and Day 3 (Nov. 6): Howard Civil Service International House

November 4 (Mon)

13:00 ~ 14:30	Registration at Center for Condensed Matter Sciences, NTU
14:30 ~ 14:50	Opening Ceremony
15:00 ~ 15:40	**Keynote Speech by Thamasak Yeemin, D.Sc.**
15:40 ~ 16:20	**Keynote Speech by Waka Sato-Okoshi, Ph.D.**
16:20 ~ 17:00	**Keynote Speech by Hsing-Juh Lin, Ph.D.**
17:00 ~ 17:30	Q&A
18:00 ~ 20:00	Welcome Party at Garden Cafeteria, 1F Howard Civil Service International House

November 5 (Tue)

08:30 ~ 09:00	Registration at Howard Civil Service International House
09:00 ~ 10:30	**Session A1 @ Room 101 | Session B1 @ Room 103**
10:30 ~ 11:00	***Coffee Break***
11:00 ~ 12:30	**Session SC1 @ Room 101 | Session S1 @ Room 103**
12:30 ~ 13:30	***Lunch***
13:30 ~ 15:00	**Session SC2 @ Room 101 | Session S2 @ Room 103**
15:00 ~ 15:30	***Coffee Break***
15:30 ~ 17:30	**Poster Presentation** Ⅰ

November 6 (Wed)

08:30 ~ 09:00	Registration at Howard Civil Service International House
09:00 ~ 10:30	**Session A2 @ Room 101 | Session B2 @ Room 103**
10:30 ~ 11:00	***Coffee Break***
11:00 ~ 12:30	**Session C @ Room 101 | Session D @ Room 103**
12:30 ~ 13:30	***Lunch***
13:30 ~ 15:15	**Session E @ Room 101 | Session F @ Room 103**
15:30 ~ 17:00	**Poster Presentation** Ⅱ
17:40 ~	Closing Ceremony & Banquet at Yueshiang Restaurant, 2F Howard Civil Service International House

Conference Information

Registration Information

For all registered participants, the symposium packages will be available at the registration desks. The desks will be located at the International Conference Hall at Center for Condensed Matter Sciences, National Taiwan University on Nov 4, and the Conference Area at Howard Civil Service International House on Nov 5, respectively. The symposium package contains symposium name badge, brochure, registration fee receipt, and relevant information.

The online registration can be available and please contact the conference staff for the further assistance.

Symposium name badge

Symposium name badge will be required to attend welcome party, banquet, and pick up lunch boxes.

- **Welcome Party Information**
  Date: November 4 (Mon), 2019
  Time: 6:00 pm
  Location: Garden Cafeteria, 1F Howard Civil Service International House
- **Closing Ceremony & Banquet**
  Date: November 6 (Wed), 2019
  Time: 5:40 pm
  Location: Yueshiang Restaurant, 2F Howard Civil Service International House

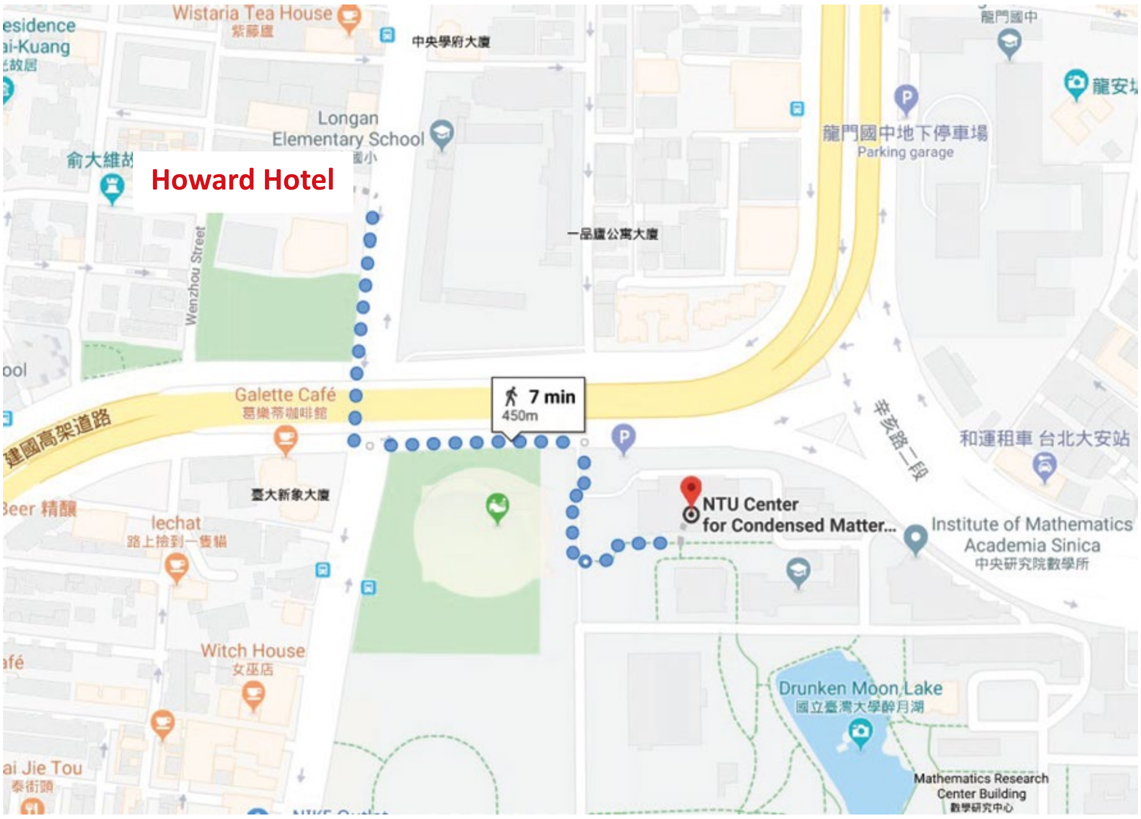
WiFi service

Free wifi service will be available at the conference area. Please follow the step-by-step instructions below

1. Find and connect to Howard-Meeting wireless service
2. Go to the login page at 192.168.254.253 with your browsers
3. Account name/password: Howard02/9dbqx8

Symposium Venue Map

Direction between
Opening Ceremony Hall (NTU Center for Condensed Matter Sciences)
and
Welcome Party (Howard Hotel)

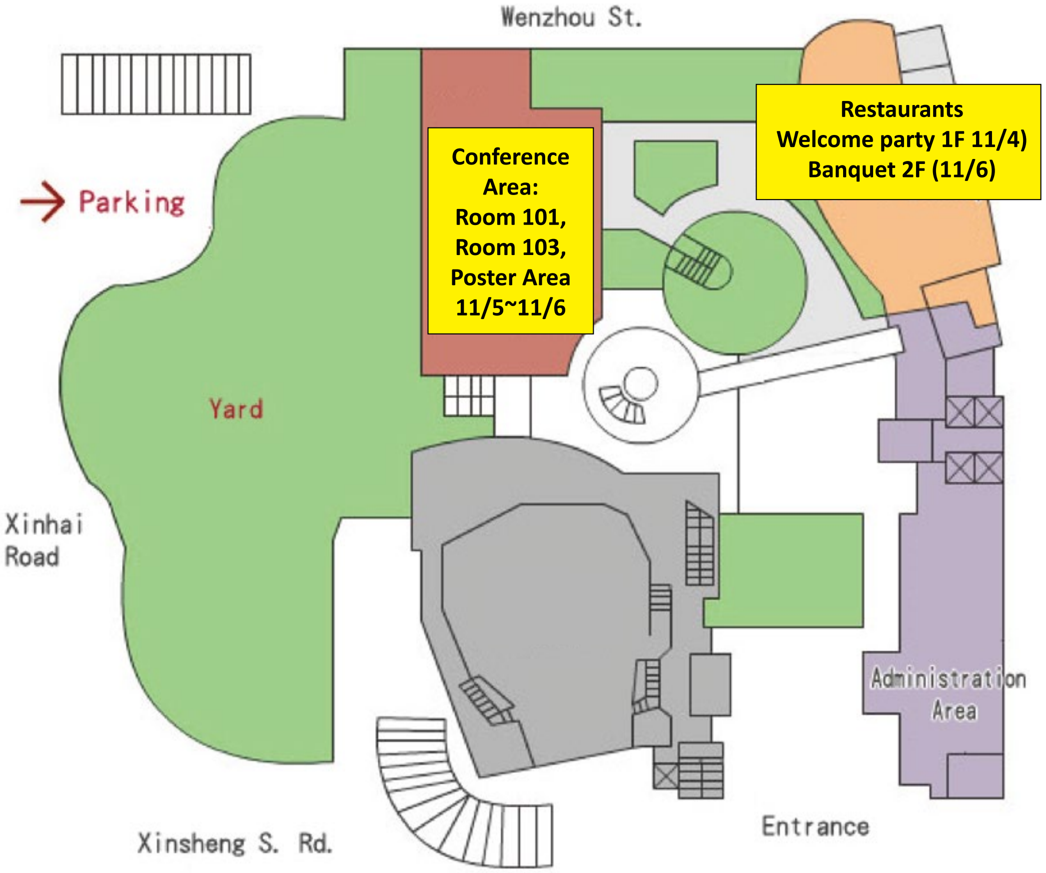


November 4 (Mon)

Registration at International Conference Hall (R204), Center for Condensed Matter Sciences, NTU

Symposium Venue Map

Room 101, 103, and Poster area are all located at the Conference Area



November 5~6 (Tue ~ Wed)

Registration at Conference Area, Howard Civil Service International House

Information for the Presenters

Oral Presentation

The presentation time is 15 minutes, including discussion.

The computer for presentation is available in each room.
Please upload your presentation file to the following link:
https://stemlab.bse.ntu.edu.tw/file/sharing/CR53zT3cc

Remarks:

You can also use your own computer but please come to test whether the file can be projected normally before the session starts.

Poster Presentation

The size of the poster is A0 (841 mm in width and 1189 mm in length).

Please put up a poster on the designated board before the poster presentation starts.
Please take off the poster right after the poster presentation ends.

Student Presentation Contest Rules

Student Oral Presentation Contest

Evaluation

1) Each presenation will have 12 minutes for presentation and 3 minutes for Q&A
2) The oral presentation will be evaluated based on:
   - Clarity of oral expression (1-5)
   - Professional knowledge (1-5)
   - Slide design (1-5)
   - Significance of the study (1-5)
3) The participant **must attend Room 101 in the designated time** and **can be disqualified if he or she is absent** during the time of oral competition session.

Student Poster Presentation Contest

Evaluation

1) The participant **must present his or her poster in the designated time** and **can be disqualified if he or she is absent** during the time of poster competition session.
2) The poster presentation will be evaluated based on:
   - Clarity of oral expression (1-5)
   - Professional knowledge (1-5)
   - Poster design (1-5)
   - Significance of the study (1-5)

Presentation Schedule

November 4th (Monday) Schedule
Center for Condensed Matter Sciences, NTU

Reception of the registration

13:00 ~ 14:30

Opening ceremony of the symposium

14:30 ~ 14:50

Keynote Speeches

Chairs: Dr. Sau-Wai Yam and Dr. Hsuan-Wien Chen

15:00 ~ 15:40

Speaker: Thamasak Yeemin, D.Sc.

Ecological resilience to climate change and anthropogenic disturbances: lessons learned from coral reef studies in the Western Pacific

15:40 ~ 16:20

Speaker: Waka Sato-Okoshi, Ph.D.

Global aquaculture activities can alter species distribution and marine ecosystem

16:20 ~ 17:00

Speaker: Hsing-Juh Lin, Ph.D.

The driving force for intertidal tropical seagrass beds over decadal timescales

Q&A Time

17:00 ~ 17:30 Chairs: Dr. Hsuan-Wien Chen and Dr. Sau-Wai Yam

Welcome Party at Howard Civil Service International House

18:00 ~

November 5th (Tuesday) Schedule
Howard Civil Service International House

Start Time	Room 101	Room 103
	Session A1 Biology and ecology of benthic animals and plankton (I) Chairs: **Yo-Jin Shiau** & **Naoko Isomura**	**Session B1** Assessment and conservation of coastal and estuarine (I) Chairs: **Chaolun Allen Chen** & **Nozawa Yoko**
09:00	A1-1 **Kenta Nakamoto,** Jun H, Tomohiko K.; Spatial variability in composition of brown algae along Sanriku Coast, northeastern Japan	B1-1 **Tzu-Hao Lin,** Florence E, Jhoanna J L,Claire A ,Pia C, Haazel A.; Ocean biodiversity listening project: an acoustic approach of marine ecosystem assessment
09:15	A1-2 **Gaël Dur,** Won E-J,Jeonghoon H, Lee J-S,Sami S.; Individual-Based Model for evaluating the post-traumatic effect of UV-B radiation on zooplankton reproduction.	B1-2 **Chaolun Allen Chen**; Unprecedent effort in conserving the critically-endangered caryophyllid coral Polycyathus chaishanensis (Scleractinia; Caryophyllidae) in the Datan algal reef, Taiwan
09:30	A1-3 **Tomohiko Kondoh,** Hirokazu A, Okoshi W- S.; Recolonization of two *Pseudopolydora* species (Annelida Spionidae) in relation to reproduction and larval development in a shallow, brackish and eutrophic lagoon after the 2011 tsunami	B1-3 **Osamu Miura,**Won E-J,Jeonghoon H, Lee J-S,Sami S.; Effect of the 2010 Tohoku earthquake tsunami on trematode community in the mud snail, *Batillaria attramentaria*
09:45	A1-4 **Naoko Isomura,** Taichiro Y.; The genes expression of hormone and neuronal transmitter receptor in relation to gametogenesis and spawning in *Acropora intermedia*	B1-4 **Felipe Monteiro Gomes de Mattos,** Thamasak Y.; Reef fish diversity in the Mu Ko Surin marine national park, Andaman sea, Thailand
10:00	A1-5 **Jun Nishikawa,** Mitsumi A.; Effect of posture on somatic growth and asexual reproduction in the polyp stage of *Aurelia coerulea*	B1-5 **Nozawa Yoko,** Villanueva R.D., Munasik Roeroe K.A, Mezak T, Kawai T, Guest J, Arakaki S., Suzuk G., Tanangonan J.J.B , P.O. ANG, Jr. P.; Latitudinal variation in growth and survival of juvenile corals
10:15	A1-6 **Chae-Lin Lee,** Yoo J-W.; Biogenic habitats as home for invertebrates: comparison of communities associated with tubeworms, oysters, mussels on Rocky shore of Masan Bay, Republic of Korea.	B1-6 **Machida Ryuji,** Matthieu L,Nancy K.; GenBank is a reliable resource for 21st century biodiversity research
10:30	***Coffee Break***	

Start Time	Room 101	Room 103
	Session SC1 Student Oral Presentation Contest (I) Judges: **Dr. Shiau Yo-Jin** **Dr. Mark Grygier** **Dr. Ichiro Imai**	**Session S1** Contributed Session: Biodiversity monitoring projects in shallow coastal habitats along the Japanese Coast Chairs: **Hsuan-Wien Chen** & **Kanaya Gen**
11:00	SC1-1 **Noboru Kitagawa,** Tsutsumi H,; The impacts of physical disturbances caused by strong waves and winds on the seasonal fluctuations of the macro-benthic community on the sandy tidal flats	S1-1 **Aoki Misuzu,** Saki T, Takuya K.; Coastal surveys (rocky shores, tidal flats, seagrass beds, and algal beds) in Monitoring Sites 1000 Projects: A long-term monitoring project in Japan
11:15	SC1-2 **Ko Hinokidani,** Ushioda A, Nakanishi Y.; A role of leaf-removing crabs in iron solubilization processes in mangrove sediments	S1-2 **Suzuki Takao,** Takeshi Y, Jotaro U.; Citizen-based monitoring projects in tidal flats along the Japanese Coast.
11:30	SC1-3 **Aziz J Mulla,** Lin C-H, Takahashi S, Nozawa Y.; Phototaxis in Pocillopora verrucosa Larvae	S1-3 **Kanaya Gen,** Kazuo K, Yasuhisa H, Masami H, Tsunenori K, Taeko K, Masanori T, Takao S, Masahiro N, Misuzu A.; Spatiotemporal variation in the macrozoobenthic biodiversity and community structure in Japanese tidal flats: Analyses based on data from the Monitoring Sites 1000 Project
11:45	SC1-4 **Jutarat Pornamnuaylap,** Monthum Y, Jitchum P; Species diversity of the coastal Phytoplankton in the Northern Andaman Sea, Thailand	S1-4 **Hirokazu Abe,** Matsumasa M,; Habitat alteration and benthic animal biodiversity in the Sanriku Coast after the 2011 earthquake and tsunamis
12:00	SC1-5 **Luna Yamamori,** Kato M; Evolution of limpet-shaped shell in trochid snails: adaptation to two different environments	S1-5 **Genki Kobayashi,** Itoh H, Kanaya G, Abe H, Kojima S; Population genetic structures of two ocypodoid crab species along the Japanese coast
12:15	SC1-6 **Manzhi Tang,** Okoshi K, Nishitani G, Okoshi W-S.; Population dynamics of *Boccardia proboscidea* and *Boccardiella hamata* (Annelida, Spionidae) inhabiting oyster beds in Sasuhama, northeastern Japan	S1-6 **Hajime Itoh,** Kanaya G, Miura O, Nakai S, Kobayashi G, Kojima S.; Phylogeographic variation in the Asian horn snail *Batillaria attramentaria* (Mollusca: Gastropoda) along the Japanese coast
12:30	***Lunch***	

Start Time	Room 101	Room 103
	Session SC2 Student Oral Presentation Contest (II) Judges: **Dr. Hsieh Chih-Hao** **Dr. Phongchate Pichitkul** **Dr. Taeko Kimura**	**Session S2** Contributed Session: Symbiosis and parasitism in Crustacea: diversity and ecology studies in Asian region Chairs: **Gyo Itani** & **Yumi Henmi**
13:30 13.35	SC2-1 **Satoshi Takahashi,** Tanu F-Z, Nakanishi Y.; Relationship between mangrove foliar δ15N and land use in some watersheds in Okinawa, Japan	(13:30~13:35) **Introduction** S2-1 **Benny K.K. Chan,** WangT-W, Lin H-C.; Are coral associated barnacles suspension feeders or they have to derive carbon from their coral hosts?
13:45 13:50	SC2-2 **Wei-Siang Hong,** Chiou H-Y, HuR-H, Tilley A, Hsu W-Y.; On the estimation of marine resource distribution of Timor-Leste by data fitting	S2-2 **Ryutaro Goto**; Diversity of bivalves symbiotic with crustaceans
14:00 14:05	SC2-3 **Chi Chen**; The characteristics and expression profile of SQOR under sulfide tolerance in hydrothermal vent crab, *Xenograpsus testudinatus* **Author:** Chiou H-Y, HuR-H, HongW-S, Tilley A, Hsu W-Y.	S2-3 **Meng-Chen Yu,** Wong Y-H, Kolbasov G-A, Chen H-J, Wada N, Tang S-L, Chan B-k.k.; Windows for animals: Understanding the functions of the unique window structure in the shell of sponge-inhabiting barnacles
14:15 14:20	SC2-4 **Pakorn Tongboonkua,** Chen W-J.; Systematics of the Bothid Flatfishes (Pleuronectiformes: Bothidae)	S2-4 **Niklas Dreyers,** Olesen J, Palero F, Grygier M, Machida R, Chan B-K; The biology and lifecycle of enigmatic crustacean y-larvae
14:30 14:35	SC2-5 **Kamonlak Ninsuwan,** Praiboon* J, Muangmai N, Yuthavisuthi P.; Comparative of various carbon sources on docosahexaenoic acid production from *Aurantiochytrium limacinum* FIKU003	S2-5 **Sungtae Kim,** Lee C-L, Hong J-S.; The effect of the isopod parasite, Gyge ovalis on the mud shrimp, *Upogebia major* in the west coast of Korea
14:45 14:50	SC2-6 **Anirut Klomjit,** Praiboon* J, Thamlikitkul V.; Phytochemical compositions and potential pharmaceutical uses of *Padina australis* extract	S2-6 **Yumi Henmi,** Itani G.; Symbiotic relationships between crustaceans and fishes
15:05		S2-7 **Akira Asakura,** Imazu M.; Species composition and seasonal abundance of ectoparasitic crustaceans on intertidal hermit crabs in the Pacific rocky shore of Japan. (15:20~15:50) **General discussion** (15:50~16:00) **Concluding remarks**
15:30	Poster Presentation I	

November 6th (Wednesday) Schedule
Howard Civil Service International House

Start Time	Room 101	Room 103
	Session A2 Biology and ecology of benthic animals and plankton (II) Chairs: **Shuh-Sen Young** & **Kenji Okoshi**	**Session B2** Assessment and conservation of coastal and estuarine (II) Chairs: **Hwa-Lung Yu** & **Akira Umehara**
09:00	A2-1 **Shuh-Sen Young,** Jhao J-S,; Suggested type and benefit of the bottom trawl for sampling macrobenthos in Taiwan coast	B2-1 **Ichiro Imai,** Kakumu A, Shimada H.; Expanded occurrences of red tides by the warm-water dinoflagellate *Karenia mikimotoi* in Hakodate Bay, Hokkaido, northern Japan
09:15	A2-2 **Kenji Okoshi**; The multiple effects of the Great East Japan Earthquake on the Pacific oyster *Crassostrea gigas*	B2-2 **Akira Umehara,** Borja A, Nakai S, Nishijima W.; Long-term changes in the benthic environment in the Seto Inland Sea
09:30	A2-3 **Li-Tzu Hou,** Ko C-Y.; Multi-scale temporal variation in phytoplankton biomass (chlorophyll-a) in the northern South China Sea	B2-3 **Wai-Zhian Soo,** Chen Y-R, Hou W-S,; Study on the Influence of Leaf Fan Form of Aeration Equipment on Dissolved Oxygen Distribution and Flow Field in Water
09:45	A2-4 **Kay Sakuma,** Ueda Y.; Validating fisheries-dependent catch and effort data with observations from trawl surveys: an example of the Pacific northern shrimp *Pandalus eous* in the Sea of Japan	B2-4 **Masaaki SATO**; Assessing local fish communities around artificial reefs using environmental DNA metabarcoding
10:00	A2-5 **Mark J. Grygier,** Dreyer N, Fujita Y, Jacobsen D-E, Chan B-K.K, Olesen J.; A new attempt to document the extraordinarily diverse form-taxa of “nauplius y” and “cypris y” (Crustacea: Thecostraca: Facetotecta) in plankton at Okinawa, Japan	B2-5 **Sommai Janekitkarn**; Diversity and Community of Composition of Coral reef fishes of the Ra Island, Pang-Nga province, Andaman Sea, Thailand
10:15	A2-6 **Chen-Lu Lee,** Liu S-L, Lin H-J, Liu P-J.; Allelopathic algae effect on coral reef fish	B2-6 **Hwa-Lung Yu**; An ecological risk assessment around a petrochemical industrial area
10:30	***Coffee Break***	

Start Time	Room 101	Room 103
	Session C Biogeochemistry of coastal ecosystem Chairs: **Chih-Yu Chiu** & **Shang-Shu Shih**	**Session D** Environment and ecosystem Chairs: **Sau-Wai Yam** & **Suchana Chavanich**
11:00	C-1 **Tomohiro Komorita,** Nizzoli D, Viaroli P-L.; Characterization of the organic matter of biodeposits derived from marine aquaculture bivalves: a meta-analysis approach	D-1 **Teerapong Duangdee,** Tsutsumi H.; Accelerated bioaccumulation of mercury in red stingray (Hemitrygon akajei) by the change of feeding habits relative to growth
11:15	C-2 **Chih-Yu Chiu,** Shiau Y-J, Cai Y, Lin Y-T, Jia Z-G; Phylogenetically distinct methanotrophs modulate methane oxidation in rice paddies and mangrove soils	D-2 **Chih-hao Hsieh**; Fluctuating interaction network and time-varying stability of a natural fish community
11:30	C-3 **Chiao-Wen Lin,** Kao Y-C,Lin H-J.; Seasonal variations of methane emissions from mangrove forests soils across Taiwan	D-3 **Hans-Uwe Dahms,** Cho M-F, Gurunathan R, Hong J-F, Liu C-H,Selvar P, Deepak C, Ambarsari W, Schizas N-V, James R A, Hwang J-S.; Shallow marine hydrothermal vents (HVs) provide valuable bioresource information
11:45	C-4 **Hsuan-Wien Chen,** Lian Y-J, Hsieh L-Y, Hsueh M-L.; From trophic contribution to ecosystem services: a mangrove case	D-4 **Do Wan Kim**; Effecive initiation diffusion model based on data of species growth
12:00	C-5 **Yo-Jin Shiau**; Biological N_2 fixation of mangrove forest soils in the western coastal of Taiwan	D-5 **Sau-Wai Yam**; Flow of metallic contaminants in food-web components within a subtropical mangrove ecosystem
12:15	C-6 **Shang-Shu Shih**; Coupling tidal creek evolution model with mangrove habitat suitability model in estuarine wetlands	D-6 **Chaolun Allen Chen**; Potential resilience of Taiwanese Coral reef in Changing Climate
12:30	***Lunch***	

Start Time	Room 101	Room 103
	Session E Fisheries and aquaculture Chairs: **Wen-Shang Hou** & **Hiroaki Tsutsumi**	**Session F** Taxonomy and phylogeny of aquatic organisms & Other general issues of marine biology Chairs: **Keryea Soong** & **Chang-Bae Kim**
13:30	E-1 **Tirawat Rairat,** Thongpiam W, Hsieh C-Y, Chou C-C.; The effects of water temperature on pharmacokinetics, optimal dosing regimen, and the occurrence of non-linear kinetics of florfenicol in Nile tilapia (Oreochromis niloticus)	F-1 **Shigeaki Kojima,** Kido M, Itoh H, Sakuma K, Shinohara G.; Evolution of deep-sea demersal fishes of the *Bothrocara hollandi* species complex around Japan
13:45	E-2 **Hiroaki Tsutsumim,** Nishi T, Duangdee T, Tunkijjanukij S.; DO control of the water at a shrimp farming pond with a micro-bubble aeration system, and its effect on the growth of shrimp	F-2 **Chang-Bae Kim,** Do T-D, Jung D-W, Kim J-I.; Morphological Examination and DNA Analysis Reveal a New Record and a New Species of Cadlina (Nudibranchia) from Korea
14:00	E-3 **Masahiro Suzuki,** Suzuki K.; The effect of rapid invasion of clam eating moon snail Laguncula pulchella on the abundance of Manila clam Ruditapes philippinarum in artificial tidal flat constructed after the Great East Japan Earthquake	F-3 **Keiichi Kakui,** Tomioka S.; Diversity of *Nesotanais* tanaidacean crustaceans in the Ryukyu Islands, Japan
14:15	E-4 **Min-Yu Tsai**; High resolution larval fish compositions of catch and by-catch species in coastal waters of Taiwan, ascribable to spatiotemporal and environmental factors	F-4 **Jintana Salaenoi,** Jaowatana N, Chuangcham K**,** Salaenoi J.; Minerals in the Sediment Collected from Blood Cockle Cultured Area at Bandon Bay
14:30	E-5 **Wai-Zhian Soo**; The effect of water quality, growth and survival of *Macrobrachium Rosenbergii* by lower power circulating water system	F-5 **Thipphawan Chothonglang,** E-kobon, Chumnanpuen P, Salaenoi J.; Antibacterial Activity in Haemolymph of the Oyster, Saccostrea commercialis
14:45		F-6 **Chananya Pinsri,** Suksangchan C, Boonprab K, Salaenoi J.; Protein and elements composition in Cephalopods ink
15:00		F-7 **Keryea Soong,** Lin P-H.; Two scientific stations open to all in South China Sea
15:30	Poster Presentation II	

Poster Presentation Schedule

※P1-1 ~ P1-25 and P1-36: Student Poster Contest

No.	Poster Presentation Ⅰ (15:30~17:30 on Nov. 5)
P1-1	**Tomo Tateishi**: Impact of torrential rain on the population dynamics of brackish water clam, *Corbicula japonica*, in the Kikuchi River Estuary, Kumamoto, Japan
P1-2	**Aika Oyama**: Seasonal changes of the distribution and population dynamics of hard clam, *Meretric lusoria*, on Midri River Tidal Flats, Kumamoto, Japan
P1-3	**Kouki Suga**: Food web analysis of benthic ecosystem with stable isotope signatures of carbon and nitrogen on Arao Tidal Flats, Kumamoto, Kyushu, Japan
P1-4	**Yuki Shimada**: Seasonal fluctuations of short-neck clam, Ruditapes philippinarum, population and its controlling factors on Shira River Tidal Flats, Kumamoto, Japan
P1-5	**Dang Do Hung Viet**: The role of sea urchins on coral recruitment in Taiwan
P1-6	**Wan-Chien Hsiao**: Identification of abiotic drivers shaping marine coastal benthic communities
P1-7	**Ploypailin Rangseethampanya**: Species composition and abundance of macrofauna at Mu Ko Chumphon, the Western Gulf of Thailand
P1-8	**Akiyuki Kenmochi**: Mass occurrence and its ecological significance of marine cladocerans in offshore Suruga Bay, Japan
P1-9	**Kohei Oshiro**: Morphological and molecular assessment of the species diversity of the genus *Phascolion* (Annelida: Sipuncula) in Japan
P1-10	**Kengo Kajiyama**: Seasonal variation in distribution and species composition of infaunal spionid polychaetes (Annelida: Spionidae) in the intertidal zone of Tokyo Bay
P1-11	**Arirush Wongnutpranont**: Seasonal variation of abundance and composition of benthic invertebrates in Phuket, the Andaman Sea
P1-12	**Kyeonglim Moon**: Changes in diversity and structure of marine benthic assemblage
P1-13	**Phunsin Kantha**: Toxic Effects of Nanoplastic Polystyrene on Developmental stages and Behavior on Zebrafish Larvae.
P1-14	**Charernmee Chamchoy**: Abundance and composition of juvenile corals on shallow reef flat and reef slope at a popular tourist destination in the Andaman Sea
P1-15	**Rocktim Ramen Das**: Surveys of coral reactions to fishing line garbage around Sesoko Island, Okinawa
P1-16	**Tomoe Kuno**: Feeding habits and niche of short-finned pilot whales and bottlenose dolphins around Kii Peninsula
P1-17	**Masaomi Shiromoto**: Genetic diversity of the red tide-forming dinoflagellate, *Noctiluca scintillans*, in Japanese and Korean coastal waters
P1-18	**Yoshiko Matsuoka**: Experiment to re-establish high-density patches of short-neck clam, *Ruditapes Philippinarum*, with protective fences to the predation by fishes on Sashiki Tidal Flats in Yatsushiro Sea, Japan
P1-19	**Kyeonglim Moon**: Spatial trends of morphology and genetic structure in seagrass *Zostera marina* on Jeju Island, Korea
P1-20	**Tzu-yu Lai**: Ready to spawn? Final gamete maturation and egg-sperm bundle formation in Acropora and Merulinidae corals

No.	Poster Presentation Ⅰ (15:30~17:30 on Nov. 5)
P1-21	**Chia-Ling Fong**: Citizen scientists reveal main threats to the foraging sea turtles in Taiwan
P1-22	**Akihiro Yoshikawa**: Molecular Phylogeny of Clibanarius Dana, 1852 from the Indo-West Pacific: Habitat Adaptation and Evolution of Pereopod Colour Pattern
P1-23	**Yucheol Lee**: A mitochondrial genome phylogeny of Mytilidae (Bivalvia: Mytilida)
P1-24	**Takahiro Sugiyama**: Interspecific or intraspecific variation?: host-specific color morphs in the parasitic scale worm *Gastrolepida clavigera* (Annelida: Polynoidae)
P1-25	**Mizuki Ohta**: Species richness of the deep-sea Asellota isopods (Arthropoda: Crustacea) off Tohoku, Japan
P1-27	**Chih-Hsien Chang**: The splash detection technology for fish feeding monitoring in cage culture
P1-28	**Sawada Hideki**: Spatial distribution of the sea cucumber Apostichopus japonicus in the natural habitat of Miyazu Bay, Kyoto, Japan
P1-29	**Jin-Young Seo**: Toxicity assessment for the wastes removed from the in-water ship's surface cleaning activities using sea-urchin embryos
P1-30	**Laongdow Jungrak**: Meiofaunal composition of sandy beach and soft-bottom of coral reefs in the Western Gulf of Thailand
P1-31	**Shoko Hosoi-Tanabe**: Distribution of toxic *Alexandrium tamaense* and *A. catenella* in Akkeshi-ko estuary and Akkeshi Bay, where oyster is cultivated on a large scale in Japan
P1-32	**Tohru Takahashi**: Microcystine (freshwater origin cyanotoxin) hibernates in the sea bottom
P1-33	**Taeko Kimura**: Long-term monitoring of macrobenthic fauna on three tidal flats in the Tokai Region, Central Japan from 2008 to 2018 (the Monitoring Site 1000 program)
P1-34	**Rumiko Kajihara**: Feeding ground function of fishing ports for fish in southwestern Hokkaido, Japan
P1-35	**Jia-Ho Shiu**: Shifting in bacteria *Endozoicomonas* is independent to coral bleaching
P1-36	**Moeko Kato**: Seasonal change of benthic diatoms in Gamo Lagoon, Miyagi Prefecture, northeastern Japan
P1-37	**Kyosuke Momota**: The importance of habitat diversity for biodiversity of benthic macrofaunal species in a semi-enclosed coastal sea
P1-38	**Sungtae Kim**: Vertical distribution of the introduced Invasive smooth cordgrass, *Spartina alterniflora* in the West Coast of Korea
P1-39	**Yu-Te Lin**: Denitrification activities in coastal mangrove soils of Taiwan
P1-40	**Shun Kawaida**: The role of crabs having cellulose digestion ability in mangrove organic carbon processing
P1-41	**Sosuke Otani**: Bioturbation of Sesarmid crab Chiromantes dehaani at reed marsh in Yodo river estuary, Japan

No.	Poster Presentation Ⅱ (15:30~17:00 on Nov. 6)
P2-1	**Mutsuo Ichinomiya**: Parmales abundance and species composition in the waters surrounding Hokkaido, North Japan
P2-2	**Yaowaluk Monthum**: Species composition and distribution for phytoplankton of Tung Nang Dam estuary in Phang-Nga Province during dry and rainy seasons in 2018-2019
P2-3	**Parinya Limviriyakul**: Host detection of symbiotic crab Tetralia rubridactyla
P2-4	**Daishi Yamazaki**: Comparative seascape genetics revealed contrasting genetic structure and habitat preferences between co-distributed closely related marine species
P2-5	**Jeong Hyeon Kim**: Summer variations of macrobenthic community structures in Gwangyang Bay, South Korea
P2-6	**Waka Sato-Okoshi**: Survey of the family Spionidae (Annelida) in Danshuei River and Estuary, north Taiwan
P2-7	**Ryo Orita**: Profiling gene expression responses of the blood clam *Anadara kagoshimensis* to anoxia by *de novo* RNA-Seq analysis
P2-8	**Che-Hung Lin**: The reef-building coral *Acropora hyacinthus* may use chemical signals to synchronize spawning timing between conspecifics
P2-9	**Seok-Hyun Kim**: Distribution patterns of some Polychaetes in the intertidal rocky shores in Jeju Island, Korea
P2-10	**Siriluck Rongprakhon**: Abundance of macro-invertebrates on shallow reefs flats in the Western Gulf of Thailand
P2-11	**Napakhwan Whanpetch**: Spatial and temporal distribution of polychaetes in seagrass bed at Kung Krabaen Bay, Chanthaburi Province, Thailand
P2-12	**Chae-Lin Lee**: On some population characteristics of the parasitic bopyrid isopod Gyge ovalis (Shiino, 1939) in the mud shrimp Upogebia major (de Haan) in Jugyo tidal flat, west coast of Korea
P2-13	**Katsumasa Yamada**: Community structure of brachyuran crab (Crustacea, Decapoda) among tidal rivers at the Ariake Sea, Kyushu, Japan
P2-14	**Chao-Kai Kang**: Investigation of marine benthic communities in sandy bed of Fangshan coast near Fenggang harbor
P2-15	**Hyun-Sig Lim**: Effect of Spartina anglica and Suaeda japonica vegetation on the macrobenthic community structure of the mud flat in Korea
P2-16	**Yu-Kai Chen**: Long-term observation of ichthyoplankton community structure and its relation to environmental factors in the Taiwan Strait in winter
P2-17	**Takefumi Yorisue**: Latitudinal gradient of cold temperature tolerance in an introduced barnacle (Balanus glandula) in Japan
P2-18	**Nami Okubo**: Microplastic disturb coral-algae symbiotic relationship
P2-19	**Pailin Jitchum**: Microzooplankton Community Structure in the Northern Andaman Sea, THAILAND
P2-20	**Wiphawan Aunkhongthong**: Assessing diversity and abundance of scleractinian corals on shallow reef flats in Mu Ko Phangan, the Western Gulf of Thailand
P2-20	**Wiphawan Aunkhongthong**: Assessing diversity and abundance of scleractinian corals on shallow reef flats in Mu Ko Phangan, the Western Gulf of Thailand
P2-21	**Wanlaya Klinthong**: Long-term monitoring of coral recruitment on settlement panels at Mu Ko Similan, the Andaman Sea after the 2010 coral bleaching event
P2-22	**Makamas Sutthacheep**: The recovery potential of corals at Mu Ko Chang, the Eastern Gulf of Thailand

No.	Poster Presentation Ⅱ (15:30~17:00 on Nov. 6)
P2-21	**Wanlaya Klinthong**: Long-term monitoring of coral recruitment on settlement panels at Mu Ko Similan, the Andaman Sea after the 2010 coral bleaching event
P2-22	**Makamas Sutthacheep**: The recovery potential of corals at Mu Ko Chang, the Eastern Gulf of Thailand
P2-23	**Sittiporn Pengsakun**: Coral community on an underwater pinnacle at a proposed dive site for marine ecotourism in the Western Gulf of Thailand
P2-25	**Wachirah JAINGAM**: THE CORRELATION OF MERCURY CONTENT OF THE LIVER AND MUSCLE OF FISHES IN AN ENCLOSED ISAHAYA BAY, KYUSHU, JAPAN
P2-26	**Suchana Chavanich**: Marine debris and microplastics in the upper Gulf of Thailand
P2-27	**Phongchate Pichitkul**: Effect of Asian Sea Bass (Lates calcarifer) Cage Culture on Benthic Communities in Estuary of the Bang Pakong River Basin at Chachoengsao Province, Thailand.
P2-28	**Hans-Uwe Dahms**: Are in silico endocrine disruption screenings useful for seafood safety predictions for children?
P2-29	**Hans-Uwe Dahms**: Risk assessment by chemcomputation of biotoxins from marine cyanobacteria
P2-30	**Hans-Uwe Dahms**: Hypersaline saltpan bacterium Pseudomonas aeruginosa provides antibacterial agents against diabetic wound infections
P2-31	**Hans-Uwe Dahms**: Hydrothermal vent bacteria from Taiwan provide antibacterials and metalloproteinases
P2-32	**Hans-Uwe Dahms**: Bacterial diversity of shallow marine hydrothermal vents at Kueishantao, Taiwan
P2-33	**Hans-Uwe Dahms**: Status of ESβL producing bacteria along the southern Indian coast
P2-34	**Hans-Uwe Dahms**: Development of a marine featured curriculum in the coastal elementary school San Gu, Tainan, Taiwan
P2-35	**Hyojin Ahn**: Seasonal changes of fish biodiversity in Hakodate Bay, Japan, revealed by eDNA metabarcoding technique
P2-36	**Chiang, Wei-Chuan**: Vertical and horizontal movements of bigeye tuna (Thunnus obesus) off southeastern Taiwan
P2-37	**Hirokazu Abe**: Identification guide to the planktonic larvae of marine annelids in Japan
P2-38	**Chang-Bae Kim**: Next-Generation Sequence for Mitochondrial Genome Construction: An Integrated Pipeline, Assembly to Annotation case of Dermatobranchus otome
P2-39	**Yucheol Lee**: Marine Mollusk Resource Bank of Korea (MMRBK)
P2-40	**Gyo Itani**: Morphological characteristics of an undescribed species of gaeticine crab (Crustacea: Brachyura: Varunidae) clinging to mud shrimp abdomen from Japan
P2-41	**Hiroaki Tosuji**: Molecular evidence of two sibling species in “*Perinereis shikueii*” (Annelida: Nereididae) and their distributions in Taiwan and Japan

Keynote Speaker Abstracts & Biographies

Thamasak Yeemin, D.Sc.

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EDUCATION

1984 B.Sc. in Marine Biology from Chulalongkorn University, Bangkok, Thailand
1986 M.Sc. in Marine Biology from Chulalongkorn University, Bangkok, Thailand
1988 M.Sc. in Biology from the University of the Ryukyus, Okinawa, Japan
1991 D.Sc. in Biology from Kyushu University, Fukuoka, Japan
1993 Diploma in Environmental Management from the Netherlands International Institute for Management, Maastricht, The Netherlands

EXPERIENCES & MAIN STUDIES

Thamasak Yeemin has worked at Marine Biodiversity Research Group, Department of Biology, Faculty of Science, Ramkhamhaeng University, in Bangkok since 1992. His education background includes a D.Sc. in Biology from Kyushu University, M.Sc. in Biology from the University of the Ryukyus, M.Sc. and B.Sc. in Marine Biology from Chulalongkorn University and a diploma in Environmental Management from the Netherlands International Institute for Management. He has studied ecology, biology, environmental science and socio-economics of coastal ecosystem management and marine protected areas. He has experience in many aspects of coastal and marine ecosystems, including management, conservation, research, and administration, based on nearly 30 years of fieldwork in Thailand and other parts of the Western Pacific. He has provided expertise to several management agencies, including local governments, national institutions, international organizations and NGOs, to design and implement management plans for coastal resources and the environment. He is a founding member of the Asia Pacific Coral Reef Society and a former councilor of the International Society for Reef Studies (ISRS). He has also worked as a consultant for some regional collaborative projects under international organizations, such as the International Maritime Organization (IMO), UNEP, ASEAN Center for Biodiversity, etc. He is currently a president of the Marine Science Association of Thailand (MSAT).

Ecological resilience to climate change and anthropogenic disturbances: lessons learned from coral reef studies in the Western Pacific

The resilience concept was introduced in an ecological context as the amount of disturbance that an ecosystem could withstand without changing self-organized processes and structures. Resilience concepts are being increasingly applied to coral reefs in the Caribbean, Indo-Pacific and other parts of the world. Large numbers of people in the Western Pacific are highly dependent on coral reef ecosystem services. However, most coral reef ecosystems are under severe threat from natural and anthropogenic disturbances, particularly coral bleaching events. Major coral bleaching phenomena have led to widespread coral mortality in the last three decades. The assessment of coral reef resilience to climate change is an important task for coral reef studies. Some coral reef resilience assessments are not practical for developing countries in the Western Pacific but some researchers developed practical resilience indices. A case study on quantitative assessment of coral reef resilience was conducted at twenty study sites in the Gulf of Thailand and the Andaman Sea, following the 2010 severe coral bleaching event. The resilience assessment was based on the percentage of non-bleached coral colonies, the percentage of surviving coral colonies and the density of juvenile corals. The results showed that coral reef resilience varied greatly among the study sites and major reef groups according to their community structure, largely due to the differing bleaching resistance and tolerance of the dominant coral species. Recent studies revealed that the speed of coral recovery from a first round of bleaching event contributes strongly to sensitivity to a second round of bleaching event. Some naturally occurring climate-resilient corals were used for coral restoration projects. The compiled coral abundance data from over 2,548 Indo-Pacific reefs to evaluate the influence of 21 climate, social and environmental drivers on the ecology of coral communities showed that high abundances of corals were typically associated with several factors, including weaker thermal disturbances and longer intervals for potential recovery, slower human population growth, reduced access by human settlements and markets, and less nearby agriculture. Resilience-based management and some management strategies have been proposed for coral reef management and conservation.

Keywords: climate change, coral reef, disturbance, resilience, Western Pacific

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EDUCATION

1979-1983	B.Sc. from Faculty of Agriculture, Tohoku University, Japan
1983-1985	M.A. from Graduate School of Agricultural Science, Tohoku University, Japan
1985-1988	Ph. D from Graduate School of Agricultural Science, Tohoku University, Japan

EXPERIENCES

1988-1991	Chief Curator, Natural History Museum and Institute, Chiba Prefecture, Japan
1991-2005	Associate, Graduate School of Agricultural Science, Tohoku University
2005-2007	Assistant Professor, Graduate School of Agricultural Science, Tohoku University
2007-2018	Associate Professor, Graduate School of Agricultural Science, Tohoku University
2018-present	Professor, Graduate School of Agricultural Science, Tohoku University
1994	Guest Researcher, University of Alberta, Canada
1996-1999	Adjunct Investigator, Center for Interdisciplinary Research, Tohoku University
1998	Expert Instructor in Aquaculture in Chile, Japan International Cooperation Agency
2000-2001	42nd Japanese Antarctic Research Expedition
2002	Deep Sea Research Expedition, Ryukyu Islands (Natsushima)
2002	Deep Sea Research Expedition, Japan Trench (Kairei)
2003	Japan-Thailand cooperative studies on fisheries science, Ministry of Education, Culture, Sports, Science and Technology, Japan
2005	Guest Professor, Murdock University, Australia
2010, 2016	Visiting Professor, Inha University, South Korea

ACADEMIC ACTIVITIES

2007-present	Advisory council of the International Polychaete Association
2009-2013	Executive committee of the Japanese Association of Benthology
2011-2015	Editor-in-Chief of “Plankton and Benthos Research”
2011-2013	Executive Editor of “Plankton and Benthos Research”
2013-2016	Council of the Japanese Society of Fisheries Science
2015-2019	Executive committee of the Japanese Association of Benthology
2019-present	President of the Japanese Association of Benthology

SCIENTIFIC INTERESTS

1. Biology and ecology of marine macrobenthos
2. Biology of polydorid complex (Annelida, Spionidae)
3. Natural and anthropogenic disturbances
4. Deep sea ecology
5. Polar biology

Global aquaculture activities can alter species distribution and marine ecosystem

Today, not only natural but serious anthropogenic disturbances are increasingly witnessed all over the world. Due to world population explosion, global environmental change and overfishing conditions, a world food shortage is conceivable, as the ocean can only sustainably nourish a fraction of this steadily growing population. With the goal of addressing this deficit, expansion of aquaculture activities has resulted in global distribution of certain commercially important animal and plant species, quicker and easier than ever before. Consequently, various species, many of which have not been identified, are transported inadvertently during the transport of these economically important species. Here, I will provide two concrete examples from our research findings of species introductions by anthropogenic means, and discuss the impacts on marine ecosystems of each.

First, Annelida is one of the biggest Phyla in the Animal Kingdom in terms of not only abundance and biomass but also species diversity. Annelids comprising the polydorid species complex of the family Spionidae, possess distinguishing morphological characteristics on the 5th chaetiger but species are easily confused due to their morphological similarities. They are observed burrowing into sand-mud sediments, and inhabiting the surface or inside of various host animals in symbiotic relationships. Some polydorid species are well-known for their boring activity into the shells of mollusks and damage commercially important mollusks by decreasing commercial value, reducing both growth rate and meat yield and causing heavy mortality. I will share some of our recent findings on polydorid species whose distribution has likely expanded due to their association with mollusks transported for aquacultural purposes. Next, asari clams of the species *Ruditapes philippinarum* are one of the most familiar bivalves consumed by Japanese people since very ancient times. However, asari clam populations in Japan have been declining steadily since 1980, although the reason for this decline is complex and requires further clarification. In northeastern Japan, for example, it is suggested that the long-standing continuous importation of asari clams from East Asia has caused the decline of native asari population due to simultaneous introduction of the associated moon snail *Laguncula pulchella*, a natural predator of asari clams. I will share a summary of the biological characteristics of the moon snail and present our hypothesis of the scheme of its introduction into Japanese waters.

Hsing-Juh Lin, Ph.D.

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EDUCATION

1983-1987	Ph.D. from Graduate School of Oceanography, University of Rhode Island, RI, U.S.A.
1990-1994	B.S. from Department of Marine Resources, National Sun Yat-sen University, Taiwan

EXPERIENCES

1994	Scientist of NOAA RV Delaware II, Woods Hole, U.S.A.
2005-2008	Adjunct Professor of Institute of Marine Environmental Chemistry and Ecology, National Taiwan Ocean University, Taiwan
2007-present	Honorary Distinguished Professor of Department of Life Sciences, National Chung Hsing University
2009-2013	Chair of Department of Life Sciences, National Chung Hsing University, Taiwan
2010-2016	Adjunct Professor of Institute of Ecology & Evolutionary Biology, Chinese Medical University, Taichung, Taiwan
2012-2013	The Evaluation Committee of Taiwan's Wetlands of Importance, Ministry of the Interior
2013-2014	Council of Agriculture
2013-2016	Director of Research Center for Global Change Biology, National Chung Hsing University
2015-2016	Environmental Protection Agency
2015-present	President of Taiwan Wetland Society
2015	The Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), United Nations Environment Programme (UNEP)
2008-present	Academia Sinica
2016	International Union for Conservation of Nature (IUCN)

MAIN STUDIES

The specialty of Dr. Lin is on the structure, function, and service of coastal ecosystems, particularly in the tropical/subtropical region. In the past 20 years, Dr. Lin have been studying on a variety of tropical aquatic ecosystems, from streams, estuaries, coastal lagoons, coastal wetlands, mangroves, seagrass beds to coral reefs, particularly Blue Carbon. He was charged in making the standard operation procedure for ecologically monitoring the wetlands of national importance in Taiwan.

The driving force for intertidal tropical seagrass beds over decadal timescales

As we know little about how disturbances such as typhoons and El Niño-Southern Oscillation (ENSO) events affect seagrass beds, diverse seagrass habitat types (*Thalassia hemprichii*) were surveyed once every three months for 17 years (January 2001 to February 2018) in southern Taiwan, which is regularly affected by typhoons and ENSO events. Environmental, seagrass and periphyton data collected in the wet season of a year without a typhoon were treated as controls. The data collected before the typhoon season (summer) and within 30 days after a total of 6 typhoons were treated as posttyphoon responses. Our results show that La Niña and El Niño events had distinct effects on the biomass and growth of *T. hemprichii*. During La Niña years, higher 1) precipitation levels and 2) seawater nitrogen concentrations (DIN) led to increases in seagrass leaf productivity, canopy height, and biomass. However, the latter simultaneously stimulated the growth of periphyton on seagrass leaves; this might lead to decreases in seagrass cover and shoot density. There were no significant overall differences in either the environmental data or the seagrass response variables in response to the typhoons. However, DIN was significantly higher and periphyton biomass declined after the typhoons. The significant losses in periphyton suggest that the typhoon impacts on the intertidal seagrass beds were primarily short-term wind events or storm surges. Relative to the chronic and persistent effects of ENSO, the typhoon effects on the intertidal seagrass beds were dramatic and rapid. Our long-term dataset revealed that intertidal tropical seagrasses are resilient to typhoons over decadal timescales.

Keywords: El Niño, La Niña, *Thalassia hemprichii*, typhoon, DIN, periphyton

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The Abstracts of Oral Presentations

Room 101

NO. A1-1 to A1-6 on Nov. 5 09:00 ~ 10:30
NO. SC1-1 to SC1-7 on Nov. 5 11:00 ~ 12:45
NO. SC2-1 to SC2-7 on Nov. 5 13:30 ~ 15:15
NO. A2-1 t A2-6 on Nov. 6 09:00 ~ 10:30
NO. C-1 to C-6 on Nov. 5 11:00 ~ 12:30
NO. E-1 to E-6 on Nov. 5 13:30 ~ 15:15

Room 103

NO. B1-1 to B1-6 on Nov. 5 09:00 ~ 10:30
NO. S1-1 to S1-6 on Nov. 5 11:00 ~ 12:45
NO. S2-1 to S2-5 on Nov. 5 13:30 ~ 15:15
NO. B2-1 to B2-6 on Nov. 6 09:00 ~ 10:30
NO. D-1 to D-6 on Nov. 5 11:00 ~ 12:30
NO. F-1 to F-7 on Nov. 5 13:30 ~ 15:15

Spatial variability in composition of brown algae along Sanriku Coast, northeastern Japan

Kenta Nakamoto[1], Jun Hayakawa[1], Tomohiko Kawamura[1]

1. International Coastal Research Center, Atmosphere and Ocean Research Institute, The University of Tokyo

Introduction

Along Sanriku Coast, northeastern Japan, marine environment is influenced by three major currents with different characters, that is the cold Oyashio, the warm Kuroshio and the Tsugaru Warm Current, and therefore largely different among seasons and places. Moreover, Sanriku area has a complex coastline with many bays of different shapes so that geographical features differ among places. These large spatial heterogeneities in marine environment and geographical features seem to cause high spatial variability in composition of marine organisms. This may be the reason why diverse marine organisms are found in Sanriku area, but this possibility has been poorly examined. In this study, we focused on brown algae which are major components of coastal benthic ecosystems, and aimed to elucidate factors affecting the spatial variability in composition of brown algae in Sanriku area.

Materials and Methods

Field surveys were conducted in July 2019 in three sites (Taro, Omoe and Otsuchi site). At five (Omoe and Otsuchi) or seven (Taro) stations in each site, a 100 m line was set at right angles to the shoreline. Each station was apart from the other stations at least 600 m. Swimming along the line using SCUBA, we set a 50 cm×50 cm quadrat at every 5 m and recorded the coverage of each species of brown alga and depth. We distinguished the bottom substrate into four types (bed rocks, boulders, gravels and artificial reefs).

Results and Discussion

In total, 17 species/taxa of brown algae were found. Total coverage and species composition of brown algae differed among the three sites. In Taro site, total coverage was 29.9 ± 35.0% (mean ± SD) and *Undaria pinnatifida* was the most dominant (7.3 ± 17.6% in coverage). In Omoe site, total coverage was 47.5 ± 41.7% and *Saccharina japonica* was the most dominant (34.0 ± 8.7%). In Otsuchi site, total coverage was 34.5 ± 35.8 % and *Sac. japonica* was also the most dominant (14.4 ± 27.0%). *Sargassum yezoense*, the second most dominant species in Otsuchi site (5.6 ± 18.9%), was never found in Taro or Omoe site. Composition of brown algae were also different among the stations and the quadrats. In Taro site, the coverage of *Colpomenia sinuosa* differed among seven stations. The coverage of *C. sinuosa* at three stations around Taro Bay (5.0 ~ 27.1% in mean) was significantly higher than that at the other four stations apart from Taro Bay (0.0 ~ 0.8% in mean; $p < 0.01$, GLMM), which may be caused by the difference in wave exposure. In Otsuchi site, the coverage of *Sar. yezoense* was significantly higher at quadrats on bed rocks than on boulders or on artificial reefs ($p < 0.001$, GLMM) at three stations where *Sar. yezoense* was found. Because *Sar. yezoense* has prostrate stems, rocks with large surface area are probably suitable for its growth. In summary, species composition of brown algae differed among places and distribution of each species was probably regulated by several factors concerning wave exposure and/or type of bottom substrate.

Keywords: macroalgae, rocky shore, subtidal zone, β-diversity

Individual-Based Model for evaluating the post-traumatic effect of UV-B radiation on zooplankton reproduction.

Gaël Dur[1], Eun-Ji Won[2], Jeonghoon Han[3], Jae-Seong Lee[3], Sami Souissi[4]

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2. Marine chemistry and geochemistry research center, Korean Institute of Ocean Science and Technology, Ansan, South Korea
3. Department of Biological Science, College of Science, Sungkyunkwan University, Suwon 16419, South Korea
4. Univ. Lille, CNRS, Univ. Littoral Cote d'Opale, UMR8187, LOG, Laboratoire d'Océanologie et de Géosciences, F62930, Wimereux, France

Solar ultraviolet radiation, especially UV-B (280-320nm) has been showed to be partially responsible for adverse effects from DNA damage to altered population dynamics in zooplankton throughout the world. To cope with such negative effects of UV-B copepods have developed several systems of protection including escaping long and intense UV-B exposition. But how much can they withstand until it affects the population remains unsolved. To evaluate the post-traumatic effect of ultraviolet B (UV-B) exposure on the reproduction of egg-carrying copepods, we developed an individual-based model (IBM) integrating results obtained in the lab. We calibrated the IBM for the small cyclopoid copepod species ,*Paracyclopina nana*, a biological model used both in ecotoxicology and aquaculture. Our finding provided a better understanding of the response to UV-B radition. Significant UV-B radiation effects were decreased reproductive success (at ≥ 0.7 KJ/m2) and decrease offspring production (at 0.6≥ KJ/m2). The model predicted fewer than 500 females from an original population of 1000 by 5 day after exposure at 1 KJ/m2, and 50% offspring suppression 8 days after exposure at 1 KJ/m2. This integrative model also highlighted the importance of female longevity in maintaining a viable population for radiation dose below 2KJ/m2 and that of hatching success for radiation over 2KJ/m2. *P. nana* appeared as a very sensitive species at 25°C but further improvement of the model such as the implementation of temperature variation effect and recovery mechanisms should be conducted to better estimate its sensitivity to UV-B.

Keywords: individual-based model, simulation, UV-B effect, emergence, population dynamics

Recolonization of two *Pseudopolydora* species (Annelida Spionidae) in relation to reproduction and larval development in a shallow, brackish and eutrophic lagoon after the 2011 tsunami

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Pseudopolydora kempi is well known as one of the common species in estuary and coastal soft-bottom habitat in Indo-West Pacific coastal waters. However, recently, it was clarified that *P. kempi* included *Pseudopolydora* cf. *kempi* and *Pseudopolydora* cf. *reticulata* which were morphologically similar to each other, occurred in sympatric and had been confused for a long time in Japan. On 11 March, megathrust earthquake and tsunami struck the Pacific coast of Tohoku district and Gamo Lagoon, which is located in Sendai Bay, Northeast Japan, suffered serious damage by the tsunami. Reproduction and larval development were considered to be one of the factors which determine the recolonization after the disturbance. The purpose of this study is 1) to determine the reproduction and larval development of the two *Pseudopolydora* species by rearing experiments, 2) monitoring of recolonization of the two species after the 2011 tsunami. We determined that the number of embryos per capsule differed between the two species: 0–16 for *P.* cf. *kempi* and 62–405 for *P.* cf. *reticulata*. Observation of the larval development revealed *P.* cf. *kempi* showed short-term planktonic development, whereas *P.* cf. *reticulata* showed long-term planktonic development. After the 2011 tsunami, Gamo Lagoon was drastically eroded and turned into open water area. In May 2011, density of benthic animals was extremely low. However, *P.* cf. *reticulata* rapidly colonized and increased its population from May to July 2011 probably because of its abundant larval supply by benefit from long-term planktonic development. In August 2011, Gamo Lagoon turned into closed water area again. From August 2011 to August 2012, *P.* cf. *kempi* colonized dense population at the inner part of the lagoon. It was considered that there was low risk to flow out the larvae of *P.* cf. *kempi* to outside of the lagoon. Therefore, the environmental condition of the lagoon was thought to be suitable for *P.* cf. *kempi*. On the other hand, *P.* cf. *reticulata* occurred with low density at entire area of the lagoon during this period. We conclude that, although two species are sister species, different reproduction and larval development resulted in the different response to the 2011 tsunami.

Keywords: Tsunami, Spionidae, life-history strategy

The genes expression of hormone and neuronal transmitter receptor in relation to gametogenesis and spawning in *Acropora intermedia*

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Coral reef produces an ecosystem in rich biodiversity. A main genus, *Acropora* in the coral reef is developed a gamete during a year and the synchronous spawning occurs once a year. It is known that the synchronous spawning is induced together with the endocrine system in response to outside environmental event, such as lunar age, tide and sea temperature. However, the reproduction mechanism is not yet clarified. This study placed focus on exploring genes expression of estrogen receptor (ER) and noradrenaline transporter (NAT) during gametogenesis and spawning in *Acropora intermedia*. Each gene expression was determined by RT-PCR and the genes expression was quantified using qPCR. As a result, ER gene is a high expression at early developmental stage in oocytes, then the expression decreased dependent on the development of the oocyte. Also, the ER gene expression increased during the spawning. While the NAT gene expression decreased. These observation s suggest ed that estrogen plays significant role on early stage in oocyte with spawning promotion In addition, neurotransmitter, noradrenaline may contribute to trigger of synchronous spawning. In future study, the detail mechanism will be elucidated due to determination of reproductive proteins in oocyte during synchronous spawning.

Keywords: Acropora, synchronous spawning, gene expression

Effect of posture on somatic growth and asexual reproduction in the polyp stage of *Aurelia coerulea*

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The polyp stage plays crucial roles in population outbreaks of jellyfish. The polyps of *Aurelia coerulea*, a typical blooming species in the coastal areas of Japan, have been known to occur mainly in the undersurface of the artificial structures, rather than upper-surface of the substrates. However, the reason for this remains unclear. We carried out laboratory experiments to test the null hypotheses that the posture of polyps do not affect the somatic growth, budding, the number of ephyrae released by polyps, and the rate of abnormal developments in ephyrae. Higher growths of polyps were observed in the individuals attached to the undersurface of the substrates than those attached to the upper-surface (GMANOVA, $p < 0.05$). On the other hand, there was no difference in the cumulative number of buds between the animals cultured with different postures (Mann-Whitney's U-test, $p = 0.92$). Cumulative numbers of ephyrae during the 20 days were higher in the "undersurface" animals than those in the "upper-surface" animals (U-test, $p < 0.05$). The rate of abmormal development in ephyrae was lower in the "undersurface" (Chi-square test, $p < 0.01$). Our study indicated that the posture has significant effects on the growth and asexual reproduction in the polyps of *A. coerulea*. This suggests that there may be possible physiological adaptations in the posture of polyps, and this may be one of the reasons for the preference of the undersurface in the wild colonies.

Keywords: jellyfish, polyp, *Aurelia*

Biogenic habitats as home for invertebrates: comparison of communities associated with tubeworms, oysters, mussels on Rocky shore of Masan Bay, Republic of Korea.

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The Rocky shore of Masan Bay, located in Southern Coast of Korea have various biogenic habitats such as Mussels, Oysters, Serpulids, and Algae. These biogenic habitats and cavities of hard substrata structures variously provide small animals with protection against predators, surfaces for food processing, sites for courtship and mating, or nurseries for rearing juveniles (Aikins and Kikuchi, 2001, Karen, 2015). Also, this area is considered as one of the important site for monitoring invasive species because this sites are near Masan Port. In 2017, the macroinvertebrates in this rocky shore were 58 species, 56,856 ind./m2, 15,168 g/m2. And the invasive species, *Monocorophium insidiosum* (Crawford, 1937) and Spionidae spp. were major dominant species. *M. insidiosum* (Crawford, 1937) was recorded 5,259 individuals/m2 (21.8%), and Spionidae spp. with 1,819 ind./m2 (7.5%). In Jan 2019, the most abundant species were Spionidae spp. and secondly dominant species were *M. insidiosum*, which accounted for respectively about 20%, 10% of total animals. *M. insidiosum* and Spionidae spp. are tube builders and suspension feeders. They might be showing substrate specificity and these biogenic habitats could be beneficial to thrive invasive species. Although the biogenic habitats were located in the similar tidal level, the community structure of macroinvertebrates tended to be separated according to the substrata. In the tube of *Hydroides ezoensis* and the surface of *Magallana gigas*, the most abundant species were Spionidae spp. and *M. insidiosum*. The macroinvertebrates in tube of Serpulids are more abundant than those of oysters. In the community of *Mytilis galloprovincialis*, Copepoda spp. were most abundant (23.7%) and Spionidae spp. were abundant (20.6%) secondly. The diversity, density, biomass of macroinvertebrates on the lower habitats were higher than habitats, upper 50cm than lower habitats.

Keywords: Rocky shore, Biogenic habitat, Invasive species, Macroinvertebrate

The impacts of physical disturbances caused by strong waves and winds on the seasonal fluctuations of the macro-benthic community on the sandy tidal flats

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The benthic environment on the sandy tidal flats is much more unstable than that on the muddy ones, since the sediment tends to be more easily movable, and washed away by the strong wind-driven current and waves. The abundance of macro-benthic animals occurring on the sandy tidal flats is apt to fluctuate dynamically, receiving the physical disturbances caused by the storm. Our study areas, Midori River Tidal Flats, which faces Ariake Bay, Kyushu, western Japan, is the largest sandy tidal flats with the areas of about 2,200 ha remained in Japanese coast. This area is located in the regions where a typhoon approaches frequently during summer and early autumn. The surface layer of the sediment is susceptible to the physical disturbances caused by the strong winds and waves, due to the typhoon. Here, two species of suspension feeding bivalves, *Ruditapes philippinarum* (short-neck clam) and *Arculatula japonica* (Asian mussel) predominate in the macro-benthic communities on the tidal flats, competing for occupation of the habitats on the surface layer of the sediment each other. In this study, we conducted quantitative samplings of the macro-benthic communities on the sandy tidal flats to describe the seasonal fluctuations of the abundance of the macro-benthic animals including these two dominant species between June in 2017 and November in 2018. We report the results of the benthic surveys, report how the strong winds and waves caused by the typhoon affect the seasonal fluctuations of the macro-benthic communities on the sandy tidal flats, and clarify how the two dominant species of the bivalves persist their populations in the unstable habitats on the sandy tidal flats, competing each other.

In May in 2017, the two dominant species of bivalve (*R. philippinarum and* A. japonica) occurred in the densities of 3,320 ind. m^{-2} and 11,290 ind. m^{-2} and the biomass of 544 gww m^{-2} and 5,182 gww m^{-2}), respectively, and these two species occupied 9.1 % and 86.7 % of the total density and biomass of the macro-benthic communities. However, between July 25 and August 21, the total density and biomass of the macro-benthic communities decreased from11,210 ind. m^{-2} to 8,550 ind. m^{-2} and from 4,502 gww m^{-2} to 2,941 gww m^{-2}, respectively. In this sampling interval, strong wind blew in our city (17.5 m^{-1} of the instant max. wind velocity) on August 6, due to a typhoon approaching the Japanese Archipelago. Surprisingly, the surface layer of the sediment up to the depth of approximately 70 cm was washed away. Before the strong wind blew, the sediment surface as thickly covered by the muddy carpet created by *A. japonica*, but it disappeared. The density of this species increased but changed to small from 3,670 ind. m^{-2} to 5,417 ind. m^{-2} and biomass of this species decreased from 1,297 gww m^{-2} to 675 gww m^{-2}, respectively. Contrasting, the dense patches of *R. phillipinarum* received little damages. This species inhabited in the subsurface layer of the sediment. The differences of the living modes on the tidal flats seem to bring the different resistances to the environmental disturbance.

Keywords: Asian mussel, Arcuatula japonica, muddy carpet, physical disturbance, sandy tidal flats short-neck clam, Ruditapes Philippinarum, typhoon

A role of leaf-removing crabs in iron solubilization processes in mangrove sediments

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Iron is a micronutrient essential for phytoplankton growth, thus attentions have been paid to iron supplying system from land to sea. Among them, we have been conducting the studies on iron supplying system from mangrove ecosystems to tropical and subtropical coastal sea. Mangrove plants contain high amounts of polyphenols such as tannins, in their bark, leaves, and roots and those polyphenols can form organic complexes with insoluble forms of manganese and iron in soils, making them water-soluble forms. However, in the intertidal zone where mangroves grow, most of mangrove leaf-litter can be exported by mainly tidal activity, which will reduce the reaction frequency of polyphenols in the fallen leaves with the forest soil. In this context, the presence of benthic animals that directly consumes mangrove leaf-litter could increase the reaction between polyphenols leached from mangrove leaf-litter and the floor sediments by their feeding activities. For example, removal leaf-litter by crabs to their burrow will promote the chemical reaction between polyphenols and iron in sediment. In order to verify the hypothesis, mangrove sediments (8 levels of sediment layer in each 10 cm depth) were collected from forest floor of the crab habitats (divided by burrow size, and dominant crab species) and we measured the amounts of polyphenol (PP) and dissolved iron (dFe) in the sediments and compared the both of contents among deferent sampling sites. As the results, the maximum amounts of PP and dFe in mangrove sediments were observed in 50 to 60 cm depth layer which the leaf-removing crabs inhabited the forest floor. On the other hands, there were no clear differences on the amounts of PP and dFe in the sediments of each layer where the crabs did not presence.

Keywords: mangroves, sediment, dissolved iron, polyphenols, leaf-removing crab

Phototaxis in Pocillopora verrucosa Larvae

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Phototactic movement of coral larvae may help mediate swimming behavior towards or against light, determining an individual's vertical distribution within the water column. Yet despite the ecological significance of larval behavior during dispersal, this phase remains poorly understood. Therefore, this study examined the role of light on *Pocillopora verrucosa* larvae. Transparent and blackened chambers were installed in the laboratory and field representing various light conditions and depths, respectively. A predetermined number of larvae were placed in each chamber and exposed to light conditions for 1 hour. On collection, chambers were separated into top and bottom sections and larvae were counted. In the laboratory, the majority of larvae (83.62%) were found in the top section of chambers compared to no light conditions where larvae were distributed equally throughout. Remarkably, larvae were observed to show a high level of positive phototaxis response to moonlight with most larvae (85.66%) counted in the top section of chambers. In the field, the majority of larvae (81.55%) were found in the top section of transparent tubes at all depths (1m, 7m, 15m). In blackened tubes under no light conditions, larvae were similarly observed to be distributed equally throughout. Collectively, these results reveal that *Pocillopora verrucosa* larvae have the ability to positively respond to light during both the daytime and the night. Thus, our understanding of larval behavior during dispersal should take into consideration the role light plays in this critical stage.

Keywords: Coral, Reproduction, Ecology, Dispersal, Physiology

Species Diversity of the Coastal Phytoplankton in the Northern Andaman Sea, Thailand

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Coastal phytoplankton community expresses as a key primary production that supports the marine ecosystem. So the high biodiversity and abundance of phytoplankton establishes the high food quality that leads to the complexity of trophic balance. Moreover the high species diversity combines with the optimal abundance that makes the strong and long-termed sustainability of marine resources. This study aimed to investigate the phytoplankton diversity index and evenness in two seasons of the coastal area, Ranong and Phang-nga Province. Samples were collected 18 stations in February (dry season) and December (rainy season) in 2018. The vertical haul was applied by a plankton net with 20 µm in mesh sizes, 30 cm. in diameters. The five environmental parameters were measured in situ. The results showed the total of phytoplankton species diversity in 126 species and 61 genera. The highest number diversity was centric diatom (47 species), followed by pennate diatom (39 species), dinoflagellate (34 species), blue-green algae (4 species), green algae (1 species) and silicoflagellate (1 species), respectively, The higher diversity index (3.51±0.06) and evenness (0.82±0.02) were recorded in the dry season more than the values (2.80 ±0.12, 0.68±0.01) were recorded in the rainy season in the northern area. Anyway, the southern area along river mouth station showed the opposite results (dry season 2.49±1.23, 0.60±0.29; rainy season 3.19±0.36, 0.77±0.06). The average abundance showed the highly fluctuation (438 - 1,214 × 103 cells.m-3) between season. Meanwhile, the environmental parameters showed quite similar values between season except the salinity decreased in the rainy season. The river mouth area was effected by the environmental variation more than the coastal zone in the northern area. Finally, a high species diversity and an optimal abundance of phytoplankton maintains and balances the coastal ecosystem. So, it may be determined that the low pollutant contaminated in this area. For the future study, the specific phytoplankton community will be drawn in the different marine ecosystem for a powerful conservation and sustainable management.

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Keywords: Phytoplankton, Species diversity, The Andaman Sea

Evolution of limpet-shaped shell in trochid snails: adaptation to two different environments

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Flattening of coiled shells has occurred in several gastropod lineages, while the evolutionary process is little known. The subfamily Fossarininae (Gastropod; Trochidae) is unique, because the four genera of this family vary considerably in extent of shell coiling/flattening. Broderipia and Roya have zygomorphic shells that have lost coiling, while the sister genera, Fossarina and Synaptocochlea have respectively turbiniform and auriform shells. We compared biology and morphology among these four genera to detect the selection pressure which has driven loss of coiling. We discovered that Broderipia iridescens live symbiotically in rock pits of sea urchins, and Roya eximia live on intertidal rock surfaces exposed to strong waves. Comparison of the morphology of soft bodies in Fossarininae revealed that the columellar muscle of flattened species has been drastically elongated as true limpet family, Nacellidae. The flattering and loss of coiling of the shell in Broderipia and Roya caused acquisition of a zygomorphic flat body, retraction of coiled visceral mass, and expansion of the foot sole. These morphological changes would have improved tolerance against strong waves and the ability to cling to rock surfaces in Roya, and would have enabled the commensal life in narrow space in sea urchin pits in Broderipia.

Keywords: torchid snail, limpet-shaped shell, algaevore

Population dynamics of *Boccardia proboscidea* and *Boccardiella hamata* (Annelida, Spionidae) inhabiting oyster beds in Sasuhama, northeastern Japan

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Spionidae is one of the largest family in Annelida and it shows diverse lifestyle and distribution in marine environment. *Boccardia proboscidea* and *Boccardiella hamata*, which belong to the family Spionidae, were found to be abundant in oyster beds in Sasuhama, Miyagi Prefecture, northeastern Japan. They are known as exotic species for the Japanese coastal environment; *B. proboscidea* is native to the Pacific while *B. hamata* is native to the Atlantic coast of North America. Larval developmental patterns of the two species are known to be different. The aim of this study is to monitor the populations of the two dominant spionids inhabiting Sasuhama oyster beds for a long-term period and discuss the factors which determine the density of the two species. The oysters were collected from the upper and lower layers of the concrete slope monthly from February 1999 to August 2000, September 2013 to November 2014 and April to September 2019. Worms were extracted from the mud in crevices of oyster shells and mud between oyster shells and concrete slope in the laboratory. Environmental factors (water temperature and salinity) were measured. After the worms were extracted from the shells, the number of males, females and immature individuals were measured monthly. The width of the fifth chaetiger is used as the criterion of the body size of each individual. Comparing the previous results of 1999 to 2000 and 2013 to 2014 with the present 2019 results, the population density of *B. proboscidea* drastically decreased in 2013 but again increased in 2019. On the contrary, *B. hamata* showed the opposite tendency that it increased in number in 2013 but decreased in 2019. Priority of the dominant species replaced in 2013, after the Great East Japan Earthquake and tsunami which occurred in 2011. There was no new recruitment of juveniles of *B. hamata* in expected season in 2019. We infer that the structure of the two species populations seemed to return to the state before the disturbance. Moreover, we will discuss the habitat preference of the two species.

Keywords: Annelid, Spionidae, *Boccardia proboscidea*, *Boccardiella hamata*, dominant species, long-term monitoring

Relationship between mangrove foliar δ15N and land use in some watersheds in Okinawa, Japan

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Eutrophication in coastal area can be induced by increasing of domestic drainage due to growth of population, and outflow of excess nutrients derived from agricultural fields. In recent years, it is considered that the outflow of excess nutrients to coral ecosystems which basically developed in low nutrient environments in tropical and subtropical sea, is the one of factors which gives stresses for coral communities. On the other hands, it has becoming clear that mangrove ecosystems in tropical and subtropical coastal area play an important role for conserving environmental water quality (bio-filter) by removing excess nutrients outflowing from inland. We have conducted studies on the bio-filter function of mangrove ecosystems, using stable isotope analysis. Stable isotope ratio of nitrogen (δ15N) is widely used as an index to estimate the origin of nitrogen in target substances. According to previous studies, the range of δ15N values of atmosphere, rain, chemical fertilizer, and organic fertilizer are 0 ‰, -8.0 to 2.0 ‰, -3.0 to 3.0 ‰, 2.7 to 15.4‰, respectively in general. In order to clarify the mechanism of bio-filter function of mangrove ecosystems, we firstly measured the δ15N value in mangrove leaves which were collected from deferent land-use area (i.e. urban, agricultural, and forest areas), to compare the values associated with the land-use conditions. The land-use ratio was calculated by using ArcGIS with data of National Land Information obtained from Geospatial Information Authority of Japan. As the results, significant positive correlations were observed between foliar δ15N values of mangrove and non-mangrove, and the area ratio of agricultural and urban areas. Moreover, as the slope of regression line for the correlation of mangrove species was larger than that of non-mangrove, it was estimated that mangrove species absorb anthropogenic nitrogen more than non-mangrove species

Keywords: mangroves, bio-filter, eutrophication, stable nitrogen isotope, ArcGIS

On the estimation of marine resource distribution of Timor-Leste by data fitting

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Tracking fishing activities is a measure to understand the distribution of marine biology, the abundance of resources, and the living conditions of fishers. This research uses experiences from the voyage data recorder (VDR) project of Taiwan to map the distribution of marine resources of Timor-Leste, an island at the southern end of Maritime Southeast Asia. Like many tropical islands, it should have an abundance of marine resources to feed its people and should be researched. Small scale fishing activities of Timor-Leste is collected by the Pelagic Data System (PDS) system. By correlating the written logbooks of catches, we can make the best matches to the PDS and map the distribution of resources. Currently, the activities of approximately 350 fishing boats are observed. Since the total number of fishing vessels is much larger than this number, by understanding the distribution of known fishing vessels, the results in this research can then be used to approximate the total marine resource of Timor-Leste more accurately.

Keywords: Big data, Small scale fisheries, Resource distribution, Data Visualization

The characteristics and expression profile of SQOR under sulfide tolerance in hydrothermal vent crab, *Xenograpsus testudinatus*

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Hydrogen sulfide is a lipophilic gas molecular which can directly pass through the cell membrane by diffusion. The toxic mechanism of H2S is the inhibition of cytochrome c, then interrupt the aerobic respiration. When animals encounter sulfide conditions, there are two strategies against the toxicity. One is sulfide detoxification, the other is anaerobic respiration. In the first step of sulfide detoxification, sulfide: quinone oxidoreductase (SQOR) transfers sulfur atoms from the high toxic sulfide to generate thiosulfate. Second, thiosulfate sulfurtransferase/rhodanese-like domain-containing protein (TSTD) and persulfide dioxygenase (ETHE1) mediates the conversion of thiosulfate to sulfite, transferring sulfur to a –SH-containing acceptor, like glutathione (GSH). In terminal step, sulfite oxidase (SO) converts thiosulfate into sulfide which has the weakest toxicity. In this study, *SQOR1* , *SQOR2* , *TSTD*, *ETHE1* and *SO* were found in transcriptomic data of hydrothermal crab. To understand the relationship between sulfide detoxification-related genes and sulfide, we compared the gene expression profiles with high sulfide conditions (field) and low sulfide conditions (raised in normal seawater > 1week). According to qPCR analysis, *SQOR1* was dominantly expressed in gill (Gi). *SQOR2* was dominantly expressed in the digestive gland (DG). Furthermore, *SQOR1* and *SQOR2* expressions were no significant difference between high sulfide and low sulfide conditions. Additionally, Western blot and enzyme activity assay showed SQORs was significantly increased in high sulfide conditions. To confirm the effect of sulfide, low sulfide conditions raised hydrothermal crab was incubated in the hydrothermal zone (HZ) and non-hydrothermal zone (NHZ) for 2 hrs. Results of hemolymph biochemical analysis revealed that sulfide metabolites: thiosulfate and sulfite were significantly increased in HZ compared with NHZ. In conclusion, these data suggested that although *SQOR* had no significant difference between high sulfide and low sulfide conditions, high sulfide conditions might induce the increase of protein level. Moreover, sulfide detoxification might not the key strategy for the hydrothermal crab to survive in high sulfide extreme environment.

Keywords: Sulfide, hydrothermal crab, SQOR, TSTD, ETHE1, SO

Systematics of the Bothid Flatfishes (Pleuronectiformes: Bothidae)

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The left-eyed flatfish family Bothidae comprises 175 recognized species in 20 genera and is the second largest family (after the Soleidae) within the order Pleuronectiformes. Bothids are benthic fishes and are widely distributed throughout the tropical and subtropical waters from the shallows to the deep sea (1,500 m). In the past, the systematics of the Bothidae was largely based on morphology. Even though the monophyly of the family is highly supported, the intrarelationships and the generic classification are still unresolved. Due to their relatively small body size, and the lack of useful diagnostic characters, the bothids are easily misidentified by morphology. Additional molecular tools and results from integrated approach in systematics are therefore essential for correct species identification and taxonomic revision. In this study, a total of 206 specimens belonging to 60 currently recognized species (14 genera) collected from 15 oceanographic expeditions under the *Tropical Deep-Sea Benthos* (TDSB) and from several fish landings in the West-Pacific were examined. Two molecular datasets (*COI* and combined) were compiled for the species delimitation and phylogenetic analyses. The *COI* dataset was primarily used to explore the species diversity and test the validity of recognized species. This dataset contained 463 sequences in which 205 were newly generated and 258 were obtained from the GenBank/Bold databases. The second dataset was composed of sequences from four genetic markers (*COI*, *EGR3*, *RAG1*, and *RH*) obtained from the representative taxa from 17 out of 20 currently recognized genera. This dataset was utilized to infer phylogenetic relationships of bothid flatfishes. Here, we presented the most comprehensive phylogeny of the family and validated a total of 108 species based on the combined evidence from phylogeny, species delimitation analyses, and others (i.e., morphology, genetic distance, geographic consideration, etc.), among them several are potentially new species. Our phylogenetic results also revealed that 4 out of 20 genera are polyphyletic including *Arnoglossus* (4 lineages), *Laeops* (3 lineages), *Parabothus* (3 lineages), and *Psettina* (2 lineages); the suggested revision on generic classification was addressed.

Keywords: Bothidae, Taxonomy, Systematics, Phylogeny

Comparative of various carbon sources on docosahexaenoic acid production from *Aurantiochytrium limacinum* FIKU003

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Aurantiochytrium, a heterotrophic protist is widely distributed in the marine environment and has a potential to produce a high concentration of Docoxahexaenoic acid (DHA). DHA is an omega-3 fatty acid that is essential for human and animal health. Fish oils are known as a source for DHA production in industrial scale. However, it associated with many problem such as unstable quality contamination and not suitable for vegeterians. *Aurantiochytrium* are considerate as an alternative source of DHA currently, which can accumulated DHA up to 30-40 % of total fatty acids. In this study, the biomass, lipid and DHA production of *A. limacinum* FIKU003 were investigated. *A. limacinum* FIKU003 were cultured with different carbon sources (glucose, crude glycerol and refined glycerol) at a concentration of 10 g/L. The highest biomass and lipid content were obtained from refined glycerol (4.95±0.08 g/L and 55.01±2.33 % dry weight). Whereas, the highest DHA content (13.00±0.80 % dry weight) was obtained from crude glycerol as a carbon sources. Later, the different concentration of crude glycerol 10, 20, 40, 80, 100 and 120 g/L were determined. Crude glycerol at 40 g/L showed the highest DHA production (15.87±0.84 % dry weight, 1.15±0.06 g/L and 230.42±12.24 mg/L/day). These results indicated that crude glycerol could be used as a low-cost substrates for DHA production from microalgae in industrial scale. However, DHA production was decrease when the glycerol concentrations increased (100 and 120 g/L), which may be oxygen supply is not enough due to viscosity issues with increasing glycerol content.

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Keywords: *Aurantiochytrium*, glycerol, docosahexaenoic acid (DHA)

Phytochemical compositions and potential pharmaceutical uses of *Padina australis* extract

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Currently, marine resources are an interesting source for pharmaceutical and cosmetics. The brown alga *Padina australis* is the most common species belonging to genus *Padina* that is mostly found in the coastal areas of Thailand. However, the utilization of this alga is limited. Therefore, this study aimed to evaluate the phytochemical compositions of *P. australis* collected from Sattahip bay. The alga sample was extracted with methanol then partitioned with *n*-hexane (Hex), dichloromethane (DCM), ethyl acetate (EA) and *n*-butanol (BuOH), respectively. The EA fraction was further purified using column chromatography to yield 8 subfractions (EA-1 to EA-8). All fractions were determined total phenolic contents, fucoxanthin contents, and the chemical compositions of EA-1 subfraction were analyzed by Gas Chromatography-Mass spectrometer (GC-MS). The results showed that the highest total phenolic and fucoxanthin contents were steadily increasing after fractionated step by step. The EA-1 subfraction was contained the highest total phenolic at 246.88±4.35 mg PGE/g extract. After the EA fraction was fractionated, the fucoxanthin contents were only found in the EA-1 subfraction at 50.40±0.22 mg/g extract. Moreover, the chemical compositions of EA-1 subfraction were analyzed by GC-MS method that the fucosterol was found as the highest amount at 23.43%. Follow by the (3β,24Z)-Stigmasta-5,24(28)-dien-3-ol (fucosterol derivative) and 1,3,5-Benzenetriol (Phloroglucinol) at 17.33% and 16.39%, respectively. In addition, the dl-α-Tocopherol and Δ-Tocopherol were found in the EA-1 subfraction at low levels (1.48% and 1.17%, respectively). The EA-1 subfraction of the brown alga *P. australis* was contained numerous bioactive compounds that have potential pharmaceutical uses such as phloroglucinol, fucoxanthin, fucosterol derivatives, and tocopherol derivatives.

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Keywords: *Padina australis*, Brown alga, Phenolic contents, Phytochemical compositions

Suggested type and benefit of the bottom trawl for sampling macrobenthos in Taiwan coast

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Macrobenthos have a variety of sampling gears, which can be roughly divided into sled, dredge, bottom trawl, corer, grab and trap. Among them, the bottom trawl is one of the best collection instruments. In Taiwan, the macrobenthic survey and research using bottom trawl mostly used research vessel or specimen vessel. However, the number of research vessel is scarce. The specimen vessel specializing in fish, crab collection, the number and diversity of macrobenthos are underestimated, furthermore, the researchers can not grasp the on-site environmental information and the investigation operation procedure, result in insufficient information during analysis.

In addition, there are many restrictions on the use of bottom trawl in Taiwan, such as regulations prohibiting bottom trawl within 3 nm from shore, vessel types and equipment not sufficient to operate bottom trawl. 2 m Agassiz trawl is a common benthic collection instrument in the world. Its advantages are light and easy to operate. By referring to the Agassiz trawl and related literature, out team revised 2 m Agassiz trawl and designed appropriate net length and mesh size suitable for the use of macrobenthos sampling in Taiwan coast. Through actual practice, it revealed 2 m Agassiz trawl has quite sampling efficiency. Comparing to research vessels and specimen vessels, can significantly reduce the towing time.

Compared with the economic bottom trawl, 2 m Agassiz trawl reduces the net width and the collection quantity is relatively low, which is not suitable for economic fishery operations. It is proposed that government agencies should be allowed to conduct surveys within 3 nm of the shore. It is also suggested 2m Agassiz trawl could be used as a standard benthic sampling gear to improve the current situation of inconsistent investigation methods and sampling efforts in Taiwan.

Keywords: marine macrobenthos, sampling, bottom trawl

The multiple effects of the Great East Japan Earthquake on the Pacific oyster *Crassostrea gigas*

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Eight years have passed since the Great East Japan Earthquake that caused huge damage to marine organisms. I divided the process of the earthquake into four main events—the initial earthquake including liquefaction, subsequent tsunamis, land subsidence and ground uplift—and examined the impact of each event on marine life including oysters. The effect of liquefaction on oysters was not confirmed this time. The tsunamis were found to have negative and positive effects on oysters. The earthquake and tsunamis resulted in the destruction of a large number of houses and buildings, which collapsed and were swept out to sea as debris. The movements of debris by the tsunami waves were likely to have crushed submerged rocks and stripped them of oysters. Huge oyster reefs that were developed at the mouth of the Matsukawa-ura Lagoon, Fukushima, northern Japan, were destroyed by the tsunamis, and pieces of the reefs, with living oysters, were spread around the muddy and sandy lagoon bottoms. As the results, new oyster reefs had formed on these redistributed pieces after the tsunami. Thus, earthquakes with tsunamis contribute to the creation of new habitats for sessile organisms. Several years after the earthquake, it is necessary to study the effects of ground elevation changes rather than the effects of the initial tsunamis. Land subsidence results in a downward displacement of the intertidal zone. At Mangoku-ura Lagoon, Miyagi, northern Japan, land subsidence of ~80 cm was observed after the earthquake and the intertidal zone was shifted to the subtidal zone. I examined species that have disappeared and those that have successfully colonized the transition area of Mangoku-ura Lagoon in the eight years after the earthquake. My observations showed that the ecological effects of land subsidence varied among species and locations. As expected, the impact of land subsidence was more severe for sessile organisms compared with mobile organisms. Due to land subsidence, the rocks, roots and trunks of cedar trees originally grown along shoreline sank below the seawater level and were used as settlement substrata by larval oysters and barnacles. I selected one rock and observed in detail the recruitment, growth, and death of oysters attached to it from 2011 to 2019. In September 2011 new juveniles were observed on the rock. The newly attached oysters grew steadily, and the oyster coverage on the rock surface increased. However, since 2016 oysters attached to the upper part of the rock have begun to die. It was found that a 40 cm uplift had occurred in the area around Mangoku-ura Lagoon by spring 2017. It is presumed that the death of individual oysters on the upper area of the rock is due to the increase in the ebb time at low tide because of ground uplift. If the uplift continues, new juveniles on the upper part of the rock will disappear, and the number of dead individuals will increase in the upper part compared with the lower part. The effect of 2011 earthquake on marine life continues in various ways.

Keywords: effect, earthquake, oyster, *Crassostrea gigas*, subsidence, uplift

Multi-scale temporal variation in phytoplankton biomass (chlorophyll-a) in the northern South China Sea

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Phytoplankton are major primary producers in marine ecosystems and can directly impact higher trophic levels. The abundance and distribution of phytoplankton are known to be related to water temperature, nutrient, light, and zooplankton grazing. Therefore, the phytoplankton dynamic is often linked to seasonal variations and mixed-layer depth (MLD). This study compiled and analyzed in situ fluorescence and chlorophyll-a (Chl-a) concentration data at the SouthEast Asia Time-series Study (SEATS, 116°E and 18°N) station in the northern South China Sea, to understand the phytoplankton dynamics in different time scales, diurnal, seasonal, and decadal scales. In situ Chl-a concentrations and water temperature were collected for 30 cruises throughout 1999 and 2019 at the SEATS station, and the euphotic depth integrated Chl-a concentrations were analyzed and compared with sea surface temperature (SST) and MLD. In the diurnal scale, the results showed the Chl-a concentrations increased during the day, decreased during the night time, and the variations could be as high as two-fold. In the seasonal scale, the Chl-a concentrations, SST and MLD showed two distinct patterns: the cold seasons (December and January) with low SST, deep MLD, and high Chl-a concentrations; the warm seasons (March to November) with high SST, shallow MLD, and low Chl-a concentrations. Seasonal Chl-a concentrations, SST and MLD also showed correlations. In the decadal scale, the 20-year data showed an increase in SST (cold season: 0.05 °C / year; warm season: 0.06 °C / year), a decrease in MLD (cold season: -0.80 m/ year; warm season: -0.52 m/ year), and a decrease in depth integrated Chl-a concentrations (cold season: -0.73 mg m-2/ year; warm season: -0.49 mg m-2/ year) at the SEATS station. The results suggest that, in short-term study, it is important to consider the diel fluctuations when conducting field sampling for phytoplankton and primary productivity studies; in the 20-year analysis, the increase of SST and the shallowing of MLD led to the decrease in Chl-a concentrations, and which may impact the ecology and resources in the northern South China Sea.

Keywords: phytoplankton, chlorophyll-a, sea surface temperature, mixed layer depth, the SouthEast Asia Time Series (SEATS) Station

Validating fisheries-dependent catch and effort data with observations from trawl surveys: an example of the Pacific northern shrimp *Pandalus eous* in the Sea of Japan

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Being one of the central issues in fisheries science and marine biology, catch per unit effort (CPUE) data has been assessed in numerous studies to infer trends in relative abundance of the species. While CPUE is a powerful tool in case where no fishery-independent observation (i.e., survey data) is available, there are many exceptions caused by various factors that can alter catchability, the proportion of the stock caught by a single unit of effort. The efficiency and accuracy of the CPUE should therefore be assessed carefully.

Here, we focused on Danish seine bottom trawlers targeting Pacific northern shrimp *Pandalus eous* Markov in the Sea of Japan, to detect historical changes of catchability and explore its potential causes. Pacific northern shrimp is common on the continental slopes from 300–1000 m depth in the northwestern Pacific and represents one of the most commercially important crustacean species in the Sea of Japan. From the beginning of its exploitation history, the fishery for Pacific northern shrimp has been unique among trawl fisheries in the Sea of Japan, as the fishing ground for the species are much deeper than those for the other species, and specific fishing gears (trawl nets) have been developed for deep muddy bottoms.

According to the official logbooks, shrimp fishery in the Sea of Japan has experienced dynamic changes throughout its history. While the total catch has fluctuated between about 900 and 3000 t from 1980s, nominal CPUE (annual catch/annual effort) has been continuously increasing through its exploitation history. The historical trends of fisheries production can be linked with the development of fisheries such as introduction of freezer and development of new fishing grounds, though such changes are not directly recorded in logbooks. As a result, nominal CPUE can mislead the interpretation of the stock status without appropriate statistical procedures.

We assessed official logbook data and standardize CPUE by two-step delta-generalized additive-models (GAM) to understand the historical changes of the shrimp fishery in the Sea of Japan. We extract effects of year, month, coordinates and prefecture of fleets from logbook for evaluating historical changes of catchability in a spatially-explicit manner. We also used the trawl survey data to better understand the geographic distribution and predict absolute abundance of the species in the Sea of Japan.

The standardized CPUE had been almost constant from late 1980s to early 2000s, then increased since 2003, which was remarkably different from the trends in the nominal CPUE. Trawl survey data also showed that the abundance of Pacific northern shrimp has been increasing after 2003, which is almost concordant with the inference from the standardized CPUE. The results suggest that there were historical changes of catchability in the shrimp fishery in the Sea of Japan and, we would further discuss the causes for such changes.

Keywords: CPUE standardization, Fisheries management, Trawl survey, Species distribution, Pacific northern shrimp

A new attempt to document the extraordinarily diverse form-taxa of “nauplius y” and “cypris y” (Crustacea: Thecostraca: Facetotecta) in plankton at Okinawa, Japan

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Uniquely within the Crustacea, the Facetotecta are known only from “nauplius y” and “cypris y” larvae and a subsequent slug-like juvenile stage, the “ypsigon”, while the adults remain unrecognized and hidden to science. Thirteen named species of *Hansenocaris* and a smaller number of other alphanumerically designated “types” of facetotectan larvae – some based exclusively on nauplii, some on cyprids, and a few on both – have been characterized in the literature, but only a handful of zoologists have had a chance to see their true diversity of form. Especially in East Asian waters, but elsewhere as well, many remain unpublished. Extensive plankton sampling and laboratory rearing of facetotectans conducted at Sesoko Island, Okinawa, Japan in 1996–1997, 2003–2005, and 2018–2019 has allowed us to recognize dozens of undescribed form-taxa there, particularly of lecithotrophic larvae. The very abundance of new forms, the technical difficulties in description posed by highly ornamented tiny creatures that undergo several molts, the refusal of some evidently planktotrophic kinds of facetotectan nauplii to molt at all in culture, and resistance in the zoological community to designating larvae as name-bearing types, have combined to make effective presentation and publication of these findings difficult. Here we present the scale of facetotectan diversity at Sesoko Island using video recordings of live specimens, SEM photographs, and stacked digital DIC photographs of late (usually last) naupliar molts. We propose to base formal descriptions of named species on combinations of such data for the last “nauplius y” instar and the corresponding “cypris y” stage of the different form-taxa, and present three examples of the procedure. Other directions for research on the Facetotecta populations of Okinawa and Taiwan, including the application of molecular systematic techniques to questions of diversity assessment and taxon delineation, will be the subject of a companion talk.

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Keywords: Facetotecta, nauplius, cypris, plankton, laboratory rearing, Okinawa, imaging methodology, larval taxonomy

Allelopathic algae effect on coral reef fish

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Coral reef ecosystem has underwent the phase shift from coral- to macroalgae-domanant system in many regions. Furthermore, some macrolage contain secondary metabolites that would repel the grazing behaviores of herbivorous reef fish, thereby slowing down the recovery of a health coral ecosystem. However, it remains unexplored if these chemical-rich macroalge have different repellent effects on different hebivore fish. In this study, we test the repllent effect of a chemical-rich macroalga, Galaxaura divaricata, on the foraging efficiency of different fish using tank experiments. This species are overgrowthing and occupied benthic substrates on many reef around Dongsha atoll, South China Sea. Our results showed that G. divaricata can have a great impact on the foraging efficiency for many fish by decreasing their grazing amount. Over all, most herbivore fish species show the avoidance behavior in contact with food treatments subjecting to G. divaricata. However, carnivore fish species show no difference between with or without G. divaricata treatments. This study revealed that the chemical-rich seaweed can affect foraging of reef fish, implying that the overgrowth of the chemical-rich seaweed might have adverse impacts on the benthic environment in the coral reef ecosystem.

Keywords: Dongsha, Galaxaura divaricata, Allelopathy, coral reef fish, herbivory

Characterization of the organic matter of biodeposits derived from marine aquaculture bivalves: a meta-analysis approach

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Bivalve aquaculture is one of the world's most important food sources for humans. However, an increase in biodeposits along with the expansion of aquaculture has led to the deterioration of the seabed. To date, there has been no consensus on the organic content and elemental ratio regarding the quality of a biodeposit. Therefore, in this study, we compiled data on the elemental content and ratio of biodeposits for the first time. Furthermore, we determined (1) the relationship between the carbon (C) contents of biodeposits and food conditions, and (2) the representative value of the stoichiometric ratio of biodeposits with reference to Redfield ratio, (3) a comparison between the taxonomic groups, such as Venerida, Pectinida, Ostreida and Mytilida of carbon/nitrogen ratio (C/N).

Nonlinear regression was performed for total particulate matter (TPM), chlorophyll a (Chl-a), and particulate organic carbon (POC) concentration, which are food concentration indicators. In addition, linear regression was performed to determine the C (%) of TPM, which is related to food quality. The response of C content of biodeposits to TPM showed a quadratic function type response, whereas that to Chl-a and POC concentration showed the Michaelis–Menten equation response. The C content of biodeposits was reduced to approximately 14% of the C (%) of TPM due to linear regression between C content of biodeposit and TPM. Biodeposit stoichiometry was estimated to be C:N:P = 141 (112–173): 13.2 (10.5–15.8): 1, which significantly differed from Redfield ratio. There was also a significant difference observed in the C/N between taxonomic groups, indicating that Pectinida is higher than Ostreida and Mytilida.

We, for the first time, showed several knowledge gaps, such as C content of a biodeposit related to a wide range of foods, the P content of a biodeposit, and data of biodeposits other than mussels with environmental variables. Using these data, we can estimate the C content of a biodeposit by using monitoring data (i.e., TPM and Chl-a) and obtain a more accurate stoichiometric ratio of a biodeposit. In the future, the influence of the differences in the elemental ratios among taxa on ecosystems should be elucidated.

Keywords: biodeposit, bivalves, aquaculture, organic matter

Phylogenetically distinct methanotrophs modulate methane oxidation in rice paddies and mangrove soils

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Methanotrophs can oxidize methane before it is emitted to atmosphere. However, the biogeographic distribution of active methanotrophs in rice paddies and mangrove soils across Taiwan was poorly understood. We used DNA-based stable isotope probing (DNA-SIP) to show that phylogenetically distinct type I and type II methanotrophs dominated methane oxidation in geographically different paddy and mangrove soils. High-throughput sequencing of soil 16S rRNA and pmoA genes under field conditions revealed that a type II methanotroph, Methylocystis, was predominant in rice paddy soils. In addition, an uncultured novel type I methanotroph cluster (Rice Paddy Clusters) was detected with the closest relatedness to Methylocaldum 16S ribosomal RNA (rRNA) genes in all rice field soils was tested. High-throughput sequencing of 13C-pmoA genes indicated the presence of novel methanotrophs that are phylogenetically distantly related to the type I methanotrophs Methylosarcina in four out of five non-acidic paddy soils studied, and the high proportions in the 13C-DNA suggested that these uncultured methanotrophs play an important role in methane oxidation. These results provide strong evidence for the environmental selection of phylogenetically distinct methanotrophs under field conditions. Moreover, community shifts in active methanotrophs likely occurred in response to environmental variations with fluctuating methane concentrations. Methanotrophs affiliated with the cluster Deep-sea-5 belonging to Type Ib methanotrophs were the most dominant methanotrophs in the fresh mangrove soils, whereas Type II methanotrophs also appeared in the fresh mangrove soils. High-throughput sequencing of the 16S rRNA gene also confirmed similar differences in methanotrophic communities at the different locations. However, several unclassified methanotrophic bacteria were found by 16S rRNA MiSeq sequencing in both fresh and incubated mangrove soils, implying that methanotrophic communities in mangrove forests may significantly differ from the methanotrophic communities documented in rice paddies.

Keywords: methanotrophs, mangrove, soils, rice

Seasonal variations of methane emissions from mangrove forests soils across Taiwan

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Coastal wetlands are important ecosystems providing multiple ecosystem services. However, these types of wetland soils such as mangrove forests were considered as sources of greenhouse gases. There are large areas of mangrove forests distribute along the west coast of Taiwan. The dominant species are *Kandelia obovata* and *Avicennia marina* in northwest and southwest coast, respectively. Nonetheless, there is little systematic research on greenhouse gas emissions from mangrove soils in Taiwan. In this study, *in situ* closed-path chamber and ultraportable greenhouse gas analyzer were applied to quantify seasonal variations of methane emissions from soils in several representative mangrove forests across Taiwan. The soil physiochemical characteristics, including temperature, redox potential, pH, salinity, electrical conductivity, density, water content, and organic matter, were analyzed to examine the effects of soil properties on methane emissions. The results demonstrate that methane emissions were higher in warm (spring and summer) than cool (fall and summer) seasons. This suggests that the methane emissions from mangrove soil are positively correlated with soil temperature.

Keywords: methane emissions, mangrove forests soils, environmental factors

From trophic contribution to ecosystem services: a mangrove case

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Chiku lagoon is the largest coastal wetland ecosystem in southwestern Taiwan. The mangrove forest located in the southeastern corner of lagoon has known for its importance on providing nursery habitats for various aquatic organisms and sustained local fishery production. While the significance of the mangrove is indisputable, the trophic contributions from mangrove to lagoon fishes as well as its subsequent ecosystem services have never been quantified. Applying stable isotopes ^{13}C and ^{15}N measures for major trophic guilds in the lagoon, the study is aimed to elucidate nutritional contribution and resultant ecosystem services of the mangrove. Result showed that Chiku mangrove contributed substantially to the organic carbon uptake by individual fish species as well as fish communities. The proportions ranged from 25% to 53% based on sampling locations within the lagoon. The lagoon food web model was then constructed using trophic relationships projected from stable isotope data. Based on this model, we estimated the nutritional contribution from mangrove to local fish biomass is around 17%, which worth roughly 47 million USD of fishery productions per year in the lagoon.

Keywords: Food web model, Stable isotope analysis, Trophic interaction, Ecosystem services

Coupling tidal creek evolution model with mangrove habitat suitability model in estuarine wetlands

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Mangrove forests provide a variety of benefits in the whole ecosystem. It is acknowledged that sea level rise effects have become increasingly severe on the impacts of mangrove ecosystem. Habitat suitability index (HSI) is an ecological model widely applied to evaluating the quality of habitats and helping integrated management. Step function was used to build the HSI models of inundation frequency and sorting coefficient corresponding with mangrove biomass per unit area. The HSI and field investigation were adopted to develop the mangrove habitat model for Wazwei wetland in the Tanshui River, northern Taiwan. The results of suitability-index function of inundation frequency proved to coincide with the field data. In addition, tidal creeks serve as critical habitat areas for shorebirds and fish in subtropical mangrove estuarine wetlands. A vertical two-dimensional evaluation model coupling with the HSI model for quantifying geomorphological changes of tidal creeks by governing the Exner equation. Dynamic mangrove biomass was incorporated into the model to demonstrate the growth effects of mangroves on mangrove productivity and sediment trap efficiency. The results illustrate that the rates of deposition and erosion on tidal creeks and tidal mudflats are different due to the energy and momentum of the different tidal prism, which would alter the amount, dimension and speed of geomorphological evolution. The model was verified by comparing with the bathymetry data investigated during the years 2007 and 2008 in Shezi mangrove wetland and revealed a reliable prediction ability. The simulations indicate that the presence of mangroves has a significant effect on declining flow velocity and bed shear stress. The mangrove has the capability of reducing the energy of tidal flow, and would thus affect the shape of the tidal creek. Also, the geomorphology would reach the dynamic equilibrium process under the situation of rising sea level.

Keywords: Mangrove, Habitat Suitability, Tidal Creeks, Mudflats, Hydrodynamics

The effects of water temperature on pharmacokinetics, optimal dosing regimen, and the occurrence of non-linear kinetics of florfenicol in Nile tilapia (Oreochromis niloticus)

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Nile tilapia (Oreochromis niloticus) is an economically important eurythermal fish species that has been reared in different climatic zones ranging from tropical to temperate. It is well known that water temperature has a significant influence on fish physiology by affecting the overall metabolic rate, blood flow, and enzyme activity. As a consequence, water temperature is among the most important factors that influence drug behavior in the fish's body. The aims of the current study was to investigate the effect of water temperature on pharmacokinetic (PK) parameters of florfenicol (FF) in Nile tilapia with the implication in optimal dosing regimen determination. Forty-two Nile tilapia (500-700 g) were reared at 3 different temperature level (24, 28 and 32°C) in laboratory condition. The FF solution was administered by oral gavage (PO) or intravenous (IV) at a dose of 15 mg/kg and the blood samples were collected at 0.25-72 h post-dosing. The sera were analyzed for FF concentration by HPLC-UV method. The PK parameters were determined by a 2-compartmental model using PKSolver 2.0 software and the optimal dosages were determined by pharmacokinetic-pharmacodynamic (PK-PD) principle, assuming that the minimum inhibitory concentration (MIC) of fish bacteria was 1, 2 and 4 µg/ml. Our results revealed that water temperature has a significant influence on PK parameters of FF. In general, higher the temperature resulted in increasing drug absorption (Ka) and elimination rate constants (β), the volume of distribution (Vd), and clearance (CL), and reducing the area under the curve (AUC) and mean resident time (MRT). In other words, the FF was absorbed and eliminated faster at 32°C compared to the lower temperatures. The calculated optimal dosages increase with increasing water temperature and target MIC levels, ranging from 2.23 (MIC 1 µg/ml at 24°C) to 34.88 mg/kg/day (MIC 4 µg/ml at 32°C). The accuracy of the calculated dosages was verified by comparing the measured serum concentration with the predicted value which suggests that the optimal dosing regimen determination by PK/PD approach is feasible provided that the drug PK behavior follows first■order kinetics. However, it appeared that at the highest dose studied, the observed serum concentration was deviated from those predicted by PK principle, suggesting that non-linearity was likely occurring. This speculation was proven by the subsequent experiment in which the fish (at 24-32°C) was orally administered FF at 4 different doses (10-45 mg/kg) and the results showed that non-linear kinetics were evident when the dose was >15 mg/kg (at 32°C) or >30 mg/kg (at 24°C). In conclusion, the recommended dosing regimen of aquaculture drugs is better based on a combination of drug PK parameters at a specific temperature level and drug susceptibility (MIC) of infecting bacteria rather than using a universal recommended dose unconditionally. The possibility of non-linear kinetics occurrence at higher doses should also be aware as it can complicate the optimal dosing regimen determination.

Keywords: Florfenicol, Nile tilapia, Optimal dosing regimen, Pharmacokinetics, Temperature

DO control of the water at a shrimp farming pond with a micro-bubble aeration system, and its effect on the growth of shrimp

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Puddle wheel or combined aeration system with blowers and air stones has been adopted widely for the shrimp culture. However, the capacity of these devices for dissolving oxygen gas to the water is fairly limited. In the shrimp farming pond, DO of the water tends to increase above the saturation level due to the oxygen production by the photosynthesis of phytoplankton during daytime, while it consumes DO of the water for respiration during nighttime. As the feed consumption increases in the pond following the growth of the reared shrimp, the decrease of DO of the water during the nighttime tends to become severer due to the respiration by the phytoplankton and the aerobic decomposition of the organic matters contained in the feces and food residues. DO of the water often falls to unhealthy levels for rearing shrimp during the nighttime, in particular, in the latter half of the culturing period.

We have developed a micro-bubble aeration system for the shrimp culture to prevent the occurrence of the unhealthy DO conditions (<5 mg O2 L^{-1}) of the water during the nighttime with extremely high capacity of the micro-bubble for dissolving oxygen gas to the water. Here, we report the results of the DO control experiment conducted at a vanammei shrimp culture pond in Chantaburi, Thailand. 440,000 individuals of young juveniles were released at each of the two ponds (80 x 80 m). The conventional aeration system with puddle wheels were installed at these two ponds. At one of them, which was referred to as “Experimental Pond”, two sets of the micro-bubble aeration system that had five nozzles for releasing micro-bubbles in a housing were set on the bottom of the pond, and released 20 L pre min. of micro-bubbles with mean diameter of 15 µm from each nozzle to the water. Another one without the micro-bubble aeration system was referred to as “Control Pond”.

In Control Pond, the daily min. DO of the water rapidly decreased to less than 3 mg L^{-1} when the daily feed consumption increased to about 240 kg d^{-1}, while the DO of the water was kept around 5 mg L^{-1} until the end of the culturing period when the feed consumption reached about 300 kg d^{-1} in Experimental Pond. These different DO conditions of the water between these two ponds were reflected to the growth of the shrimp. In Control Pond, 7,948 kg of the shrimp was harvest 105 days later from the start, when it grew to the mean body weight of 18.7 gww. In Experimental Pond, the growth of the shrimp was significantly accelerated to that of Control Pond. It reached the mean body weight of 20.0 gww, and 8,500 kg was harvested 82 days later from the start. The survival rate of the shrimp was estimated as about 97 % in both of the two ponds. Consequently, the food conversion rate (FCR) of the shrimp culture was improved from 1.72 in Control Pond to 1.15 in Experimental Pond.

Keywords: DO, micro-bubble generator, growth, shrimp culture

The effect of rapid invasion of clam eating moon snail Laguncula pulchella on the abundance of Manila clam Ruditapes philippinarum in artificial tidal flat constructed after the Great East Japan Earthquake

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The invasive naticid gastropod *Laguncula pulchella* (*Euspira fortunei*) introduced with the imported Manila clam *Ruditapes philippinarum* from China and Korea from 1990s, has become a new, strong predator of the clam stocks. At Mangoku-ura Lagoon near Oshika Peninsula, northern Japan, land subsidence of ca. 80 cm was observed after the earthquake occurred 11th March 2011 and the intertidal zone was shifted to the subtidal zone. Sediments from mountains have been added artificially to entrance of the Lagoon since October 2013 to maintain a shallow littoral zone and create tidal flats, where the Manila clam population could colonize and develop. There hardly inhabited living marine organisms in the artificial tidal flat just after the construction. Artificial tidal flat is a unique field, because it is possible to examine the process of how clams and moon snail recruit to, grow and settle in an artificial tidal flat. This is also important opportunity to investigate individuals that mature and reproduction for the first time in their life history in *L. pulchella* and the effect of clams in the early stages of recruitment. This study aimed to estimate predation amount of Manila clam by *L. pulchella*, and to ascertain the process of invasion in the artificial tidal flat. Sampling was conducted in two sites where constructed in 2014 (St. A) and 2016 (St. B) for the comparison of inhabiting situation and predation amount. Living moon snails, their egg masses and drill-hole shells by prey of the *L. pulchella* were found in second year after the artificial tidal flat was constructed in each study site. In St. A, *L. pulchella* grew to 18 mm in one year, matured and laid egg masses. The size of the egg mass was the smallest among the egg masses collected from northern Japan, where survival of *L. pulchella* was confirmed after the earthquake. Growth performance of *L. pulchella* and biomass of Manila clam in St. A was significantly higher than St. B. These results suggest that the time to maturity is different between the two sites. *L. pulechella* preyed most bivalves mainly Manila clam in all terms. The amount of clam predation in 2016 by *L. pulchella* was comparable amount of clam harvested by fishers in 2017 and 2018. Predation of clams by *L. pulchella* severely damages clam stocks that are recovering after the earthquake. Continuous individual and egg mass control is important for sustainable use of clam resources.

Keywords: moon snail, alien species, Laguncula pulchella, aquaculture, Manila clam, predation, artificial tidal flat

High resolution larval fish compositions of catch and by-catch species in coastal waters of Taiwan, ascribable to spatiotemporal and environmental factors

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"Bua fisheries" is the larvae fisheries targeted at Engraulidae (Anchovies) and Clupeidae (Herrings). It is commonly practiced in the coasts of Japan, Taiwan and mainland China, and the catches were mainly composed of Engraulis japonicas, Encrasicholina heteroloba, and Encrasicholina punctifer. The catch composition of Bua fisheries showed significant seasonal and geographical shifts in parts of waters around Taiwan based on previous studies with monthly samplings. To explore the catch composition variance in a shorter time period, we collected and analyzed weekly Bua catch in Taiwan waters from Ilan, Hualien, Pingtung, Kaohsiung, Taichung and New Taipei City in 2018, and the satellite environmental data at these locations. Generalized additive model investigated the relationships of environmental and biotic factors between bycatch rate and bycatch diversity. In this study, samples were clustered into five groups, including four groups related to anchovies and a group was composed of round herring (Dussumieria elopsoides), which was seldom discussed in the past. Models showed the sea surface temperature, location and length of anchovies significantly affected the bycatch rate. Likewise, location and length of anchovies significantly affected the bycatch diversity. Results from this study indicated high frequency sampling may provide more information about the Bua fisheries, and the resource of round herring might be underestimated in previous studies. Location or the mixed factor that location represented might affect the bycatch rate and diversity more than the environmental data we used in the study. We speculated larger anchovies have enhanced-movement behavior to form small pelagic fish schooling, and which might simplified the composition in unit space and decrease the bycatch rate. We suggest long-term and high frequency samplings should be considered to assess fisheries resource comprehensively.

Keywords: Bycatch rate, Bycatch diversity, Bua fishery, Dussumieria elopsoides, Larval fish

Ocean biodiversity listening project: an acoustic approach of marine ecosystem assessment

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Information on marine ecosystem dynamics is essential for effective management of marine conservation. Many sensing techniques have been developed to acquire variations of ocean physical properties, but it remains difficult to acquire information on marine biodiversity effectively. Ocean sound has been recognized as an essential ocean variable in the Global Ocean Observing System in order to understand how noise affects marine life, and how acoustic sensing can assess biodiversity and ecosystem health. However, acoustics-based ecosystem assessment has not been widely employed due to the challenge to separate sounds from environmental, biological, and anthropogenic sources. In this presentation, we propose an Ocean Biodiversity Listening Project, which aims to collect broadband and long-duration audio data from various marine ecosystems. By integrating machine learning in audio source separation, an underwater soundscape can be effectively separated into biological and non-biological components. The separation of biological sounds thus allows for a more efficient investigation on the species identification and behavioral observation of soniferous animals. In order to demonstrate the feasibility of the Ocean Biodiversity Listening Project, we present the audio data collected in Cebu, Philippines. Our results showed that underwater soundscapes of seagrass and coral reef habitats changed with diurnal, tidal, and lunar cycles, but different habitats display their own specific changing patterns. The analysis of acoustic diversity indicated that coral reefs harbor a higher diversity of marine animals, such as soniferous fish and crustaceans. Despite the diverse biological sounds, coral reefs are still suffering from tourism activities that generate prominent shipping noise in the daytime. By recording ocean sounds, we show that managers of marine protected areas and ecological researchers can obtain ecological observations with high temporal resolution. The audio data can also be shared in an open data platform to facilitate ecological education, citizen science, and inter-disciplinary collaborations. This year, we created a Python-based open toolbox, Soundscape Viewer, to assist soundscape information retrieval. With the open-sourced tools and cloud computing resources, people can assess ecosystem dynamics and potential change of ecosystem service in an acoustic point of view.

Keywords: Ecoacoustics, marine soundscape, ocean sound, acoustic diversity, soniferous animal

Unprecedent effort in conserving the critically-endangered caryophyllid coral Polycyathus chaishanensis (Scleractinia; Caryophyllidae) in the Datan algal reef, Taiwan

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Polycyathus chaishanensis is a symbiotic caryophyllid coral described from a single population in a tidal pool off Chaishan, Kaohsiung, Taiwan. Due to its rarity, P. chaishanensis was declared a critically-endangered species under the Taiwan Wildlife Protection Act. In May 2017, a *P. chaishanensis* colony was discovered in the intertidal area of the Datan algal reef, Taoyuan, Taiwan. To confirm whether this is a stable population in the algal reef, a demographic census—including occurrence, distribution, and measurement of colony size—was carried out in the algal reef in southern Taoyuan. Intertidal censuses and sediment collections were conducted at five different sections—Baiyu, Datan G1, Datan G2, Yonghsin, and Yongan algal reefs—during the monthly spring low tide from July, 2018 to January, 2019. In total, 84 colonies—23 in Datan G1 and 61 in G2—were recorded in the tidal range between -160 cm and -250 cm, according to the Taiwan vertical datum 2001 compiled by the Central Weather Bureau. No *P. chaishanensis* was found in Baiyu, Yonghsin, or Yongan. The *P. chaishanensis* colony sizes ranged from 2.55 to 81.5 cm in diameter, with the larger *P. chaishanensis* present in the lower intertidal zone. Extremely high sedimentation was found, with monthly site averages ranging from 3818.26 to 29166.88 mg cm^{-2} d^{-1}, and significant difference between sites and months, affecting the distribution of P. chaishanensis in the algal reef. Our studies confirm the existence of a second population of *P. chaishanensis* in Taiwan, which highlights the importance of the Datan algal reef for the survival and protection of this critically-endangered caryophyllid coral and why it is so urgent that the reef is conserved.

Keywords: Polycyathus chaishanensis, Datan algal reef, critically-endangered, Taiwan Wildlife Act

Effect of the 2011 Tohoku earthquake tsunami on trematode community in the mud snail, *Batillaria attramentaria*

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Coastal organisms of northeastern Japan were heavily affected by the 2011 Tohoku earthquake tsunami. The tsunami can have long-term effects on coastal ecosystems. Since trematode parasites have complex life cycles and infect multiple hosts in different trophic levels, they can be used as indicators of disturbance and recovery of coastal ecosystems. We examined trematodes in the mud snail, *Batillaria attramentaria*, at five study sites in Sendai Bay for 2 years prior to and eight 8 years after the tsunami to evaluate the effect of the tsunami on trematode community. Our ecological monitoring demonstrated that the prevalence and species richness of trematodes in the intertidal snail host were significantly reduced after the tsunami, and their community structure has not recovered 8 years after the tsunami. The instability of the trematode community structure could be explained by the alteration of first and second intermediate host communities. Our study suggests that it will take more time for the recovery of the trematode community and the associated coastal ecosystem in the Tohoku region.

Keywords: Tsunami, The Great East Japan Earthquake, Disturbance, Parasite

Reef fish diversity in the Mu Ko Surin marine national park, Andaman sea, Thailand.

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Reef fish fauna was surveyed at 9 different sites in the Mu Ko Surin national park, Thailand, during three different expeditions, January, March and November 2018, with the goal of determining how species are distributed within its waters and its local characteristics. Data was collected by underwater visual census, compiled and analyzed using R statistical software. Among the 197 species found in Mu Ko Surin, damselfishes were always dominant, but a shift in dominant species was observed between sites. Ko Satok had the highest diversity but also the largest deviation. While the sites with lowest diversity (Ao Meh Yay and Chong Khad) were less variable. As for richness, Ao Pakkad had the highest mean species count per census (32.7±10.1). Overall diversity was high compared to other sites in Thailand, as H' index mean values varied from 5.6 to 9.2. Shannon's gamma diversity was also high (23) and similar do the averaged (alpha) richness per transect (27.6±7.2). In addition, beta diversity (3.27) indicates a number of 3 effective communities within Mu Ko Surin. Pairwise analysis show no significant difference between Ko Satok and other sites. However, Chon Khad held the largest dissimilarities, with $p<0.05$ when compared to four other sites, followed by Ao Meh Yay, significantly differing to 3 sites. Finally, pairwise results indicate significant changes to the community on November only, while January and March were not dissimilar. This might be due to the different water conditions in this month, shortly after monsoon rains. In conclusion, Mu Ko Surin presents a highly diverse reef fish community, supporting the importance and effectiveness of this marine park in Andaman sea waters.

Keywords: Reef fish, Mu Ko Surin, Andaman sea, Thailand, Diversity

Latitudinal variation in growth and survival of juvenile corals

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Reef-building corals inhabit a wide range of temperature and irradiance environment from the tropics to subtropics, up to >30 degrees in latitudes. However, we know little about the latitudinal variation and its extent in their biological performance. Here, we examined annual growth and survivorship of juvenile corals at 11 locations over 17º S to 33º N latitude in the central and western Pacific, and compared results among four common coral genera; two fast-growing taxa (Acropora and Pocillopora) and two slow-growing taxa (Dipsastraea and Porites). Exponential regression estimated 16 and 14% increase in growth rates for Acropora and Pocillopora, compared to 6 and 1% for Porites and Dipsastraea, for each degree Celsius increase in annual average seawater temperature. Survivorship of juvenile corals did not show clear latitudinal patterns. This study provided the first step toward better understanding of latitudinal variation in coral biological performance. Given the size-dependency of coral demography, the results suggest a significant latitudinal variation in coral dynamics, especially, in fast-growing coral taxa.

Keywords: Coral, growth, mortality, latitude, temperature

GenBank is a reliable resource for 21st century biodiversity research

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Databases of taxonomically annotated DNA sequences have revolutionized ecological and evolutionary research. The accuracy of these annotations has been questioned but never examined comprehensively. In the present study, we estimate the taxonomic accuracy with a distance-based clustering analysis of metazoan mitochondrial gene sequences in GenBank. We found, contrary to expectation, little evidence for major errors in taxonomic annotations, with fewer than 0.05% being mislabeled at the order level or above. Even at the genus level, estimates of incorrect assignments ranged from only 0.52-2.9%, with the lower estimate more likely to be accurate. This encouraging result is of particular importance in light of the rapidly growing use of high-throughput sequencing for community analyses without vouchers for characterization and monitoring of biodiversity.

Keywords: Biodiversity, DNA reference, Mitochondrial genes

Coastal surveys (rocky shores, tidal flats, seagrass beds, and algal beds) in Monitoring Sites 1000 Projects: A long-term monitoring project in Japan

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Monitoring Sites 1000 Projects

Japan consists of both large and small islands, spanning from the subarctic to the subtropics. The islands have winding coastlines and undulating mountains. The variation in topography means that animals and plants adapted to different environments are found in various locations throughout Japan. In 2003, The Ministry of the Environment of Japan launched a long-term ecosystem-monitoring project called "Monitoring Sites 1000 Projects," based on the Second National Biodiversity Strategy of Japan. This ongoing project aims to detect qualitative and quantitative changes in various ecosystems in the Japanese archipelago, such as alpine zones, forests, "satoyama", inland waters, and coastal regions. This project established over a thousand monitoring sites, which will be surveyed for 100 years.

Monitoring the coastal regions

As a part of this project, we are involved in ecosystem surveys that cover coastal regions (rocky shores, tidal flats, seagrass beds, and algal beds), with the objective of monitoring biodiversity in these wetlands. These coastal surveys have been conducted for 12 years, using both qualitative and quantitative methods to assess biodiversity. The data obtained in the project are published on the webpage of the Ministry of the Environment of Japan. It is expected to be used for analyzing long-term fluctuations of the biota and flora in each of the studied regions, the elucidation of the factors behind such fluctuations, as data accumulate in the future. In addition, novel information on the invasion of alien species and the occurrence of endangered species will be obtained. These data will be used for planning conservation measures, such as preventive measures for alien species, the protection of endangered species, and identification of Red List Species. Furthermore, some of the data obtained from the coastal surveys will be shared through two global databases, the Ocean Biogeographic Information System (OBIS) and the Global Biodiversity Information Facility (GBIF), to help elucidate the long-term fluctuations in biota and flora on a global scale. On a regional scale, the biota and flora data are also used to meet the criteria for registration with the Ramsar Convention, directly contributing to wetland conservation.

Keywords: Long-term monitoring, The Ministry of the Environment of Japan, Coastal region, Biodiversity

Citizen-based monitoring projects in tidal flats along the Japanese Coast.

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The quantitative surveys of the benthos communities performed during the Monitoring Sites 1000 Project's Coastal Area Survey are suitable for analyzing community dynamics. However, long-term studies over a wide area are time-consuming and expensive.

In comparison, citizen-based monitoring technique (Suzuki & Sasaki 2010) is simple, quick, and inexpensive, and yields accurate data on species diversity.

Therefore, using citizen volunteers, we conducted long-term monitoring of the benthos communities in the tidal flats along the coast of Tohoku district, which was severely affected by the tsunami caused by the 2011 East Japan Great Earthquake disaster. Benthos species richness decreased sharply just after the tsunami. Subsequently, the benthos species recovered and the community compositions gradually approached the pre-tsunami condition in most tidal flats. Nevertheless, the species compositions and dominant species of benthos differed in tidal flats located near the shore. Therefore, the indigenous composition of each tidal flat must sustain the diversity of the meta-community as a whole (β diversity).

These results suggest that this investigation technique is effective for long-term monitoring of wide areas.

In addition, we aimed to educate citizens regarding environmental conservation at the tidal flats at Obitsu river estuary (Chiba), Ena estuary (Kanagawa) and Waka-ura (Wakayama). In the Yatsushiro Sea (Kumamoto), we applied the citizen-based investigation technique to clarify the benthos fauna along the coastal zone. At Minami-Sanriku (Miyagi) and Arao (Kumamoto), we performed an investigation involving high school and primary school students to help them understand the biodiversity of tidal flats.

Keywords: Citizen-based monitoring, long-term monitoring, tidal flat, species richness, after the tsunami

Spatiotemporal variation in the macrozoobenthic biodiversity and community structure in Japanese tidal flats: Analyses based on data from the Monitoring Sites 1000 Project

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The structures of macrozoobenthos assemblages were monitored at eight tidal flats (Kabira, Nagaura, Nakatsu, Nanki-Tanabe, Shiokawa, Banzu, Matsukawaura, and Akkeshi) that span the Pacific coast of Japan, from 2008 to 2016, as a part of the Monitoring Sites 1000 Project of the Ministry of the Environment (MOE), of Japan. Surveys are conducted at each site once a year, during spring and summer, and combine qualitative surveys by scientists and quantitative sampling. The datasets for the first 9 years showed a clear latitudinal gradient in macrozoobenthic diversity, which was highest in southwestern sites (293–322 taxa in Kabira, Nagaura, and Nanki-Tanabe) and lowest in the northeastern site (110 taxa in Akkeshi). In the 2008 to 2016 surveys, 161 endangered species on the MOE Red List were found, including 41 species in classes I and II. There were more endangered species at the southwestern sites (45–56 taxa in Kabira, Nagaura, Nakatsu, and Nanki-Tanabe) than at the other sites (5–32 taxa). Multivariate analyses (nMDS, cluster analysis, and ANOSIM) showed that the macrozoobenthic community structure was unique to each site and showed clear geographical gradients from southwest to northeast. The community structure was also unique to the several sampling areas in each site, showing the patchiness and heterogeneity of faunal diversity across various spatial scales, representing α-, β-, and γ-diversity. Multivariate analysis detected drastic interannual variation in the community structure at the Matsukawaura site, which experienced the 2011 Tohoku Earthquake tsunamis. These findings suggest that long-term monitoring projects in tidal flats on a broader spatial scale are necessary to detect natural and anthropogenic changes (and subsequent recovery) caused by factors such as climate change, disasters, biotic invasions, and anthropogenic habitat degradation.

Keywords: Macrozoobenthic community, biodiversity, geographical change, long-term monitoring, tidal flat, Japanese Archipelago

Habitat alteration and benthic animal biodiversity in the Sanriku Coast after the 2011 earthquake and tsunamis

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The environments along the coastline of the 'Sanriku' region in northern Japan were severely damaged by the Tohoku earthquake in 2011. Tsunamis and subsidence caused by the earthquake had created and restored a lot of intertidal areas of various sizes along the Sanriku Coast. In addition, some of reconstruction works by humankind created and modified estuarine and coastal environments unconsciously and/or intentionally. There is no doubt that both these natural and artificial habitat alterations affect the coastal biodiversity, so that we have been monitoring shallow-water benthic faunas of a variety of habitats including the newly created and restored intertidal areas. Quick colonization of diverse benthic animals indicates the potential of contribution to ecosystem services, and the newly created as well as restored tidal flats have been free from the alien predatory snail *Euspira fortune* (Reeve, 1855) so far. This direct-developing species has been unintentionally introduced with its prey Manila clam *Ruditapes philippinarum* (Adams & Reeve, 1850), which is an important fishery resource, to northern Japan and are having a great impact on its prey bivalve community including the clam populations. On the other hand, the non-indigenous invasive pigmy mussels, *Xenostrobus secures* (Lamarck, 1819), have been found and are increasing in an artificial marsh, Furukawa-numa that connects with the Kesen River flowing into the Hirota Bay. This is the first record of this invasive species in the Sanriku region, and the introduction probably via a large number of shipping arriving at the mouth of the Kesen River. Since it is well known that the invasive mussel *X. secures* has a strong impact on benthic community structure, a careful monitoring and control of the mussel population should be continued for maintaining the benthic biodiversity of the Sanriku Coast.

Keywords: alien predatory snail, artificial marsh, ecosystem services, invasive pigmy mussel, newly created and restored tidal flats

Population genetic structures of two ocypodoid crab species along the Japanese coast

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Biodiversity includes three levels, i.e., ecological, species, and genetic diversities. Genetic diversity represents the variation of genetic characteristics within a species, which could positively influence the survival of species by facilitating adaptation to environmental changes and/or enhance resilience to the changes. The Pacific coast of northeastern Japan (the Sanriku region) is an ecologically diverse region where several currents meet, making the region a fascinating and important field for studying the population genetic structure of marine organisms. The Tsushima Current flows into the Pacific from the Sea of Japan through the Tsugaru Straits. The Kuroshio Current flows northward along the Pacific coast of Japan, and then leaves the coast eastward from central Japan. Two genetically deviated groups co-occur in local populations of some coastal species in the Sanriku region; this divergence may be attributed to the independent origins of each individual, i.e., the upper streams of the Tsushima and Kuroshio Currents. On the other hand, some coastal species are absent in the Sea of Japan in spite of widely distribution along the Pacific coast of the Japanese mainland. Their northern local populations exist further north than the extent of the Kuroshio Current in the Pacific coast and therefore these species can show unique genetic structures in northern populations. However, their population genetic structure remains unknown. We focused on two intertidal ocypodoid crab species that do not inhabit Japanese coasts along the Sea of Japan, i.e., *Macrophthalmus japonicus* and *Scopimera globosa*, to examine genetic diversity and population connectivity among local populations based on analyses of the mitochondrial cytochrome *c* oxidase subunit I. Over 80 haplotypes were obtained form 154 individuals of *M. japonicus* collected at 10 sites from Tohoku (northern Japan) to Kyushu (southern Japan) regions. Haplotype and nucleotide diversities of *M. japonicus* were relatively high in most of the local populations (haplotype diversity, Hd = 0.92–0.99, nucleotide diversity, $\pi = 0.00629–0.00946$) but low in the northernmost station (Hd = 0.68, $\pi = 0.00382$), which is further north than the extent of the Kuroshio Current. Pairwise F_{ST} analysis also clearly showed differentiation between the northernmost and other local populations. Contrastingly, only seven haplotypes were obtained from 170 individuals of *S. globosa* collected at 12 sites from Hokkaido to Kyushu areas. Genetic diversity was low (Hd = 0–0.52, $\pi = 0–0.00209$) compared with *M. japonicus*. Especially, a single haplotype was recovered from the Pacific coast from the northern (Hokkaido) to southern Japan (Wakayama prefecture). We revealed that the two similarly distributed ocypodoid species differed in the population genetic structure. In the presentation, we will discuss mechanisms which caused differences in genetic structures between these ocypodoid species and other species in the Japanese coast, such as the forktongue goby *Chaenogobius annularis* and “*Clymenella*” *collaris* (Annelida: Maldanidae).

Keywords: Dotillidae, Macrophthalmidae, Ocypodoidea, shallow water

Phylogeographic variation in the Asian horn snail *Batillaria attramentaria* (Mollusca: Gastropoda) along the Japanese coast

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The Asian horn snail *Batillaria attramentaria* is a ubiquitous intertidal gastropod in Japanese coastal areas. A previous study based on nucleotide sequences (384 bp) of the mitochondrial cytochrome *c* oxidase subunit I (COI) gene classed *B. attramentaria* individuals into two phylogenetically distinct groups, each distributed along a different warm current. Such a genetic structure of *B. attramentaria* was attributed to its low dispersal ability which relates to the direct development. Similar spatial patterns of genetic variation have been reported for organisms living on the Japan coast and are considered to reflect historical environmental changes. Unintentional transportation of *B. attramentaria* among clam and oyster seedlings for aquaculture has been reported within and outside of Japan. Therefore, the present distribution of *B. attramentaria* is thought to have been affected by historical major environmental changes such as the glacial-interglacial cycle and by human-mediated transport. In the current study, nucleotide sequences of the COI gene (1020 bp) and genotyping data for 14 microsatellite loci were obtained from B. attramentaria collected from 56 sites in Japan and two sites in Korea to clarify its population genetic structure in greater detail, and to detect individuals dispersed by human-mediated transport. As observed in the previous study, molecular phylogeny of the COI gene showed two genetically distinct groups distributed along two warm currents; however, Bayesian clustering of the microsatellite data showed three groups, mainly distributed in (1) coasts along northern Kyushu Island, the Japan Sea, and Hokkaido, (2) Pacific coasts of the Tohoku district, and (3) Pacific coasts from the Kanto to Kinki districts. The results of our genetic analyses indicate that isolated populations on the Japan Sea and Pacific coasts of Japan expanded northward separately, and were reunited on the coast of the Tohoku district. In addition, human-mediated transport related to aquaculture was confirmed in several populations.

Keywords: Phylogeography, *B. attramentaria*, genetic structure

Are coral associated barnacles suspension feeders or they have to derive carbon from their coral hosts?

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There are several groups of barnacles that are associating with fire and scleratinian corals. Within the superorder Thoracica, the family Pyrgomatidae are exclusive coral-inhabiting species. The barnacle *Wanella milleporae* is also exclusively live on fire corals and this genus is suggested to be housed in its own family based on recent molecular data. The bases of pyrgomatid and *Wanella* are embedded in the coral skeletons. In the family Balanidae, Megabalanus ajax are large size barnacles that only growth on the surface of fire corals. The superorder Arothoracica contains the genus Berndita, which bores in the scleratinian corals. The trophic modes of coral associated barnacles have not been extensively studied. It is believed that these barnacles are epibionts on corals and rely on filtering zooplankton as their main diets. However, the bases of some pyrgomatid barnacles have perforations and it is believed there may be some chemical mediations between the barnacles and its coral hosts through those perforations. In the present study, we used a mixed model analysis to examine the δ13C and δ15N stable isotopes of coral associating barnacles including species in Pyrgomatidae, Balanidae and Acrothoracica. Results revealed that *Berndtia* (Acrothoracica) and *Megabalanus* (Balanidae) are truely suspension feeders and feed on zooplankton as their major diet. Pyrgomatid species had mixed signatures (corals and zooplankton) of δ13C and δ15N stable isotopes suggesting there are some kinds of chemical mediations between corals and pyrgomatid barnacles.

Keywords: Coral reefs, barnacles, symbiotic

Diversity of bivalves symbiotic with crustaceans

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Biotic interactions are one of the key drivers of evolution and diversification of organisms. Bivalves are the second largest group of mollusks, with more than 9,000 species. They are highly successful in various marine and freshwater habitats and exhibit extreme morphological and ecological diversity. Predation by crustaceans has been well recognized as a major selective force in the morphological and behavioral evolution of bivalves. However, compared to that, how symbiotic interactions with crustaceans affect their evolution remains less studied. In this talk, I will review the diversity, evolution, and adaptation of bivalves symbiotic with crustaceans. Bivalves symbiotic with crustacean hosts are known from at least three marine families (i.e., Galeommatidae, Myidae, and Ostreidae). Among them, Galeommatidae is distinctive because it includes the largest number of crustacean-associated species (> 40 spp.) and the highest host crustacean diversity (e.g., mantis shrimps, mud shrimps, ghost shrimps, hermit crabs, crabs, and tanaids). Most crustacean-associated galeommatids are commensals that live on the host burrow walls, and some are known as ectocommensals. Recent molecular analyses suggest that galeommatid evolution includes at least 13 independent colonization events into the crustacean hosts, including repeated colonizations of the same host taxa by different lineages. Galeommatids ectosymbiotic with crustaceans often show a high degree of morphological and behavioral specialization and some of them represent an evolutionary convergence. Furthermore, I will show that not only host shift but also microhabitat shift within the same host can dramatically change the morphological and ecological characteristics of galeommatids. Overall, symbiotic interactions with crustaceans make significant contributions to the morphological and ecological diversity of this bivalve group.

Keywords: Galeommatidae, host shift, molecular phylogeny, Mollusca, specialization, symbiosis

Windows for animals: Understanding the functions of the unique window structure in the shell of sponge-inhabiting barnacles

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Sponges are common habitats of marine ecosystems and housed diverse commensals, but the relationships between associates and host sponges are unclear. Sponge barnacles are one of common sponge-associated fauna and some species have hollow openings between shell plates or so called “windows”. These windows are covered by the specialized membrane. We examined the windows of two species of sponge-inhabiting barnacles Acasta sandwichi and Acasta crucibasis (Thoracica: Acastinae). Under SEM (scanning electron microscope) observation, many sphincter-like opening structures (about 5 µm in diameter) were distributed on the membranes. This structures may be related to symbiotic adaptions and involved in chemical mediations between the barnacles and hosts. However, when these sponge barnacles were isolated from their hosts and cultured in the aquarium, they exhibit a gradual closure of the windows (recorded by daily photos). We used CT (computerized tomography) scan to confirm the calcification starts from the margin to the center of the windows. To further examine any microbial relationships through these windows, we made paraffin sections of a decalcified A. crucibasis specimen and performed H & E (hematoxylin and eosin) and Hoechst (cell nuclei) staining. The sections of a freshly fixed Sponge barnacle specimen showed a lot of small hematoxylin stained and Hoechst stained spots around the mantle cavity, especially in the tissue behind the window membranes. These small spots disappeared when the barnacles started to close the windows. We confirmed these small spots are bacterial cells by FISH (fluorescence in-situ hybridization) analysis using bacteria RNA probe. Further studies will address the nature of these bacteria and examine whether they are present in the sponge hosts as well.

Keywords: Symbiosis, marine sponge, sponge-inhabiting barnacle, FISH, CT scan

The biology and lifecycle of enigmatic crustacean y-larvae

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The vast majority of marine animals have been allocated to higher taxon, family or species, whether that be planktonic larvae or adult stages. Yet, one widely distributed group remains an enigma in zoology: crustacean “y-larvae”. As the adult stage of y-larvae is undiscovered still, they rank among the most elusive metazoan taxa. Next-generation sequencing and larval morphology revealed 50+ previously unknown species of y-larvae from a single tropical harbor in Sesoko Island, Japan. We show that y-larvae are likely highly specialized, and entirely overlooked, endoparasites in still-unknown hosts. First, six naupliar stages emerge in the plankton (dispersal). Then, a single cypridoid larva emerges after a dramatical metamorphosis from within the last nauplius larva (attachment, injection). Subsequently, a slug-like ypsigon larva, excites the cyprid cuticle (endoparasite). TEM, CLSM and LM revealed that this is entirely unsegmented and has no appendages, mouth, gut, eyes or even primordial testes or ovaries. Thus, this is an entirely new crustacean larval form. Additionally, it possesses a complex anterior nervous system and powerful muscles. By using a pair of antennular claws and a spiny, spear-shaped labrum, it is believed that the cyprid attaches to and subsequently pierces the host, whence the ypsigon escapes and initiates its endoparasite life. Our results are important in unravelling the evolution and origins of larval dispersal and the morphology of sensory and attachment structures in the most specialized invertebrate larva, the cyprid.

Keywords: Crustaceans; Y-larvae; unknown parasites; nauplii; cyprid; larval evolution; attachment; TEM; SEM; CLSM; LM

The effect of the isopod parasite, *Gyge ovalis* on the mud shrimp, *Upogebia major* in the west coast of Korea

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The sudden prevalence of mud shrimp, *Upogebia major* on the tidal flat in 2012 has been still a threat to the clam culture in the west coast of Korea. According to our preliminary study, more than 15% of the shrimp population was infected with bopyrid isopod, *Gyge ovalis* (Shiino, 1939). Therefore, the purpose of this study is to investigate the effects of this parasite infection on the host shrimp population.

Mud shrimps were collected monthly from February 2012 to December 2015 for about four years. Samples were categorized by infection first and then sex ratios, growth, ovigerous female and timing of infection were examined. As a result, 29% of the shrimp population was infected by various species of macro-invertebrates, of which 94% were infested by the most dominant parasite *G. ovalis*. There was a difference in infection rates between females and males, which was higher in females. During the study period, two cohorts of the shrimp population appeared. In 2010 cohort, mean carapace length (CL) of non-infected and infected groups both was about 21 mm at the beginning of the study. Three years later, however, shrimps of the non-infected group grew to 30 mm (CL), while those of the infected group only reached to 25 mm (CL). It is noteworthy to find the infection of the newly settled juveniles of 5 mm (CL) in size in 2014 cohort. In the other hand, the growth impact of the shrimp started from one year after the settlement. Condition factor appeared significant between the non-infected and infected groups. The weight of infected group was about 10% lower. We also observed that infected females were always non-ovigerous.

Keywords: Bopyrid, *Gyge ovalis*, Host-parasite interaction, Mud shrimp, Parasitic isopod, *Upogebia*

Symbiotic relationships between crustaceans and fishes

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Shrimp burrows are used by a variety of gobies for symbiotic associations. Compared with well-studied obligatory mutualistic relationships between gobies and alpheid shrimps, much fewer studies have been conducted for gobies commensally or facultatively associated with shrimps.

Firstly, I will introduce the symbiotic relationships between gobiied fishes and mud shrimp. The burrow utilization by the estuarine goby *Eutaeniichthys gilli* was quantified in aquaria where mud shrimp *Upogebia yokoyai* burrows were constructed in laboratory aquaria. The goby frequently entered and exited the shrimp burrows, with bout durations of several seconds to several minutes. It is suggested that *E. gilli* feeds on small-sized crustaceans and other organic matter on the mud surface frequently utilizing shrimp burrows for possible predator avoidance even when no predator is present. In contrast, commensal crab and shrimps (*Sestrostoma toriumii*, *Athanas japonicus* and *Stenalpheops anacanthus*) stayed in the mud shrimp burrows much longer time. These commensal crabs and shrimps are believed to feed on organic matters that enter the burrow with water currents created by the host shrimp.

Secondly, gobiied fishes facultatively associated with alpheid shrimps will be introduced. Alpheid shrimp burrow morphology was investigated because it may reflect the behavior of the burrow inhabitants. The objective was to elucidate the effects of *Acentrogobius* sp. on the burrow morphology of *Alpheus brevicristatus*. Through mesocosm experiments, 12 and 14 burrows made by shrimp without goby (solitary treatment) and shrimp with goby (symbiotic treatment), respectively, were recovered. The average value of each burrow parameter was not different between treatments. In the solitary treatment, almost all the burrow parameters showed a high correlation with shrimp carapace length, suggesting that the burrow size was optimal for the shrimps. Contrarily, no significant correlation was observed between most of the burrow parameters and shrimp size in the symbiotic treatment. Smaller burrows may not function for the shrimp, and larger burrows require more energy to construct and maintain, suggesting that gobies negatively affect shrimps.

Keywords: alpheid shrimp, burrow morphology, burrow utilization, commensal, facultative, mudflat, mud shrimp

Species composition and seasonal abundance of ectoparasitic crustaceans on intertidal hermit crabs in the Pacific rocky shore of Japan.

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To examine the prevalence of rhizocephalan and isopod parasites, we sampled three species of hermit crabs, *Pagurus filholi* (n=5738), *P. maculosus* (n=720), and *Clibanarius virescens* (n=2436) for 13 months from an intertidal rocky shore on the coast of Boso Peninsula, Pacific coast of the middle Japan. Species of the Peltogastridae (Rhizocephala: *Peltogaster paguri*) and species of the Athelginae (Isopoda: Bopyridae: *Athelges takanoshimensis*) were found on abdomens of the hermit crabs and, species of the Pseudioninae (Isopoda: Bopyridae: *Pseudione*) occurred in branchial chambers of the hermit crabs. Regarding bopyrid isopod infection, 10.06% of *P. filholi* , 4.12% of *P. maculosus* , and 0.93 % of *C. viresens* were in total infected with these parasitic isopods. No conspicuous seasonal difference was detected in infection rates of these parasites in the all species of hermit crabs. In *P. filholi* , 12.21% of males and 8.32% of females were infected with the rhizocephalans, and 0.05% of males and 0.06% of females were infected with the athelgins; the infection rates of the rhizocephalans and the athelgins tended to increase with crab size. The rhizocephalans more frequently parasitized upon males than females, but the infection rates of the athelgins were not significantly different between the sexes. In *P. maculosus* , 1.40% of males and 0.58% of females were infected with the rhizocephalans, 2.80% of males and 2.90% of females were infected with the athelgins, and 0.35% of males and no females were infected with the pseudionins; the infection rates were not significantly different between the sexes in all these parasites. In *C. virescens* , 0.27% of males and 0.43% of females were infected with the athelgins, and 0.36% of males and 0.78% of females were infected with the pseudionins; the infection rates were not significantly different between the sexes in these parasites.

Keywords: Crustacea, Bopyridae, Rhizocephala, parasites

Expanded occurrences of red tides by the warm-water dinoflagellate *Karenia mikimotoi* in Hakodate Bay, Hokkaido, northern Japan

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In the coastal area of western Japan, harmful red tides have frequently occurred due to the dinoflagellate *Karenia mikimotoi* and have caused mass mortalities of cultured marine organismss. In Hakodate Bay, Hokkaido, the occurrence of *K. mikimotoi* red tide was recorded for the first time in northern Japan in October 2015, and the fishery damages such as squids and chum salmon were reported. In this study, we monitored the bloom dynamics of *K. mikimotoi* together with environment parameters in Hakodate Bay, Hokkaido, and tried to evaluate the effective factors for the occurrences of red tides. The seasonal distribution of *K. mikimotoi* was monitored at the quay of Hakodate International Fisheries and Ocean Research Center (Stn. HKK, water depth 10 m), during the period from May 28, 2015 to October 19, 2017. The surface water was collected once to three times a month, and water samples from 5m and 9 m depths were collected and the environmental factors were also measured. When the appearance of *K. mikimotoi* was first confirmed, a weekly survey was conducted until the disappearance.

During the survey period, the water temperature fluctuated in the range of 5 – 24.5ºC and the salinity ranged from 29.2 – 34.0. The annual survey of 2015 – 2017 confirmed that K. mikimotoi increased in every autumn. A red tide was formed (up to 630 cells / mL) in 2015, small bloom (<35 cells / mL) in 2016, and no bloom in 2017 (<2 cells / mL). The first detection of *K. mikimotoi* was also in August in 2017. The light intensities were strong and diatoms maintained a high cell densities of 1000 cells / mL or higher until the beginning of October, and *K. mikimotoi* showed consistently low cell densities. The growth of K. mikimotoi was considered to be limited by abundant diatom populations with cell densities of 1000 cells / mL or more. Sunny days in September presumably contributed to the growth of diatoms. Blooms of *K. mikimotoi* disappeared when a water temperature decreased to reach 10ºC. It is considered that the climate warming probably brings warm-water harmful algal blooms to the northern areas.

Keywords: red tide, dinoflagellate, *Karenia mikimotoi*, diatoms, Hakodate Bay

Long-term changes in the benthic environment in the Seto Inland Sea

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The rapid industrial development, urbanization, and tourism have imposed deleterious impacts on the coastal marine ecosystem in the last four decades. The Seto Inland Sea is the largest semi-enclosed coastal sea in Japan (23,203 km2). This sea is located in the western part of Japan and is connected to the Pacific Ocean via its western and eastern channels. In the Seto Inland Sea, policies for reduction of organic matter and nutrient loads from land have been enforced since the period of high economic growth in the 1950s–70s. Consequently, the policies have successfully prevented the increase in the total discharge of pollutant, and the deterioration of water quality has been brought under control, with some evidence of water quality improvement, such as the reduced number of occurrences of red tide. Some researchers suggested that the Seto Inland Sea is now becoming oligotrophic due to the reductions in nutrient loads from lands. Therefore, the benthic environment assumed to be changed with the improvement of the water quality in the Seto Inland Sea. In the present study, benthic quality assessment was conducted using biotic index (multivariate AZTI Marine Biotic Index: M-AMBI) with macrobenthos data and the physico-chemical parameters of the sediment such as TOC content collected by Ministry of Environment at approximately 400 stations in the 1980s, 1990s, 2000s, and 2010s. From the results, we will clarify the spatio-temporal changes of the ecosystem health based on the M-AMBI and the physico-chemical parameters of the sediment in the Seto Inland Sea.

Keywords: the Seto Inland Sea,M-AMBI,benthic quality

Study on the Influence of Leaf Fan Form of Aeration Equipment on Dissolved Oxygen Distribution and Flow Field in Water

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Study on the Influence of Leaf Fan Form of Aeration Equipment on Dissolved Oxygen Distribution and Flow Field in Water

Yi-Ron Chen , Wen-Shang Hou , Wai-Zhian Soo

Abstract:

The oxygenation method of traditional outdoor culture ponds mostly increases the dissolved oxygen in the water by the paddlewheel aerator, and the dissolved oxygen level and distribution of culture pond, which is related to the harvest of aquaculture organisms. Due to the large-scale water mass relationship in the culture pond, there is a situation in which the oxygen distribution is heterogeneity, or the oxygen in the entire water mass is insufficient. Therefore, the aquaculture industry is equipped with aerator equipment in the culture pond to keeping the water quality stable, it can also supply oxygen and reduce stratification.

Most of the aeration equipment used in Taiwan's outdoor culture ponds are impeller-type paddlewheels. The impeller-type paddlewheels push the stilling pool to raise the water, which to promotes the water in the culture pond is brought into contact with the oxygen in the air to produce an oxygen supply and the water body is circulated. The oxygen enrichment benefit is analysis by the dissolved oxygen distribution result. The high dissolved oxygen diffusion range of the impeller type paddlewheel reveal at epilimnion, but as the water depth is deeper and the distance from the paddlewheel is farther, the dissolved oxygen diffusion is lower. The efficiency of oxygen transfer to the water and to the rear of the water flow field is limited. Therefore, this study an experimental analysis and discussion on the oxygen supply method of aeration equipment.

In this study, the leaf fan mode of aeration equipment was changed from traditional vertical aeration to horizontal aeration. The shape and configuration of leaf fan mode were different. Firstly, CFD was used to simulate the flow field analysis of the leaf fan stirred. The 1:20 scale model was printed in 3D for laboratory testing. After confirming that the simulated water flow field distribution was consistent with the small flow field experiment distribution, the 1:1 ratio entity manufacturing application was carried out, and the invention patent was obtained in May 2018. The aeration equipment invented in this study has a 2HP aerobic water depth of up to 4M, an aeration rate of 5,000 tons of water mass can be raised from 2ppm to 6.5ppm in only 5 minutes, and the water flow exhibits horizontal diffusion without vortex stirring sediment. The aeration can replace at landscape lakes, deep water channels, wastewater and sewage plants and culture ponds, so the aeration can be applied extensively.

Keywords: #Aerator, #Aquaculture

Assessing local fish communities around artificial reefs using environmental DNA metabarcoding

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Environmental DNA (eDNA) metabarcoding has been shown as a powerful tool to assess marine biodiversity. This method can be an alternative to underwater visual survey in coastal waters, but few studies compared the two methods simultaneously. Here we report the results of eDNA metabarcoding assessing fish communities in two artificial reefs in June and October 2018, and January 2019. Using a universal PCR primer targeting the mitochondrial 12S rRNA gene of fish (MiFish), eDNA sequence data were obtained and compared to simultaneous underwater visual survey. While underwater visual survey recorded 34 species during the study period, the eDNA metabarcoding detected 63 fish species including pelagic species, which were rarely observed by visual census. We found a positive correlation between species richness of the two methods (R^2 = 0.59), but a multivariate analysis indicated significant differences in detected fish communities between the two methods. The results of eDNA metabarcoding may reflect local fish communities in artificial reefs, but this method may additionally detect pelagic fish species or capture eDNA from wastewater of houses or fishing ports.

Keywords: Artificial reef, eDNA, fish community, habitat structure

Diversity and Community of Composition of Coral reef fishes of the Ra Island, Pang-Nga province, Andaman Sea, Thailand

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Abstract:

The Ra island is part the Tung Nang Dam Gulf which classified as one of the nation's biggest estuarine ecosystem on the Andaman Sea. As marginal part, therefore, the Ra Island which locating on the ecotone region are comprising of both brackish and marine ecosystems. As the island had contained several coral reef patches, especially at the west part. By the way, information on coral reef fish from this area is rather scarce.

As the area is important of ecotone between marine and brackish water, understanding of species diversity and community of coral reef fish might be help scientist to understanding more on migratory system and adjustment of fish to changing of water salinity. In order gather this value information, the underwater videos were recorded from 3 line transects of coral reef on the Kuning bay, National park bay on the northern part of the Ra Island. Videos were take back to analyzed for fish species and counting for each species at Kasertsart University. The species account was classified after Leiske and Myerss (2001).

Total 11 families 18 genera and 22 species of coral reef fish was recorded and density of fishes was ranging between 0.52-0.82 tails/ sq./m. while the range number of species line was between 10-14 species and the 3 most dominance species was the Neopomacentrus azyron, Sphyraena obtusata and Caesio cunning respectively. The Shannon-Wienner diversity Index was ranging between 1.29-1.48 which considering low due to present of species that living in a big shoal such as damsel fishes. Results showing that fish diversity that associated with massive and hump corals was significantly low comparing to the nearby island. This might due to unstable of environmental factors such as salinity, turbidity and strengthen of wave current. Species that found in coral reef from this study were also found on rocky beaches which found around the island. Fish community on the National park which contain more clam environmental situation were small size (juvenile stage) of several coral reef species. The coral reef might be the good nursery ground for coral reef fishes.

Keywords: Coral reef fishes, Andaman Sea, fish communities, Ko Ra fishes, Thailand

Accelerated bioaccumulation of mercury in red stingray (Hemitrygon akajei) by the change of feeding habits relative to growth

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Bioaccumulation of hazardous substances such as heavy metals, PCB, dioxin, etc. in the coastal aquatic ecosystem is one of the serious environmental problems that we are still facing in our daily life, since we have utilized various fishes and invertebrates as ones of the major protein resources in diets. Among these harmful substances, our research has focused on mercury, because 7,400 tons of mercury is still emitting to the environment per year throughout the worlds not only from anthropogenic sources but also natural ones such as volcanos etc., and most of the mercury is finally discharged to the sea. The people who live in the coastal areas tend to rely on sea foods more for diets, and take in more mercury through them. In latest field studies on the bioaccumulation of total mercury (THg) in the aquatic ecosystem in Isahaya Bay, which is an inner Bay of Ariake Bay located in Kyushu, Japan, extremely high content of THg exceeded 3,000 ng g-1 d.w. was found from red stingray, Hemitrygon akajei. The source of THg seems to be derived from an active volcano, Mt. Unzen, located on the southern side of the bay. In this study, we collected various sizes of 22 individuals of red stingray in Isahaya Bay on April and June 2019 to determine their THg concentrations and stable isotope ratios of carbon and nitrogen of their muscles tissues, and to examine their stomach contents. We report these results, and discuss the THg accumulation in the body of the red stingray.

The specimens contained 240.6 to 1,366.6 ng g-1 d.w. of THg. The mature individuals with larger body weights tend to accumulate more THg than the immature ones with smaller body weights, although the trophic position in the food chain was apt to descend as its growth. The immature individuals (730 ± 1,769.04 gww, mean ± S.D., n=9) had nitrogen isotopic values of 15.7 ± 0.6‰, while the mature ones between 6,315 and 9,540 gww had δ15N values of 15.1 ± 0.6‰, n=11). The wide variations of δ13C values of both of immature and mature individuals (– 17.4 to -14.9 ‰ and – 16.2 to -13.8‰, respectively) indicate that they utilized a variety of animals for diets. The results of the stomach content analysis showed that the major food items of the immature individuals were mainly shrimp (54% in IRI (Percentage of the index of relative importance)), pelagic and demersal fishes (29%), and polychaete (16%), while the mature ones more relied on benthic animals such as bivalves (42%) and crabs (10%). Since the these benthic preys except shrimp had relatively higher THg contents, the switching of food items to the benthic preys by the mature individuals seem to accelerate the bioaccumulation of the mature individuals.

Keywords: Hemitrygon akajei, bioaccumulation, mercury, Ruditapes phillipinarum

Potential resilience of Taiwanese Coral reef in Changing Climate

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Coral reefs in the Anthropocene are being subjected to unprecedented levels of stressors, including local disturbances—such as overfishing, habitat destruction, and pollution—and large-scale destruction related to the global impacts of climate change—such as typhoons and coral bleaching. Thus, the future of corals and coral reefs in any given location will depend on their level of resilience, from individual corals to entire ecosystems. Herein we review the environmental settings and long-term ecological research on coral reefs, based on both coral communities and coral-Symbiodiniaceae associations over time and space, in Kenting National Park (KNP), Hengchun Peninsula, southern Taiwan, wherein fringing reefs have developed along the coast of both capes and a semi-closed bay, known as Nanwan, within the peninsula. These reefs are influenced by a branch of Kuroshio Current, the monsoon-induced South China Sea Surface Current, and a tide-induced upwelling that not only shapes coral communities, but also reduces the seawater temperature and creates fluctuating thermal environments which over time have favoured thermal-resistant corals, particularly those corals close to the thermal effluent of a nuclear power plant in the west Nanwan. Although living coral cover (LCC) has fluctuated through time in concordance with major typhoons and coral bleaching between 1986 and 2019, spatial heterogeneity in LCC recovery has been detected, suggesting that coral reef resilience is variable among subregions in KNP. In addition, corals exposed to progressively warmer and fluctuating thermal environments are show not only a dominance of associated, thermally-tolerant Durusdinium spp. but also the ability to shuffle their symbiont communities in response to seasonal variations in seawater temperature without bleaching. We demonstrate that coral reefs in a small geographical range with unique environmental settings and ecological characteristics, such as the KNP reef, may be resilient to bleaching and deserve novel conservation efforts. Conservation efforts that use resilience-based management programs to reduce local stresses and meet the challenge of climate change for Taiwanese coral reef is urgently needed.

Keywords: Changing climate, coral reef, Taiwan, resilience, thermal-tolerant, living coral cover, upwelling

Shallow marine hydrothermal vents (HVs) provide valuable bioresource information

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Marine hydrothermal vents (HVs) are unique, extreme environments that share several similarities with marine systems under projected global and climate change scenarios (e.g., low pH due to high concentrations of carbon dioxide and sulfite compounds, high temperature and turbidity, high loads of toxic chemicals such as H2S and trace metals). Particularly shallow HVs are easily accessible and amenable to short and long-term experiments. Research on organisms from shallow HVs provides insights in the molecular, ecological, and evolutionary adaptations to extreme oceanic environments by comparing them with evolutionary related but less adapted biota. A shallow water HV system at northeast Taiwan (Turtle Island) has been intensively studied by several international research teams. These studies revealed astounding highlights at the level of ecosystem (being fueled by photosynthesis and chemosynthesis), community (striking biodiversity changes due to mass mortality), population (retarded growth characteristics), individual (habitat attractive behavior), molecule (adaptations to elevated concentrations of heavy metals, low pH, and elevated temperature). Subsurface marine HVs may provide a particular advantage to better understand evolutionary conditions of the early earth environments and future climate predictions for marine life. The potential of shallow HVs both in their use as a template for global change scenarios and as a source for diverse bioresource information for applied technologies are highlighted here. Particularly, the rare shallow water HVs are valuable assets and sights for both research and education and deserve particular protection for their substantial bioresource information potential as rare and extreme environments and as natural heritage sites at national and international level.

Keywords: Hydrothermal vents, Climate change, Turtle Island

Effecive initiation diffusion model based on data of species growth

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The logistic model has been successfully used in population dynamics and applied to diverse fields related to growing objects to reliably forecast the future changes.In general, the logistic function is S-shaped, so that it might be called a sigmoid. When employing the traditional logistic models to analyze the growth features, however, there must occur problems if we need to know when it begins. Inspired from this viewpoint, we propose a new logistic model to have the ignition time or starting time that lets us know when it starts. The importance of the starting time is laid on the fact that the invasion of exotic species into regions of the country is related to an environmental change or human mistakes in transportation. The starting time is able to verify what reason triggers the occurrence of the exotic species. In general, the conventional logistic models have three parameters to be determined from the data whereas the effective ignition logistic model newly proposed in this paper has four parameters because of the ignition time. For the cases of the exotic species named Spartina that has invaded some regions of Korea, we estimate the starting time and doubling period during the beginnings of invasion.

Keywords: Effective diffusion model, starting time, doubling period, Spartina

Fluctuating interaction network and time-varying stability of a natural fish community

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Ecological theory suggests that large-scale patterns such as community stability can be influenced by changes in interspecific interactions that arise from the behavioural and/or physiological responses of individual species varying over time. Although this theory has experimental support, evidence from natural ecosystems is lacking owing to the challenges of tracking rapid changes in interspecific interactions (known to occur on timescales much shorter than a generation time)6 and then identifying the effect of such changes on large-scale community dynamics. Here, using tools for analysing nonlinear time series and a 12-year-long dataset of fortnightly collected observations on a natural marine fish community in Maizuru Bay, Japan, we show that short-term changes in interaction networks influence overall community dynamics. Among the 15 dominant species, we identify 14 interspecific interactions to construct a dynamic interaction network. We show that the strengths, and even types, of interactions change with time; we also develop a time-varying stability measure based on local Lyapunov stability for attractor dynamics in non-equilibrium nonlinear systems. We use this dynamic stability measure to examine the link between the time-varying interaction network and community stability. We find seasonal patterns in dynamic stability for this fish community that broadly support expectations of current ecological theory. Specifically, the dominance of weak interactions and higher species diversity during summer months are associated with higher dynamic stability and smaller population fluctuations. We suggest that interspecific interactions, community network structure and community stability are dynamic properties, and that linking fluctuating interaction networks to community-level dynamic properties is key to understanding the maintenance of ecological communities in nature.

Evolution of deep-sea demersal fishes of the *Bothrocara hollandi* species complex around Japan

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A Japan Sea eelpout *Bothrocara hollandi* has been known as the most dominant deep-sea demersal fish of the Japan Sea, where it is distributed from 200 to 2000 m in depth. Our molecular phylogenetic analyses based on the nucleotide sequences of the nuclear Internal Transcribed Spacer 1 (ITS1) region and microsatellites showed that the Japan Sea individuals consist of two genetically distinct species (sp. 1 and sp. 2). Most individuals can be classified into one of these species based on some morphological characters such as number of vertebra and color in an oral cavity. In the Japan Sea off the San-in district, the westernmost part of the Japanese mainland (Honshu Island), the frequency of sp. 2 individuals within the *Bothrocara hollandi* species complex was the highest around a depth of 400 m and decreased with both increasing and decreasing depths. Individuals of this species complex are also distributed in the Okhotsk Sea and the northwestern Pacific Ocean. Complete genetic deviation between the individuals of the Japan Sea and these neighboring sea areas was shown in our previous analyses based on nucleotide sequences of the mitochondrial control region (CR) and a non-coding region between tRNA (Thr) and tRNA (Pro) genes. A single sp. 2 individual, however, shared an ITS1 sequence with an individual from the Pacific Ocean. Molecular phylogenetic analyses based on the mitochondrial genome showed the monophyly of individuals of the Japan Sea although no CR haplotype (nucleotide sequence) was shared between the two species in the Japan Sea. On the other hand, analyses based on the nuclear ITS1 gene showed that ancestors of the two species of the Japan Sea were deviated from Pacific individuals independently. Furthermore, our microsatellite analysis showed that the sp. 2 individuals of the Japan Sea are more closely related to individuals of neighboring sea areas than to sympatric sp. 1 individuals. Pacific individuals are, especially, closely related to sp. 2, which suggests that the ancestor of sp. 2 migrated into the Japan Sea through the Tsugaru Strait between Hokkaido and Honshu Islands, long after the migration of the ancestor of sp. 1, and the Pacific-type mitochondrial DNA of sp. 2 might have been replaced with that of sp. 1 through the two unidirectional introgression events. Evolutionary history of this species complex was estimated by the Coalescent-theory based analyses.

Keywords: *Bothrocara hollandi*: the Japan Sea: cryptic species: bathymetrical distribution

Morphological Examination and DNA Analysis Reveal a New Record and a New Species of Cadlina (Nudibranchia) from Korea

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Cadlina is a widespread genus of sea slugs in the family Cadlinidae. Until now the genus is represented by 25 species. Among them, three *Cadlina* species recorded in Northwestern pacific region: *C. japonica, C. kamchatica* and *C. umiushi*. However, there was only one species of this genus, *C. japonica*, recorded in Korea. It is potential that there are more *Cadlina* species present in Korea waters. In the attempt of studying, we collected several *Cadlina* species from Korean Eastern sea by SCUBA diving. The morphology of collected samples was investigated by stereo and scanning electron microscopes. Also, genetic variations of the specimen's nuclear 18S ribosomal RNA (18S) and Histone 3 (H3) genes and mitochondrial cytochrome c subunit 1 (COI), 16S ribosomal RNA (16S) genes were studied. Obtained sequences were used for blast on Genbank database and construction of phylogenetic tree. Our results identified three *Cadlina* species, including *C. japonica, C. umiushi* (first record for Korea), and *Cadlina sp*. (new species). The new species was described in detail and illustrated. Its external morphology was close to *C. umiushi* but body shape, thin mantle edge and radula morphology distinguished this new species. Sequence comparison and phylogenetic tree analysis based on four molecular markers confirmed morphological finding.

Keywords: Cadlina, first record, new species, morphology, markers

Diversity of *Nesotanais* tanaidacean crustaceans in the Ryukyu Islands, Japan

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The order Tanaidacea is a benthic crustacean group with about 1400 species. Most members are marine but brackish-water species are also known. *Nesotanais* is one of brackish-water genera; four species have been reported so far, one of which, *Nesotanais ryukyuensis*, was described from Okinawa Island, Ryukyu Islands, Japan. In this study, we conducted a faunal survey of *Nesotanais* tanaidaceans in Ryukyu Islands, and found them in Tanegashima, Yakushima, Amami-Oshima, Kakeroma, Okinawa, Ishigaki, Miyako, and Iriomote Islands. In our specimens, four molecularly distinguishable lineages were detected based on their 18S rRNA data, and some of them were distributed in two or more islands. Tanaidaceans are benthic animals and lack a planktonic larval stage (obligate dispersal phase) in their life cycle and *Nesotanais* is a non-marine genus. Their distribution across seas thus possibly resulted from human activities (e.g., mangrove rehabilitation).

Keywords: Tanaidacea, phylogeny, taxonomy, distribution

Minerals in the Sediment Collected from Blood Cockle Cultured Area at Bandon Bay

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Bandon Bay, Surat Thani Province, is the place for aquaculture and fisheries including crabs, fishes and shellfishes. Blood cockle is one of the famous aquatic animals in this area confirmed by their characteristics and taste. The aim of this study was to find the composition of the minerals deposited in the sediment of the blood cockle cultured area of the east side (Tha Tong estuary) and the west side (Tha Chang and Phumreang estuaries) of Bandon Bay compared to the mouth of Tapi river. The sediment was collected from 8 stations in rainy season (August), kept cool, pretreated before observed by X-Ray Fluorescent technique (XRF). The result showed that there were 12 types of minerals; silicon dioxide (SiO_2), aluminium oxide (Al_2O_3), iron oxide (Fe_2O_3), potassium oxide (K_2O), chloride (Cl), magnesium oxide (MgO), sodium oxide (Na_2O), sulfite (SO_3), calcium oxide (CaO), titanium oxide (TiO_2), manganese oxide (MnO) and phosphorus pentoxide (P_2O_5). The majority was silicon dioxide found in all station followed by aluminium oxide and iron oxide, respectively. Station No. 5 found the highest proportion of all three elements up to 90.82%. Sediment from Tha Thong estuary showed the higher proportion of the other elements than those from Tha Chang and Phumreang estuaries, except for sodium oxide and chloride. It seemed the stations in the eastern had a variety of minerals than those in the western, mainly calcium oxide and sulfite, indicated more activities occurred in this area.

Keywords: Mineral, Sediment, X-Ray Fluorescent technique (XRF)

Antibacterial Activity in Haemolymph of the Oyster, Saccostrea commercialis

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Oyster is a popular shellfish deal to the tasty and nutrition. Fresh eaten, cooked, fried and spicy salad are normally served for oyster. It was reported the properties of oyster on stimulation the reproductive system, reduce blood fat levels and treatment of hepatitis B virus. This study was aimed to determine the antibacterial activity of the oyster (Saccostrea commercialis) haemolymph on Vibrio parahaemolyticus, Escherichia coli and Staphylococcus aureus. Oyster was collected from the fresh market, kept cool until dissected. Four Oyster hemolymph forms; fresh hemolymph, boiled hemolymph at 100 °C for 15 sec, boiled hemolymph at 100 °C for 5 min and fresh hemolymph mixed lemon juice, were tested. The results showed that no antibacterial activity was found on fresh hemolymph, boiled hemolymph at 100 °C for 15 sec, boiled hemolymph at 100 °C for 5 min. Fresh hemolymph mixed lemon juice had the antibacterial activity to V. Parahaemolyticus, E. coli and S. aureus with percentage of the inhibition at 73.08±2.38, 65.64±5.91 and 65.45±6.61, respectively. It was indicated that acidity of lemon juice had the ability on the resistance of V. parahaemolyticus, E. coli and S. aureus that may be found contaminated in haemolymph, while heat didn’t effect on antibacterial activity in Oyster hemolymph.

Keywords: Oyster, Heat, Lemon Juice, Antibacteria

Protein and elements composition in Cephalopods ink

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Ink is one of the squid by-products come from household consumption or seafood industry. The disposal of ink is seemed to cause environmental pollution. Ink is sometimes made high value added by mixing into some kinds of food for creation or increasing nutrition. This research aimed to study the content of protein and minor elements composed in cephalopod ink 3 species: Bigfin reef squid (Sepioteuthis lessoniana), Pharaoh cuttlefish (Sepia pharaonis) and Marbled octopus (Amphioctopus aegina). It was found that all ink showed the characteristics as concentrated liquid and had different colors; dark blue for Bigfin reef squid ink, dark brown for Pharaoh cuttlefish ink and black brown for Marbled octopus ink. The highest amount of protein content was from Bigfin reef squid ink (144.15±5.48 mg/ml), followed by Pharaoh cuttlefish ink (136.24±0.60 mg/ml) and Marbled octopus ink (104.17±0.68 mg/ml), which was shown significantly different ($P<0.05$). The samples were analyzed by AAS technique for minor elements and found that Pharaoh cuttlefish ink and Marbled octopus ink consisted of calcium (29.020±0.11 and 24.552±0.50 mg/g), sodium (19.823±0.02, 15.690±0.11 mg/g), magnesium (19.795±0.49, 15.068±0.08 mg/g), potassium (7.664±0.19 and 6.830±0.05 mg/g) and iron (0.022±0.00 and 0.200±0.01 mg/g), respectively, while those concentrations in Bigfin reef squid and melanin standard were 12.754±0.28, 25.097±0.12 mg/g, 15.060±0.01, 33.027±0.11 mg/g, 10.335±0.06, 23.299±0.05 mg/g, 6.267±0.00, 0.396±0.00 mg/g, and 0.050±0.01, 0.067±0.01 mg/g, respectively. Interestingly, Bigfin reef squid ink was shown the same order content (sodium, calcium, magnesium, potassium and iron, respectively) as melanin standard (Sigma). It was concluded that the ink from different species revealed the different content of nutrients.

Keywords: Ink, Squid, Cuttlefish, Octopus, Element

Two scientific stations open to all in South China Sea

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Dongsha Atoll, at 20 degree N, in northern SCS, is an area of about 500 km*2* with diversified habitats, e.g., coral reefs, seagrass beds, sand, all in shallow water. A marine station has been established with the help of Marine National Park and coast guards since 2012. Jet ski and various boats from 12 ft to 42 ft long are available for scuba diving, or instrument deployment. Weekly flights and monthly supply ships make the atoll very accessible to scientists. There is no civilian on the island. The internal waves of the greatest magnitude in the world, the high marine biodiversity near The Coral Triangle, plus the relatively advanced stage of ocean acidification of SCS all make the site attractive to scientists. Dozens of papers have been published based on the marine station. Taiping Island, at 10 degree N, part of Spratly Islands, is a new addition as a scientific station. it is accessible to scientists by collaboration with coast guard ships. Room and board as well as scuba are provided for scientific investigation. All services mentioned above are accessible by international scientific community. These facilities are part of our effort to promote scientific collaborations in South China Sea among countries.

Keywords: Atoll, South China Sea, coral reefs, seagrass beds, marine stations

The Abstracts of Poster Presentations

NO. P1-1 to P1-41 on Nov. 5 15:30 ~ 17:30

NO. P2-1 to P2-42 on Nov. 6 15:30 ~ 17:00

Impact of torrential rain on the population dynamics of brackish water clam, *Corbicula japonica*, in the Kikuchi River Estuary, Kumamoto, Japan

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According to the IPCC report, there are no doubts that the earth climate is warming since the 19th century. As the global temperature rises, more water tends to be contained in the atmosphere, and consequently frequency of torrential rain increases. Once the torrential rain occurs, the amount of river flow increases remarkably in a short time, and it often causes dramatic changes of the topography of the estuary, and brings strong disturbances on its ecosystem. In this study, we focus on the negative impact of the environmental disturbance caused by the torrential rain during the rainy season on the population of brackish clam, *Corbicula japonica*, which predominates in the macro-benthic community in the Kikuchi River estuary, Kumamoto, Japan.

Here, we set five sampling stations (Stn 1 to 5) in the range of 1 to 5 km upstream from the river mouth, and conducted the environmental assessment of the sediment and quantitative samplings of the clam population on the sand banks that appeared at low tide at these stations, 15 times between March 2017 and February 2019. We report the results of these surveys, and discuss the negative impact of the torrential rains on the population dynamics of *C. japonica*.

One of the brackish water species, *C. japonica*, physiologically is able to adapt to the environment ranged between Stn 3 and Stn 5 in the gradient of salinity of the water in the estuary. The total precipitation in June and July including the rainy season in 2017 and 2018 was 562 mm and 739 mm, respectively. We compared how the difference of the precipitation during the rainy season influenced the downward movement of the *Corbicula* population in the estuary between these two years. In 2017, the largest patches of the *Corbicula* occurred with the density of 1,787 ind. m^{-2} and biomass of 1,012 gww m^{-2} at Stn 3 in August just after the rainy season. 65.4% of the individuals of the *Corbicula* population was made up of the reproducible adults with the shell length of larger than 10 mm. In 2018, contrastively, the downward movement of the *Corbicula* in the estuary during the rainy season went over the physiologically adaptable range. The high density patches with 1,047 ind. m^{-2} were found at Stn 1 in July. These individuals faced mass mortality due to intolerable high salinity of the water. At Stn 3 in August, the largest patches with the density of 733 ind. m^{-2} were found, but the total wet weight of the patches was 250 gww m^{-2}, which was equivalent to about one third of the biomass in 2017. The ratios of reproducible individuals decreased to 16.4% in the patches. Thus, the reinforcement of the downward movement to the *Corbicula* population by the occurrence of heavier torrential rain brings not only the mass mortality due to high salinity but also the marked decrease of reproducible individuals.

Keywords: *Corbicula japonica*, global warming, torrential rain, population dynamics

Seasonal changes of the distribution and population dynamics of hard clam, *Meretric lusoria*, on Midri River Tidal Flats, Kumamoto, Japan

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Hard clam, *Meretrix lusoria*, widely distributed on the sandy tidal flats in Japanese coasts until the mid-1970s. However, it disappeared almost of all the habitats except the sandy tidal flats that face Ariake Bay in Kumamoto Prefecture in the past four decades, and designated as "endangered species" by the Ministry of the Environment in 2012. Since the populations declined very rapidly in its main habitats, its basic life history and the detail of ecological characteristics are still not clear. In our study area, Midori River Tidal Flats, which is the largest sandy tidal flats (2,200 ha) remained in Japanese coast, it occurs in relatively high densities, and 100 to 200 tons are harvested every year. In this study, we set eight stations toward the offshore at the intervals of about 100 m on the upper part of the tidal flats, and conducted field surveys to monitor the seasonal changes of its distribution every three months and monthly quantitative samplings for population study between April in 2018 and April in 2019. We report the results of these surveys, focusing on the mechanisms of its larval settlement on the tidal flats and the growth of the juveniles, and discus about the factors that determine its distribution on them and how it grows adapting to the brackish water conditions on the upper parts of the tidal flats near the river mouth.

The larval settlement concentrated on the areas where the mud content accounts for about 40% of the sediment in the breeding season in June to July, while the adult clam mainly distributed on the sandy areas where the mud content was less than 1%. To explain these different distribution patterns of the clam between the young juveniles and adults, we offer two possibilities on the mechanism of the larval settlement on the tidal flats. One is active sediment selection. The larvae favor the muddy sediment as settling sites, and then move to the sandy areas as they grow up. Another one is passive settlement on the sediment. The larvae are caught up in the coagulative precipitation of fine particles suspended in the water caused by van der Waals force, forced to settle on the muddy sediment once, and move to the sandy areas with physiologically favorable environment on the tidal flats. After the young juveniles moved to the areas with sandy sediment, it grew to 1.5 mm in shell length after one year and 4.5 mm after two years, according to the analysis of the size frequency distribution of the clam population. I will discuss about the reasons why the clam grew slowly.

Keywords: distribution, hard clam, *Meretrix lusoria*, sandy tidal flats, settlement

Food web analysis of benthic ecosystem with stable isotope signatures of carbon and nitrogen on Arao Tidal Flats, Kumamoto, Kyushu, Japan

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Abstract:

On the tidal flats, the occurrence of macro-benthic animals are sustained by the food supply not only from the phytoplankton suspended in the water, but also various primary producers that grow thickly on the sediment including benthic micro- and macro-algae. These abundant primarily produced organic matters often enable the macro-benthic animals that feed them to establish dense patches, and they are exploited by various carnivorous animals as the secondary consumers. Our study have focused on the detail structure of the food web system of the macro-benthic community existed on the sandy tidal flats, Arao Tidal Flats, that faces the inner part of Ariake Bay, Kumamoto, Kyushu, Japan. The tidal flats are one of the largest sandy tidal flats (about 1,600 ha) remained in the Japanese coast. Here, we set 7 sampling stations from the uppermost area to the shoreline at the interval of 400 m at low tide over the distance of about 2.5 km. We carried out quantitative samplings of macro-benthic animals at these stations to describe seasonal changes of the abundance of dominant species of the macro-benthic communities, collected various organisms including macro-benthic animals and primary producers on the tidal flats and phytoplankton in the water, and examine the food web structure of the macro-benthic community, using their stable isotope signatures of carbon and nitrogen. In this study, we report the characteristics of the food web system of the macro-benthic community established on the tidal flats, and discuss how the macro-benthic animals exploit diets, shaping the prey-predator relationship each other.

On the tidal flats, we often found primary producers including benthic microalgae sea lettuce (*Ulva pertusa*), and several other macro-algae, and dominant species of macro-benthic animals such as suspension feeding bivalves (*Ruditapes philippinarum*, *Arcuatula senhousia*, *Mactra verneriformis*) and herbivorous snail (*Batillaria multiformis*) as primary consumers, and several species of carnivorous snails such as including tiger moon snail (*Natica tigrina*) and veined whelk (*Rapana venosa*) as secondary consumers. Thus, the macro-benthic community was mainly shaped by the animals located at three different trophic positions. Further, it was shown that there were two food chains (food chain 1 and 2) with different primary producers. In the food chain 1, the primary producers consisted of phytoplankton and benthic microalgae, and they were mainly fed by bivalves such as *R. philippinarum*. In the food chain 2, sea snail (*Batillaria multiformis*) was noted as one of the dominant species among the primary consumers, but we could not find the primary producers that sustained the occurrence of the secondary consumers.

Keywords: bivalves, carnivorous snails, stable isotope signature, tidal flats

Seasonal fluctuations of short-neck clam, Ruditapes philippinarum, population and its controlling factors on Shira River Tidal Flats, Kumamoto, Japan

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Introduction:

In Japanese coastal areas, clam harvesting fisheries have declined markedly in the past four decades, partly because dense patches of one of the most popular edible clams, short-neck clam (*Ruditapes philippinarum*), had disappeared from the sandy tidal flats extensively. Many previous studies have focused on this issues, and found various causes in each fishery grounds for harvesting the clam, which are reclamation, over-harvesting, wave corrosion, predation, sediment deterioration etc.

In our study area, Shira River Tidal Flats (about 1,100 ha in area), Kumamoto is one of the largest sandy tidal flats remained in Japanese coasts. Here, we also have experienced the collapse of the dense patches of the clam in the 1980s to 1990s, and they have been never re-established again until today. In this study, we set five sampling stations from the shore toward the shoreline at 200 m intervals and conducted quantitative surveys to describe the seasonal fluctuations of *Ruditapes* population at these stations on the tidal flats monthly at low tide between April 2018 and April 2019, and tried to find the reasons why the dense patches of the clam disappeared on the tidal flats. We report the results of this surveys, and discus the ways to re-establish the dense patches of the clam on the tidal flats.

Results and discussion:

On July 2018, the clam occurred at the densities of max, 1,567 ind m^{-2} at the five sampling stations on the tidal flats, but the density had decreased during the summer and autumn, and recorded 20 to 193 ind m^{-2} at these stations in December. In contrast, Asian mussels (*Arcuatula senhousia*), which has a breeding season in May to June, settled densely on the tidal flats just after the breeding season, and established dense patches with max, density of 13,056 ind m^{-2} in St. 4, creating thick muddy carpet on the sediment surface widely on the tidal flats. Most of the clam received the negative influence from the development of reduced conditions in the muddy carpet during the summer, and seems to die out in it by December. During the winter, both of the remaining clam and dense patches of Asian mussel almost disappeared from the tidal flats, except the young juveniles of the clam that newly settled on the tidal flats in the autumn breeding season (November to early December). The reasons of the disappearance of these two species of bivalves are not clear still, but we suspect the possibility of predation by the fishes such as ray and shore birds as ducks. Therefore, if we are able to protect them from the predators using some tools such as cages, we may succeed to re-establish the dense patches of the clam.

Keywords: Arcuatula senhousia, muddy carpet, predation, Ruditapes philippinarum

The role of sea urchins on coral recruitment in Taiwan

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Sea urchins play an important role in coral reef ecosystems. Via grazing algae, sea urchins create open space for coral settlement and facilitate coral recovery. There are many studies documented on the relationship between sea urchins, algae, and corals in the Caribbean and the Great Barrier Reef. However, few such studies have been conducted in Southeast Asia. Accordingly, in this project, we investigated the quantitative relationship between sea urchins, algae, and corals at 30 sites in three representative coral reefs in Taiwan from 2016 to 2017. Structural complexity at two size scales (decimeter, meter) of reef substrata was also measured as a key abiological factor influencing the relationship. Depth and wave exposure also were observed. Results indicated that large-sized sea urchins, Echinothrix spp. and Diadema spp. prevailed over herbivorous fishes and gastropods in many reef sites. We also found that sea urchin was the strongest predictor for juvenile coral across all the surveyed sites, and it was consistently top-ranked among all predictors in three locations while other factors were inconsistent. Because juvenile coral is a proximate indicator of coral resilience, our finding demonstrated that the large-sized sea urchins facilitate coral resilience in some reefs in Taiwan. Given widespread overfishing of herbivore fishes, this may occur not only in Taiwan but also in neighboring countries of Southeast Asia.

Keywords: sea urchin, diadematidae, coral recruitment, coral resilience

Identification of abiotic drivers shaping marine coastal benthic communities

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At a global scale, human activities and their effects on climate jeopardized the future of tropical reef ecosystems by decimating scleractinian corals. At a regional scale, a panel of communities are available in a given set of temperature and light conditions, which suggest that other local abiotic variable may have the last word on the community eventually thriving. Here, we propose to uncover the determinism of marine coastal benthic communities by a detailed investigation of their response to small-scale change of their environmental conditions including physical, chemical and geological drivers.

At each ten locations in Northern Taiwan (confounding site and depth factors), , communities were delineated using a morpho-functional classification of benthic organisms observed on five photo-transects. Seawater temperature, photosynthetic active radiation, water flow, sedimentation, chlorophyll concentration, dissolved organic carbon, and nutrient concentration were recorded locally, as well as the dominant substrate type on each transect.

Biotic and abiotic components of the ecosystems were integrated into a decision tree framework using Multivariate Regression Tree (MRT) combined with Boosted regression models. Aside from large scale climatic drivers, local environmental conditions such as variations in light, nutrient concentrations, and composition of substrate strongly constrain benthic communities and give rise to certain dominant species at different locations.

Our results demonstrate that regional reefs are moving toward distinct trajectories with the difference of local environmental conditions As large-scale climatic changes are acting in synergy with local stressors, it is critical to have insights on the significant processes that determine the trajectory of the benthic communities. Results of this study will have direct implications in terms of conservation and management of the marine coastal ecosystems with further potential ramifications on their dynamics.

Keywords: Benthic communities, Abiotic drivers, Decision tree

Species composition and abundance of macrofauna at Mu Ko Chumphon, the Western Gulf of Thailand

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Coral reefs are the most complex and diverse marine ecosystems in the world and provide valuable ecosystem services to human well-being. The complex structure of coral reefs leads to support a high diversity of marine organisms. This study examined the species composition and abundance of macrofauna on coral reefs in Mu Ko Chumphon, Chumphon Province, the Western Gulf of Thailand. Field surveyed were carried out at eight reef sites, including Ko Ngam Yai, Ko Ngam Noi, Ko Ma Prao, Ko Raet, Ko Mattra, Ko Lawa, Ko Rang Kachiu and Ko Kula using a belt transect census. The results revealed that reef-associated macrofauna at Mu Ko Chumphon was high diversity. The dominant macrofauna were a blue sponge *Neopetrosia* sp., a sea anemone *Heteractis magnifica*, a sea whips *Junceella* sp., a tube worm *Sabellastarte* sp., a gastropod *Cypraea tigris*, bivalves *Arca ventricosa*, *Spondylus varius* and *Beguina semiorbiculata*, the crown of thorns starfish *Acanthaster planci*, a sea star *Echinaster* sp., a sea urchin *Diadema setosum*, and a sea cucumber *Holothuria leucospilota*. The highest population density of reef-associated macrofauna was *A. ventricosa*. The population densities of *D. setosum* and *H. magnifica* were also high. This study provides important scientific information for understanding the diversity and abundance of reef-associated macrofauna in the Gulf of Thailand.

Keywords: abundance, coral reef, Gulf of Thailand, macrofauna, species composition

Mass occurrence and its ecological significance of marine cladocerans in offshore Suruga Bay, Japan

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Although cladocerans have been reported > 620 species around the world, only 8 species are known to be marine. Since cladocerans establish their plankton population from the resting egg deposited on the ocean floor, their habitat restricted to shallow coastal area in general. However, we found mass occurrence of cladocerans in offshore waters with the depth of > 1000 m in Suruga Bay during the summer of 2014. To clarify whether this phenomenon occurs regularly, population dynamics of cladocerans in offshore Suruga Bay was investigated for 5 years. In addition, stable isotope compositions (δ^{15}N and δ^{13}C) of mesozooplankton were measured in order to examine the role of cladoceran populations in the offshore food-web. Samplings were conducted monthly from June 2014 to December 2018 at fixed stations in Suruga Bay. The mass occurrence of cladocerans were observed every year during the study period, suggesting that the phenomenon seems to occur regularly in the Bay. Mesozooplankton communities could be divided into two groups based on cluster analysis: group A, copepods-dominated, and group B: cladocerans occurred abundantly or dominated communities. In between these communities, while chaetognaths and copepods Eucalanus showed similar ^{15}N values, carnivorous copepods of the genus Euchaeta showed much lower δ^{15}N values in the cladoceran-dominated communities (B). The results suggest that cladocerans may be preyed by these carnivorous copepods, and thus affect the food-web structures in the offshore area of Suruga Bay.

Keywords: Marine cladocerans, Population dynamics, Stable isotope analysis, Suruga Bay

Morphological and molecular assessment of the species diversity of the genus *Phascolion* (Annelida: Sipuncula) in Japan

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Sipunculans are members of Annelida that are characterized by an unsegmented body trunk and an anterior retractable proboscis. About 150 species in 16 genera and six families are described. They are known from intertidal to hadal depths in all the seas and oceans of the world. Most of them burrow into sediments or live beneath stones or in algal holdfasts. However, species of the genus *Phascolion* (Golfingiidae) have a unique characteristic of using gastropod or scaphopod dead shells as their shelter, like a hermit crab. According to the morphological classification, *Phascolion* in the Japanese water comprises four subgenus and eight species. However, considering that some of them are recorded from a highly wide bathymetric and geographical distribution, they may contain cryptic species that are morphologically similar but differ in the distribution. The purpose of this study is to estimate the number of species based on the DNA data of *Phascolion* collected in Japan and to clarify the morphological and ecological differences between species.

We collected *Phascolion* from various localities in Japan: Mutsu Bay, Aomori (at a depth of 15 m), off Shimoda, Shizuoka (~200 m), Maizuru Bay, Kyoto (53 m), off Kumanonada, Mie (57–409 m), off Tanabe, Wakayama (185–800 m), Bisesaki, Okinawa (1 m) and, by various methods (e.g. dredge, beam trawl, or snorkel sampling). Among the collected *Phascolion*, 54 specimens were identified by morphological observation and molecular phylogenetic analysis using the nuclear-cording gene for histone H3.

Our morphological identification suggested that our specimens include at least 11 species. Also, molecular phylogenetic analysis revealed that they are divided into genetically at least 11 groups. Seven morphologically identified species were confirmed by the molecular analyses. However, the species "*Phascolion strombus strombus*" identified by morphological observation was divided into three genetically distinct groups. In addition, three morphologically identified species were genetically not distinguished from each other by the molecular analysis. Furthermore, we compared the habitat depths and shell use among genetically distinct groups collected in Kumanonada and Tanabe. Although some species coinhabit the same depth, the interspecific difference in habitat depth was also identified. Regarding the shell use pattern, each species used shells of a wide range of gastropod and scaphopod families as shelters. This suggests that these species of *Phascolion* do not have a specific preference for their carrying shells.

Keywords: Sipuncula, Phascolion, Phylogeny

Seasonal variation in distribution and species composition of infaunal spionid polychaetes (Annelida: Spionidae) in the intertidal zone of Tokyo Bay

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The family Spionidae is a group of polychaetes, which found from deep sea to brackish water around the world. The species belonging to the family usually live in sandy or muddy bottom sediments, or boring into calcareous substrates such as molluscan shells, and majority of them can switch between suspension and deposit feeding by using their palps. Infaunal spionid polychaetes are often found dominantly in tidal flats, having an important role in the food web as a food resource for benthic fish and migration birds and in the material recycling through bioturbation. Nevertheless, they have many unclear points regarding life history and population dynamics. The aims of this study are to investigate how the density and species composition of the spionid polychaetes in Tokyo Bay fluctuates seasonally and spatially, and to obtain basic information about inhabiting species and their life history characteristics. Sampling of spionid polychaetes carried out in the intertidal zone of Kasai Seaside Park (Kasai), Funabashi Sanbanze Seaside Park (Sanbanze), and Edogawa channel in Tokyo Bay during the period from December 2018 to August 2019. There was a difference in the species composition of spionid polychaetes at each site. Density of Rhynchospio glutaea complex sp. increased from winter to spring and maintained high population densities in summer in both Sanbanze and Edogawa channel, although the density slightly decreased in summer. These population expansions attributable to life history characteristics of the species: it has been reported that this species have long breeding season and recruit at least three times from spring to autumn in southern Japan. Spio sp. occurred in both Sanbanze and Edogawa channel in winter and summer, but not in spring. On the other hand, in Kasai, Spio sp. did not appear, the density of R. glutaea complex sp. decreased from winter to summer, and Prionospio japonica, which did not occur in winter, increased from spring and predominated in summer. In this study site, salinity fluctuated widely from 0.90 to 29.6 ‰ during the period from winter to summer with influence of freshwater inflow from the Arakawa-river. For this reason, P. japonica, one of the famous brackish species, may have increased in population in spring and summer. Rhynchospio glutaea complex sp. in Kasai decreased their population size in spring and summer probably due to the low salinity. In the present study, totally 9 spionid species were collected from intertidal zones in Tokyo Bay and it was clarified that each species shows different habitat preference and life history characteristics.

Keywords: Spionidae, Polychaete, Tokyo Bay, seasonal variation, species composition, Population dynamics

Seasonal variation of abundance and composition of benthic invertebrates in Phuket, the Andaman Sea

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Benthic invertebrates are important components of marine and coastal ecosystems. Some locations of Phuket and its vicinity are important areas for small-scale fisheries. Therefore it is essential to study benthic invertebrates in these areas. Knowledge about the composition and abundance of benthic invertebrates is related to fisheries. It is also needed to understand the complexity of food webs in marine and coastal ecosystems. This study aimed to investigate the composition and abundance of benthic invertebrates living in the soft bottom in Phuket, the Andaman Sea. The results revealed that polychaetes and bivalves were the major groups of benthic invertebrates in the soft-bottom areas. The population densities of benthic invertebrates in the wet season were much higher than those of the dry season. The population densities of the bivalves *Corbula* spp. and *Anadara* spp. were the highest in the wet season while the population density of the cirratulid polychaetes was the highest in the dry season. The spionid, cirratulid, and capitellid polychaetes and the bivalves *Corbula* spp. were found abundantly in both seasons. This study highlights the importance of benthic invertebrates to the local economy of small-scale fisheries as well as ecosystem indicators, mariculture, and natural products for pharmaceutical industries.

Keywords: abundance, Andaman Sea, benthic invertebrates, population, small-scale fisheries

Changes in diversity and structure of marine benthic assemblage

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We investigated diversity and structure marine benthic assemblages in coastal areas near the Jang Bogo Antarctic Research Station in Terra Nova Bay during the 2012–2018 summer seasons. Additionally, the recovery pattern of marine benthic organisms following the disturbance due to the Jang Bogo Station's construction was examined in Terra Nova Bay. A total of 26 taxa were identified in the study area during the experimental period. Species number and diversity indices (richness, evenness, and diversity) were relatively low compared to data previously reported from Terra Nova Bay. *Sphaerotylus antarcticus*, *Clavularia frankliniana*, *Hydractinia* sp., *Iridaea cordata*, *Fragilariopsis* spp., *Alcyonium antarcticum*, and *Metalaeospira pixelli* were the dominant species in this area. Of these, the diatom *Fragilariopsis* spp. were the most abundant species, indicating their key role in maintaining the marine benthic community and controlling biogeochemical cycling. During the construction of the Jang Bogo Station, sediment coverage increased and diatoms declined due to the release of sediment into the coastal area. In February 2014, one month after the disturbance due to cyclone, the diatom coverage increased dramatically and thereby species number, richness index, and diversity index steadily rose from 2015 to 2018. However, non-metric multidimensional scaling ordination analysis of species similarities among sampling times showed that community structure had not completely recovered by 2018. Thus, long-term monitoring is required to elucidate the post-disturbance settlement mechanisms of marine benthic organisms at the study area in Terra Nova Bay.

Keywords: Jang Bogo Station, Terra Nova Bay, Marine benthic organisms, Community structure, Diversity index, Recovery

Toxic Effects of Nanoplastic Polystyrene on Developmental stages and Behavior on Zebrafish Larvae.

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The increasing load of plastic pollution in the environment has become a significant concern, especially in nanosized of plastic. Polystyrene (PS) is found abundantly at sea, one of the most common major polymers used in daily life product. Because of careless management, accidental littering lead to its quantity levels increasing in the environment. Researchers found that this tiny nano-spheres capable of penetrating the zebrafish embryos' chorion and accumulating in the organs such as eyes and digestive tract. However, little known about the basic toxicities of polystyrene nanoparticles (PS NPs) on the fish embryo, especially on their skin cells. Therefore, the study uses zebrafish embryos as an animal model for toxicity testing. The zebrafish embryos were therefore exposed to three different levels of PS NPs (10, 25, 50 mg/L) for 120 hpf. The PS NPs, manufacturer to be spherical 25 nm, was used in this experiment. I examined the effect in developmental stages include deformation survival rate and hatching rate of the zebrafish embryos. In behavior locomotion and touch evoke response were tested in the same experimental context. The result showed that the mortality rate in every constant concentration, no significant difference. However, at 120 hpf, there is a substantial difference in hatching rate, morphological assessment; body length, bending index, yolk sac area, pericardium area, and eye area. The behavior study reveals that around half of zebrafish larvae were affected by 50 ppm of PS NPs. Taken together, these PS NPs can affect general developmental physiology also a neurological disorder of zebrafish embryo.

Keywords: Zebrafish, Polystyrene, Nanoparticle, toxicity, embryo, environment,

Abundance and composition of juvenile corals on shallow reef flat and reef slope at a popular tourist destination in the Andaman Sea

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Elevated seawater temperatures in summer months of the year 2010 were associated with widespread coral bleaching and resulted in high rates of coral mortality in the Andaman Sea. Knowledge of temporal and spatial variation in coral recruitment patterns is very important for understanding population dynamics. It is also necessary for measuring coral reef resilience. The present study examined the recovery potential of coral reefs on the shallow reef flats and the reef slope at a popular tourist destination, Mu Ko Surin National Park, the Andaman Sea. At each study site, quadrats (16 cm x16 cm for each) were randomly placed on available substrates using SCUBA diving and the number of juvenile coral colonies (≤ 5 cm in diameter) was carefully observed and counted. The densities of juvenile corals on shallow reef flats were less than on reef slopes at all study sites except at Ao Pakkaad. The juvenile coral densities on shallow reef flats and reef slopes were in the range from 5.6 to 15.3 and 16.1 to 22.7 colonies/m2, respectively. The major juvenile corals were also high diversity, including *Acropora* spp., *Ctenactis* spp., *Cyphastrea* spp., *Diploastrea heliopora*, *Favia* spp., *Favites* spp., *Fungia* spp., *Galaxea* spp., *Goniastrea* spp., *Leptastrea* spp., *Lobophyllia* spp., *Montipora* spp., *Pachyseris* spp., *Pavona* spp., *Pectinia* spp., *Pocillopora* spp., *Porites* spp., *Psammocora* spp., and *Symphyllia* spp. Certain reef sites at Mu Ko Surin showed recovery potential after the coral bleaching events, therefore, the tourism management strategies for protection of these coral communities are urgently required to enhance coral recovery and resilience in the Andaman Sea.

Keywords: Andaman Sea, juvenile coral, recovery, reef flat, reef slope

Surveys of coral reactions to fishing line garbage around Sesoko Island, Okinawa

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The rate of coral mortality and damage due to fishing line has been reported as high in popular fishing spots around the world. Such damage to corals can be a source of coral disease outbreak. However, some coral colonies have been observed to overgrow or change their morphologies in response to these foreign materials. Unfortunately, there have been only a few photographic records from a few locations, and quantified data are sparse. In this study, surveys were conducted around Sesoko Island, Okinawa, Japan, and we observed a total of 87 colonies including soft corals that were observed entangled with monofilament lines. Of these colonies, 78% of colonies had partially or fully overgrown fishing lines, whereas only a few (5.7%) showed signs of direct physical damage. Apart from colonies showing physiological stress characterized by changes in tissue color such as pigmentation responses, no other major diseases were observed. Acropora was the most encountered genus and had the highest rate of fishing line overgrowth. We theorize that the gross colony morphology of acroporids (arborescent, digitate, or tabulate) makes them comparably more viable with regards to entanglement with fishing lines when compared to other coral forms such as massive colonies.

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Keywords: Coral Reefs, Fishing Lines, Sesoko Island

Feeding habits and niche of short-finned pilot whales and bottlenose dolphins around Kii Peninsula

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The feeding habits of small toothed whales may be important to identify their ecological niche. The prey of bottlenose dolphins (*Tursiops truncatus*) and short-finned pilot whales (southern form, *Globicephala macrorhynchus*) around Kii Peninsula in Japan were studied. Bottlenose dolphins captured in 1999, 2000, and 2002 had mainly consumed *Eucleoteuthis luminosa*, *Enoploteuthis chunii*, and *Watasenia scintillans* among cephalopods, and *Diaphus garmani*, *Diplophos taenia*, *Ichthyococcus* sp., and *Engraulis japonicus* among fishes (Nakatsuka, 2004). Subsequently, the main cephalopod prey remained *E. luminosa*, but there was an increase in epipelagic and demersal fish (Nojiri & Matsuzaki, 2015; Ashida, 2016). The main prey species for short-finned pilot whales captured in 1999, 2000, and 2002 were *Moroteuthis loennbergii*, *Euculeoteuthis luminosa*, and *Ommastrephes bartramii* among cephalopods, and for those captured in 1999 were *Ruvettus pretiosus* and *Lepidocybium flavobrunneum* among fish (Isoda, 2000; Aoki, 2005). However, their feeding habits of have not been studied since. The varied diet of small toothed whales categorizes them as opportunistic feeders, and their diet is expected to change over the long term. Moreover, temporal changes in diet considering the niche of sympatric species have not been studied. In this study, we compared stomach contents, diversity index of prey species, and prey size of both whale species captured before 2003 and in 2012 to identify their niche. We collected stomach contents of short-finned pilot whales and bottlenose dolphins captured by small-type coastal whaling and hand-harpoon fishery fisheries in Taiji, Wakayama Prefecture. Thirty-five short-finned pilot whales were captured in 1999, 2002, and 2003, and 6 in 2012; 24 bottlenose dolphins were captured in 1999, 2000, and 2002, and 18 in 2012. Prey from stomach contents were identified from the morphology of fish otolith, cephalopod beaks, and we estimated dorsal mantle lengths (DML) from the size of beaks. Prey diversity of short-finned pilot whales and bottlenose dolphins was showed negative correlation between cephalopod and fish, but not significant difference, respectively r^2 =0.192, p= 0.7111 and r^2= 0.516, p= 0.0657. The DML mode of *E. luminosa* was 200–220 mm for short-finned pilot whales, and 120–140 mm for bottlenose dolphins, and prey size for both species did not change between 2003 and 2012.It is assumed prey size distinguishes the sympatric niche of short-finned pilot whales and bottlenose dolphins. Furthermore, the prey of short-finned pilot whales is less generalized than that of bottlenose dolphins. Accordingly, bottlenose dolphins may avoid competition by changing prey species. However, we must collect more sample of stomach contents because not enough to define prey diversity.

Keywords: toothed whales, feeding habits, niche

Genetic diversity of the red tide-forming dinoflagellate, *Noctiluca scintillans*, in Japanese and Korean coastal waters

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The heterotrophic marine dinoflagellate, *Noctiluca scintillans*, is the species most frequently involved in the formation of red tides from temperate to tropical coasts around the world. Two types of *N. scintillans* are known by their color, red or green. The red type occurs in a wide range of waters, including Japan, while the green type is distributed only in Southeast Asia and Indian coasts. On the Japanese coast, the distribution has been widely confirmed from Hokkaido to Okinawa, with higher density near the surface layer from spring to autumn. It is unclear whether the dinoflagellate forms cyst, and the mechanism underlying the occurrence of these blooms has not yet been elucidated. The blooms are probably formed through the process of feeding, growing, and accumulating at coastal areas, and a small number of cells that serve as seeds are supplied by the water currents from the open ocean. To determine the mechanism underlying the occurrence of blooms of this species, genetic information from populations in Asia is necessary. The nuclear ITS region analysis of *N. scintillans* (red type) has been reported in Chinese and American populations, but the level of mutations is insufficient for analysis. Therefore, we developed a new primer set for PCR amplification of the mitochondrial COI region, and compared the sequences of *N. scintillans* collected from eight areas in Japan and Korea.

A total of 154 natural cells of *N. scintillans* were obtained; 12 cells from the coast of Miyagi, Japan (May 2018), 7 cells (June 2018) and 18 cells (July 2019) from the coast of Mie, Japan, 37 cells from the coast of Busan, Korea (April 2019), 13 cells from the coast of Yamaguchi, Japan (April 2019), 14 cells from the coast of Hiroshima, Japan (April 2019), 20 cells from the coast of Kyoto, Japan (April 2019), 30 cells from the coast of Aomori, Japan (August 2019), and 3 cells from the coast of Kumamoto, Japan (September 2019). The isolated cells were placed in individual tubes, DNA was extracted, and single-cell PCR was performed using the primers developed in this study. Direct sequencing was performed to create a molecular phylogenetic tree.

A total of 72 haplotypes were obtained from the 154 cells analyzed. Therefore, this method was effective for population genetic analysis of this species, and the genetic variability of this species is considerably higher than other dinoflagellates. The phylogenetic tree divided the populations into two groups, the Japanese populations and the Korean population. As the 2018 and 2019 populations isolated from Mie Prefecture formed the same cluster, the annual variation in genetic diversity seems to be relatively low. Of the 20 cells isolated from Kyoto Prefecture, four cells were included in the cluster of Korean populations. Considering the geographical location between the two points, there is a possibility of seed transfer by ocean current. However, the seed origins in Japan and Korea

Experiment to re-establish high-density patches of short-neck clam, *Ruditapes Philippinarum*, with protective fences to the predation by fishes on Sashiki Tidal Flats in Yatsushiro Sea, Japan

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Dense patches of one of the post popular edible species of bivalve, short-neck clam, *Ruditapes philippinarum*, had collapsed widely from the sandy tidal flats in Kumamoto Prefecture until the 1990s, including our study area, Sashiki Tidal Flats, that faces Yatsushiro Bay. We have conducted the population study of this clam to reveal the reasons why the dense patches of the clam disappeared from the tidal flats, and to find the ways to re-establish them again.

The results of the population study of the clam indicate that two major factors have prevented the establishment of dense patches of the clam on the tidal flats, which are a strong predation pressure by red ray (*Hemitrygon akajei*) and Japanese black seabream (*Acanthopagrus schlegelii*), and development of reduced conditions in the sediment through the formation of muddy carpet on the sediment surface by Asian mussel, *Arcuatula senhousia*. In this study, we conducted the cage experiment to protect the clam juveniles from these two disturbing factors against the development of the clam population, and to re-establish dense patches of the clam in the cages. Two sets of the protective net fences were set on the tidal flats as they fully cover the sediment surface of two meters square of the areas. To the inside of one of them, approximately 26,000 ind. of artificially cultured young spats of the clam (about 11.3 mm of the shell length) were dispersed on the sediment after the surface layer of the sediment up to the depth of 5 cm was scraped off to remove the young spats of Asian mussel on 15 April 2018. Although the young spats of the clam dispersed inside of the protective fences suffered from a high mortality due to a large amount of sand deposition carried from the upstream areas of the river during the rainy season, about 6,200 ind. of the clam, which was equivalent to about 26% of the initial number of the dispersed young spats, survived, and grew up to the adult sizes with the mean shell length of 26.8 mm. We could harvest about 21 kg of the clam finally from the inside of the protective fences on 25 October. Contrastively, none of the clam and very few other macro-benthic animals occurred around the protective fences on the tidal flats.

Thus, the results of the experiment demonstrate that the dense patches of the clam can be re-established on the tidal flats, if the sediment surface is properly protected from the predation activities of benthic fishes, and disturbed to prevent the formation of muddy carpets by Asian mussel.

Keywords: Asian mussel, muddy carpet, predation, protective fences, *Ruditapes philippinarum*, Sashiki Tidal Flats, red ray, short-neck clam

Spatial trends of morphology and genetic structure in seagrass *Zostera marina* on Jeju Island, Korea

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Nine seagrass species are distributed in coastal waters of Korea. *Zostera marina* is the dominate seagrass species in Korea, and there are only one seagrass species *Z. marina* has been observed on the coasts of Jeju Island, Korea. Six seagrass species including *Z. marina* are management as “Marine Organisms under Protection” in Korea due to significant loss of seagrass meadows. However, available data for conservation and restoration of seagrass habitats are insufficient in Jeju Island. In this vein, we aim to establish guidelines for future conservation and restoration projects of seagrass. The geographical distribution and current status of *Z. marina meadows* on Jeju Island were investigated. We also examined genetic structure and assessment genetic diversity of *Z. marina* populations in Jeju Island. Localized ten *Z. marina* meadows were observed in Jeju Island. Shoot height (34.4 to 98.5cm), total density (140.8 to 622.5m^{-2}), and biomass (126.0 to 569.2 g DW m^{-2}) at each study sites varied significantly. Genetic diversity of *Z. marina* populations in Jeju Island was lower than previous studies conducted on southern Korea. Genetic diversity of *Z. marina* population showed a significant positive relationship with habitat size (R^2 =0.605). This result indicates genetic diversity was large affected by habitat fragmentation. The values of genetic differentiation (F_{ST}) were significantly higher among all pairwise populations. Additionally, no correlation between genetic differentiation and geographical distance was observed suggesting that limited gene flow among *Z. marina* populations in Jeju Island. Thus, establish conservation and restoration strategies are required for future management of *Z. marina* in Jeju Island. We hope this study provides useful data for conducting conservation and restoration projects for protected species, *Z. marina* in Jeju Island.

Keywords: seagrass, *Zostera marina*, Jeju Island, current status, morphological variability, genetic structure

Ready to spawn? Final gamete maturation and egg-sperm bundle formation in Acropora and Merulinidae corals

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The majority of coral species are spawners, yet our understanding of this process is still limited. Before spawning, corals need to complete the final gamete maturation; i.e. nucleus migration (NM) towards the oocyte membrane and subsequent germinal vesicle break down (GVBD) in oocytes. Many also need to form egg-sperm bundles. However, information regarding this process remains almost undocumented. Here, we examined the process of NM and GVBD in four coral species(*Acropora nasuta*, *Dipsastraea speciosa*, *Favites colemani*, *F. pentagona*) via histological examinations with tagged colonies sampled daily for 5–10 days until spawning. We also examined egg-sperm bundle formation in *A. nasuta*, A. *gemmifera* and *F. colemani*, through anatomical and histological examinations, with samples collected every 3–4 hrs, for a 24 hr period until spawning. Preliminary results show that in the *Merulinidae* corals, in all samples one day before spawning, NM had occurred but GVBD had not. Most examinations are still underway. During the presentation, we will provide more detailed descriptions and discuss their timing in the entire spawning process. Deeper understanding of such mechanisms will provide crucial information in relation to predictions of spawning timing.

Keywords: coral reproduction, germinal vesicle break down, nucleus migration, egg-sperm bundles

Citizen scientists reveal main threats to the foraging sea turtles in Taiwan

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"TurtleSpot Taiwan" is a citizen scientist project using social media as a platform to collect sighting and photograph records of sea turtles. Photographs are then used to identify individual turtles by their facial scute pattern. The collected information was then used to establish an online sea turtle database. We have received more than 673 records, identifying 308 individuals (287 of *Chelonia mydas*, 20 of *Eretmochelys imbricata* and 1 of *Lepidochelys olivacea*) since June 2017 to December 2018 (still updating). Liuchiu island, the most densest foraging habitat for sea turtles in Taiwan, comprised of 80.2 % of the records and 20% of individuals are injured or clinically abnormal. Most of the injuries and casualties are related to boat strikes and fishing entanglements. We wish to raise conservation needs and the awareness of sea turtles in Taiwan through these cooperation platform and immediate information exchanged on sea turtles.

Keywords: sea turtle, citizen science, open data, conservation, photo identification

Molecular Phylogeny of Clibanarius Dana, 1852 from the Indo-West Pacific: Habitat Adaptation and Evolution of Pereopod Colour Pattern

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The hermit crab genus *Clibanarius* Dana, 1852, currently includes 59 species, 37 of which are distributed in the Indo-West Pacific. Species of *Clibanarius* usually inhabit intertidal and shallow waters, including both hard substrates (e.g., rocky shores and coral reefs) and soft sediments (e.g. mudflats, estuary flats and mangrove forests), making them one of the most successfully adapted groups of intertidal and shallow water hermit crabs. However, the evolutionary relationships for habitat adaptation have not yet been clarified. In addition, the species in this genus are morphologically very similar to, and often indistinguishable from, each other but can be distinguished by species-specific color patterns on the pereopods, (1) bright color transverse band(s) on the whole surfaces, (2) longitudinal stripe(s) on the lateral and mesial faces, (3) scattered bright color spots on the whole surfaces, (4) solid color, and (5) dactyls with solid color distinctly brighter than those of the propodi. The phylogenetic relationships and evolutionary history of these color elements have not yet been investigated using a molecular approach.

We, therefore, reconstructed the phylogenetic relationships of Clibanarius based on three mitochondrial DNA markers [12S rRNA, 16S rRNA and cytochrome oxidase I (COI)] and a nuclear DNA marker (histone H3) from the perspective of the origin of the different color elements and habitat shift. Our findings suggested that evolutionary adaptation from hard substrates to mudflats and soft sediments may have occurred at least twice. In addition, the results also suggested that the striped and solid color elements have evolved multiple times independently, with the ancestral color pattern potentially being scattered, bright color spots with a bright color band the whole surfaces.

Keywords: Intertidal area, adaptation

A mitochondrial genome phylogeny of Mytilidae (Bivalvia: Mytilida)

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The family Mytilidae is a family of bivalve mussels that are distributed worldwide in diverse marine habitats. Within the family, classification systems and phylogenetic relationships among subfamilies remain not yet fully resolved. In this study, we newly determined 9 mitochondrial genome sequences from 7 subfamilies: Bathymodiolus thermophilus (Bathymodiolinae), Modiolus nipponicus (Modiolinae), Lithophaga curta (the first representative of Lithophaginae), Brachidontes mutabilis (Brachidontinae), Mytilisepta virgata (Brachidontinae), Mytilisepta keenae (Brachidontinae), Crenomytilus grayanus (Mytilinae), Gregariella coralliophaga (Crenellinae), and Septifer bilocularis (the first representative of Septiferinae). Phylogenetic trees using maximum likelihood and Bayesian inference methods for 28 mitochondrial genomes (including 19 previously published sequences) showed two major clades with high support values: Clade 1 ((Bathymodiolinae + Modiolinae) + (Lithophaginae + Limnoperninae)) and Clade 2 (((Mytilinae + Crenellinae) + Septiferinae) + Brachidontinae). The position of the genus Lithophaga (representing Lithophaginae) differed from a previously published molecular phylogeny. Divergence time analysis with a molecular clock indicated that lineage splitting among the major subfamilies of Mytilidae (including the habitat transition from marine to freshwater environments by ancestral Limnoperninae) occurred in the Mesozoic period, coinciding with high diversification rates of marine fauna during that time. This is the first mitochondrial genome-based phylogenetic study of the Mytilidae that covers nearly all subfamily members, excluding the subfamily Dacrydiinae.

Keywords: Mitochondrial genome, Molecular phylogeny, Mytilidae, Bivalvia, Mollusca

Interspecific or intraspecific variation?: host-specific color morphs in the parasitic scale worm *Gastrolepida clavigera* (Annelida: Polynoidae)

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Body color similar to that of hosts has been known broadly among ectoparasites. Such a camouflage is supposed to help ectoparasites avoid detection from predators and thereby increase their survivorship. Interestingly, some of ectoparasites that use multiple host species represent multiple color morphs, each of which is specific to different host. Recent molecular phylogenetic studies have revealed that many parasites that were thought to use multiple hosts include cryptic species associated with different host. Taking this into account, perhaps, some of host-specific color morphs may contain cryptic species. A parasitic scale worm, *Gastrolepidia clavigera* Shmarda 1861, is distributed widely in the Indo-West Pacific and lives on the body surface of holothurians. This scale worm shows polymorphism in the body color, such as black, white, and reddish brown. It was suggested that each body color of *G. clavigera* matches to that of host holothurians, which makes *G. clavigera* cryptic, although quantitative assessments remain not done yet. In this study, we asked the following questions for *G. calvigera*: (1) Is the body color of *G. clavigera* truly host-specific?, and if so, (2) does host-associated body color of *G. clavigera* reflect the interspecific or intraspecific variation? First, we collected *G. clavigera* from various holothurian hosts in intertidal flats in Okinawa Island, southern Japan, and found eight distinct color pattern of *G. clavigera* matching to that of each host holothurian: black morph from *Stichopus chloronotus*; black morph with white spots from *Holothuria (Halodeima) atra*; brown morph from *Actinopyga mauritiana*, *Bohadschia argus* and *B. bivittata*; dark green morph from *S. variegatus*; dark purple morph from *S. horrens*; gray morph with a black streak from *S. horrens*; reddish brown morph from *H. atra*; and white morph from *B. argus* and *B. bivittata*. Two color morphs found on *B. argus* and *B. bivittate* used different color parts of the host body, which match to each color morph. We then tested cryptic species hypothesis for eight color morphs of *G. clavigera* by comparing their cytochrome c oxidase subunit I (COI) sequences. Our results show that there is no genetic difference among seven color morphs except for reddish brown morph; the latter is distinguished from the others by about 17% difference in the COI sequences, which is usually considered as an interspecific variation in Annelida. This suggests that host-specific body color of *G. clavigera* is basically due to intraspecific variation, but also contains interspecific variation. We further investigated the phylogenetic relationships between *G. clavigera* from Okinawa (seven color morphs vs reddish brown morph) based on the combined dataset of 18S, 28S and 16S ribosomal RNA and COI genes, with additional sequences of *G. clavigera* from French Polynesia and other representatives of Polynoinae registered in GenBank. Our result suggests that *G. clavigera* is monophyletic but comprises three clades corresponding to different species (seven color morphs: sp. A, reddish brown: sp. B, French Polynesia: sp. C). *Gastrolepida* sp. A was sister to *G.* sp. C, and *G.* sp. B was sister to the clade including the other two species.

Keywords: camouflage, COI, cryptic species, holothurians, host specificity

Species richness of the deep-sea Asellota isopods (Arthropoda: Crustacea) off Tohoku, Japan

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Isopods inhabit various environments from alpine to hadal zones below 10,000 m depth. Asellota is one of the most dominant and species-rich taxa in the deep-sea bottom of the world. Species richness of this group, however, has not yet been sufficiently revealed in the northwestern Pacific. In addition, cryptic speciation has been often reported with the development of molecular phylogenetic analyses. In order to elucidate the diversity of this group, systematic sampling and analyses based on both molecular and morphological characteristics is required.

Information concerning species diversity and geographical distribution of constituent species is essential as the first step for better understanding the diversification mechanisms of deep-sea organisms. In this study, Asellota isopods were collected on a dense spatial scale along two transects in the bathyal and upper abyssal zones off Otsuchi and Onagawa, and at sites off Namie-cho, Tohoku region, the northeastern Japan where information of Asellota species have yet been limited. I attempted to reveal their bathymetrical and geographical patterns of species diversity by molecular phylogenetic analyses and closely morphological examinations.

During 2012-2019, 278 specimens were collected from 19 sampling sites between depths of 236 m and 3,547 m. Nucleotide sequences of a part of mitochondrial COI gene (658 base pairs) were determined to construct a molecular phylogenetic tree. The morphology of representative individuals of each clade on the phylogenetic tree was observed and they were identified mainly based on the structures of the dorsal and lateral processes of the body.

Most of collected Asellota isopods are classified into the families Munnopsidae, Janirellidae, and Janiridae. For the Munnopsidae, the most dominant isopod group in the deep seas of the world with 336 described species, 72 individuals are collected and classified into 14 species of 8 genera. In present study, most of the identified species are unreported from Japan or undescribed species. For the Janirellidae, 34 species are known in the world, 58 individuals are collected and classified into 8 species of a single genus, most of which were identified as undescribed species.

For some species, identical nucleotide sequences were obtained from sites located 80-95 km away, suggesting that such a horizontal distance has not promoted the genetic deviation of deep-sea Asellota isopods off Tohoku.

Most individuals of the Munnopsidae and Janirellidae were collected at three sites around 3,000 m depth. In the depth zone below 3000 m, species richness of the Janirellidae is higher than those of the Munnopsidae. On the other hand, in the shallower zone (<1,500 m), only munnopsids were collected. In contrast to the Munnopsidae that are distributed over a wide depth range from bathyal to hadal zones, the Janirellidae is endemic to areas below the lower bathyal zone.

For Janiridae, 130 individuals are collected. They are now identifying and analyzing. Several specimens were classified into the families Haploniscidae, Desmosomatidae, and Munnidae.

We plan to perform intensive sampling from the lower abyssal to hadal zones off Tohoku.

Keywords: deep-sea, Asellota isopods, species richness, off Tohoku

The splash detection technology for fish feeding monitoring in cage culture

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Feeding monitoring is a highly important part of the cage culture. Reducing feed waste can reduce feeding costs, increase profits, reduce water pollution, make the living environment of fish clean and maintain fish health. As for the fish feeding method, manual operations, coupled with determination of the adequately-fed condition by the naked eye, are generally used. The basis of determination is the degree of splash caused by fish fighting for food, with the highest degree of splashing at the beginning of feeding and less splashing toward the end of feeding. In this study, the splash detection was carried out using the image recognition technology. The detection of splash was mainly done by segmentation, separating splash from the background and determining the degree of splash based on the splash dynamic pattern (distribution range and size). The background waves were random dynamic disturbances that may have affected the determination results. The splash detection technology constructed in this study utilizes the ability to analyze and identify fishes feeding activity images in order to assist in determining feed switching and unit feed volume. At the same time, to reduce the cage culture production costs and waste, but also to reduce the pollution arising out of the sea environment.

Keywords: Cage culture, Image recognition, Fish feeding monitoring

Spatial distribution of the sea cucumber Apostichopus japonicus in the natural habitat of Miyazu Bay, Kyoto, Japan

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[Background]

In Japan, the sea cucumber *Apostichopus japonicus*, which is one of the most valuable temperate-water sea cucumber species, is harvested from its natural (wild) populations, as opposed to the farmed population. To manage and enhance the stocks of A. japonicus, various conservation efforts are carried out.

In Miyazu Bay, located in the south part of the Sea of Japan, *A. japonicus* fisheries are managed vigorously by the local fishermen and some public agencies, such as a prefectural fisheries office. They employ several controls for catching *A. japonicus*, including limiting the type of fishing gear, total daily catch, minimum harvestable size, closed seasons or areas.. However, the population structure, distribution, and abundance of *A. japonicus* in this bay have not been quantitatively surveyed. Furthermore, the distribution of *A. japonicus* in its natural habitats, including those in China, has not been sufficiently assessed. In this study, we investigated the spatial distribution of *A. japonicus*, and the environmental factors after its aestivation season, to determine the appropriate habitat for them, with the help of local fishermen.

[Methods]

Trawling surveys were conducted in Miyazu Bay, in January 2017 and 2018, prior to the opening of the beam trawl fishing season of *A. japonicus*. The deepest area of this bay is 25 m deep. Trawling surveys were performed at 13 sites distributed across the bay, with survey lines at 5, 10, 15, 20, 25 m depths, parallel to the contour. Six local fishermen with their fishing boats participated in the surveys, and their beam trawls (opening length 2.5 m or 2.7 m, height 0.4 m) were dragged for 15 minutes along each line. Wet weights of collected sea cucumbers were recorded individually. Sediment samples were collected by a grab sampler along each line. Grain size distributions of sediments, total organic carbon (TOC), and total nitrogen (TN) were determined. Geographic parameters, such as slope of the sea bottom, distance to the coastal line, and fetch distance as a wave exposure Index were calculated using geographical information systems (GIS) and the R language.

[Results and Discussion]

The spatial plot of the wet weight of individuals of *A. japonicus* in Miyazu Bay appeared to be higher at the mouth of the bay than the inner parts, for both 2017 and 2018. Statistical analysis also showed that the wet weight was positively correlated with the depth and fetch distance, and negatively correlated with the median grain size (mm) and the sorting index. The density of *A. japonicus* was higher at the near-shore sites, and was positively correlated with the fetch distance and median grain size (mm), and negatively correlated with the total organic carbon. The spatial plot showed that small sea cucumbers were abundant at the inner parts of the bay along the shallow lines (5, 10 m depth), despite the deeper line (15 m depth) showing only a few individuals. Such a distribution pattern differed from that observed at the mouth of the bay, where some large individuals were collected along the deeper lines (15, 20 m). This information will aid in the stock enhancement of *A. japonicus* including the decision of releasing area of reared juveniles or the decision of the protected areas from fishing in the natural environment. Moreover, this information may be useful for improving the farm environment.

Keywords: depth, holothurians, organic matter, stock enhancement, the Sea of Japan

Toxicity assessment for the wastes removed from the in-water ship's surface cleaning activities using sea-urchin embryos

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This study was conducted to assess the toxicity of the wastes removed from ship's surface by the in-water cleaning and water jet cleaning activities on the marine benthic animals. To evaluate the toxicity of wastes, sea urchin (Mesocentrotus nudus) embryos were used. Materials for this toxicity test were collected from the antifouling paint wastes removed by on dock water jet cleaning from the R/V EARDO and R/V ISABU, and also those from in-situ cleaning water (ICW) and filtered ICW (FICW) from the R/V EARDO and R/V ONNURI. Heavy metals and biocide contents in the wastes from cleaning operations and all the final stock solutions were analyzed. In the case of the R/V EARDO, the fertilization rate exposed on water jet samples were 79±5.8% at the 0.1% diluted solution, 2.3±1.4% and 0.2±0.5% at 1% and 10% solutions, respectively. The fertilization rate for ICW was 0% at 10% and 100% solution, but it was over than 90% at both the 0.1% and 1% solution. The fertilization rates on the ICW and the FICW were similar; the EC50 values of fertilization rate for ICW and FICW were 2.7% and 3.1%, respectively. In the case of the R/V ISABU, fertilization rate was 0% exposed on the 10% solution or less diluted solution from water jet samples. The concentration of copper in the water jet samples was higher at R/V ISABU than R/V EARDO, while those of copper and zinc were higher at R/V EARDO. Among the biocides, higher concentrations of CuPT and ZnPT were detected in water jet samples from the R/V EARDO and R/V ISABU. In the case of the R/V ONNURI, the fertilization rate on ICW and FICW were 53.8±5.6% and 94.0±5.4% at the 10% diluted solution. The EC50 values of fertilization rate for ICW and FICW were 10.9% and 26.8% diluted solution, respectively.

Keywords: : antifouling paint waste, toxicity, in-water cleaning, water jet cleaning, sea urchin embryo

Meiofaunal composition of sandy beach and soft-bottom of coral reefs in the Western Gulf of Thailand

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Meiofauna is an important component of marine benthic habitats and it plays a major role in coastal biological processes, particularly facilitating biomineralization of organic matter and enhancing nutrient regeneration. Understanding connectivity between the coral reef and its associated communities is required to investigate and the complexity of food webs in marine and coastal communities. Studies on the gradient of meiofauna communities between the sandy beach and soft bottom area of coral reef at the same study site are very limited. This study investigated composition and abundance of meiofauna living in sandy beaches, soft bottom parts of shallow reef flat, reef slope and deep soft bottom zone in the Western Gulf of Thailand. The sediment samples for the meiofauna study were collected at Ko Mattra, Chumphon Province by using a PVC meiocore of 3.5 cm diameter which was randomly inserted into the sediment down to a depth of 10 cm. The results revealed that eight taxa of meiofauna were commonly observed at the study sites, including Foraminifera, Turbellarian, Nemertea, Nematoda, Polychaeta, Ostracoda, Copepoda and Bivalvia. The highest density of meiofauna was found at the sandy beach and the lowest one was observed at the deep soft bottom zone. The most dominant meiofaunal groups were copepods at the sandy beach, foraminifera at shallow reef flat and nematodes at reef slope. This study highlights future applications of meiofauna for a bioindicator of sandy beach and coral reef ecosystems. Our results could serve as scientific information for further studies on the connectivity of sandy beaches and coral reefs in the Gulf of Thailand.

Keywords: bioindicator, coral reef, Gulf of Thailand, meiofauna, sandy beach

Distribution of toxic *Alexandrium tamaense* and *A. catenella* in Akkeshi-ko estuary and Akkeshi Bay, where oyster is cultivated on a large scale in Japan

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Akkeshi-ko estuary and Akkeshi Bay, Hokkaido, is one of the most famous area, where oyster is cultivated on a large scale. The first occurrence of paralytic shellfish poisoning was reported in this areas, around the 1980s and the causative algae was though to be the toxic dinoflagellate *Alexandrium tamaense*. After this incident, and the paralytic shellfish poison in this area is thought to be due to this species. However, since no strict identification survey has been conducted at the genetic level, it is still unclear whether the damage is caused just by this species. In this study, the causative species to paralytic shellfish poison was identified and distribution of identified species in this area was surveyed by metagenomic analysis and Real-Time PCR. Furthermore, core samples were collected, and the time when causative toxic species were introduced to and settled at Akkeshi area was estimated by real-time PCR and sedimentation rate measurement.

We collected core samples in September 2014 and soil samples on the bottom at 15 sites in December 2015 and November 2016 in Akkeshi-ko estuary and Akkeshi Bay. The collected core was divided into 1 cm intervals and every 5 cm layers were used sed as a sample. DNA was extracted from all these samples, and Real-Time PCR targeting *Alexandrium tamaense* and *A. catenella* was performed. Metagenomic analysis was also done for comprehensive analysis, showing the phytoplankton community in this area. The sedimentation rate was calculated using the 210Pb data

As a result of Real-Time PCR, just *A. tamarense* was causative species in the Akkeshi coastal area, but *A. catenella*, which is another most serious toxic species was not detected at all. The number of *A. tamarense* cells was different among the sampling sites, and the number of cells was small near the much eelgrass field, suggesting that *A. tamarense* might not grow due to the algicidal bacteria attached to the surface of the eelgrass. Metagenomic analysis showed that the existence of a large number of harmful toxic algae, including also species which have not been reported in Akkeshi-ko estuary and Akkeshi Bay. The sedimentation rate was estimated t0.266 ~ 0.276g / cm^2 / y 210Pb radioisotope. Real-time PCR and this rate indicated that causative species of the first paralytic shellfish poisoning at Akkeshi-ko estuary and Akkeshi Bay 1980s was just *A. tamarense*, and this species was existed since the late 1950s before the shellfish poison occurred around this area.

Keywords: paralytic shellfish poisoning, Alexandrium, real-time PCR, metagenomic analysis, eelgrass, algicidal bacteria

Microcystine (freshwater origin cyanotoxin) hibernates in the sea bottom

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In many of the world eutrophic wetlands, dams, artificial reservoirs, blooming of toxic cyanobacteria is becoming frequent, and influence on hydrosphere ecosystem including drinking water is concerned about. However, not enough interest has been paid to the fate of the toxin after a large quantity of water including the toxin was discharged in the sea area probably because it has been thought that cyanobacteria perish by high salinity in the sea and the toxin is degraded by bacteria. However, in Isahaya Bay, Nagasaki, Japan, Microcystins (MCs) content of sediment raised after a large discharge from the reservoir, and we confirmed that MCs in the sea floor remains throughout the year. In addition, MCs were transferred and accumulated in benthos. The content of MCs in the sediment and benthos were high in winter season (non-blooming season of cyanobacteria) rather than the blooming season. It is probably because the absence of MCs degrading bacteria or low activity of degrading enzymes. Such a situation is not considered to be limited in Isahaya Bay. For instance, we collected the sediment of Naktong River, Korea in December, 2016, where large scale blooming of toxic cyanobacteria repeatedly occurring every summer, and MCs have been detected in the sediment. Most of toxic cyanobacteria occurred in fresh water area finally arrive at the sea area. As for the MCs pollution in nearshore waters, actual situation is just begun to be clarified.

Keywords: microcystin, cyanobacteria, bioaccumulation

Long-term monitoring of macrobenthic fauna on three tidal flats in the Tokai Region, Central Japan from 2008 to 2018 (the Monitoring Site 1000 program)

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Since 2008, long-term changes of macrobenthic fauna have been monitored at eight sites on Japanese tidal flats by multiple research groups under the Monitoring Site 1000 Program (the Ministry of Environment). Of these sites, our group has monitored the fauna at sites on three tidal flats (i.e., Shiokawa flat in Mikawa Bay, Aichi Pref.; Matsunase flat in Ise Bay, Mie Pref.; a flat in Ago Bay, Mie Pref.) located in the Tokai Region along the Pacific coast, central Japan. Three times (one time between April and July) in 2008, 2013 and 2018, abundance data on collected macrobenthic species together with sediment characteristics were obtained along two transect lines set on each flat. For sampling macrobenthos, we set up two or three points along any transect line on each flat: Five sediment samples were collected at each point using core sampler (covering a surface area of 176.6 cm^2, and a depth of 20 cm). Throughout the investigation, both averages of abundance (ind./sample) and species number (spp./sample) were the highest on the Shiokawa while the lowest was on the Mastunase, indicating a close relationship between abundance and species number. Dominant species was different among three flats for the above three times: *Ceratonereis erythraeensis*, *Batillaria multiformis* and Cirratulidae spp. on the Shiokawa, *C. erythraeensis*, *B. attramentaria* and *Gnorimosphaeroma* spp. on the Matsunase, *B. multiformis*, *Pirenella nipponica* and *B. attramentaria* on the Ago, respectively. According to multivariate analysis (nMDS and cluster analysis), macrobenthos community structure on the flats was separated to each other as related to sediment characteristics. nMDS analysis detected a marked spatio-temporal variation in community structure on the Matsunase, probably caused by various habitats on the flat and due to heavy rainfall.

Keywords: long-term monitoring, microbenthic fauna, Japanese tidal flats

Feeding ground function of fishing ports for fish in southwestern Hokkaido, Japan

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For the purpose to propose a method to strengthen the nursery function for aquatic organisms within the waters of fishing ports, such as the basin, in cold region, field surveys to obtain fundamental biological and physico-chemical knowledge for evaluating its function as feeding grounds considering benthic ecosystem were conducted in Suttsu fishing port located in southwestern Hokkaido, Japan.

Through the study period, the waters in the fishing port were calmer than the outside waters of the fishing port. However, there were no drastic differences between the inside and outside waters of the fishing port in water salinity and temperature. The bottom water dissolved oxygen was always higher than 6 mgO $_2$ /l at the inside waters of the fishing port, thus the water column was always an aerobic environment. Although the density of the zooplankton was not significantly different between the inside and outside waters of the fishing port. The density and biomass of macrozoobenthos at the most inside waters of the fishing port area were significantly higher than the outside waters of the fishing port. In addition, the surface sediment at the most inside waters of the fishing port had higher standing stocks of Chl. *a*, organic carbon and NH_4 contents than the outside waters of the fishing port. Various life stages and styles of fish also were observed to inhabit at the waters in the fishing port. Moreover, the dominant species of macrozoobenthos at the waters in the fishing port were found in several fish stomachs.

These results indicate that various fish use the fishing port as feeding grounds. Furthermore, the stable seafloor environment contributes to maintaining the sustainable benthic ecosystem combined with the planktonic ecosystem that supports the feeding ground function of the waters in the fishing port.

Keywords: Fishing port, nursery function, feeding ground, benthic ecosystem

Shifting in bacteria *Endozoicomonas* is independent to coral bleaching

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The coral-associated bacteria *Endozoicomonas* are a potential indicator of coral health. Their relative abundance usually decreases in bleached corals and is proposed to be positively correlated with Symbiodiniaceae abundance. However, some reports suggest that shifts in *Endozoicomonas* are unrelated to Symbiodiniaceae abundance. This study used dark-induced bleached corals to remove the factors of temperature and test the relationship between shifts in *Endozoicomonas* and coral bleaching. 16S rRNA gene sequencing revealed bacteria communities and *Endozoicomonas* were quantified by qPCR with specific primers. We detected high relative abundance of *Endozoicomonas* in the dark-induced bleached *Euphyllia glabrescens* over three months. The results indicate that changes in the relative abundance of *Endozoicomonas* are unrelated to the dissociation of Symbiodiniaceae.

Keywords: coral microbe, coral bleaching, *Endozoicomonas*, Symbiodiniaceae

Seasonal change of benthic diatoms in Gamo Lagoon, Miyagi Prefecture, northeastern Japan

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Gamo Lagoon is located on the north side of the Nanakita River Estuary in Sendai Bay, northeastern Japan and well known as stopping point for migratory birds and nursery area for fish juveniles. Benthic diatoms, which cover the bottom surface of Gamo Lagoon, are thought to be important as primary producers and support the biological production in lagoon. They are also expected to use as environmental indicators. However, their abundance and composition in the field are mostly unknown. This research aimed to reveal the community structure and seasonal change of benthic diatoms in Gamo Lagoon. Monthly field investigations were conducted at two sites from April 2018 to August 2019. Environmental factors (water temperature, mud temperature, salinity, nutrients conc., chl *a* conc., stable isotope ratio) were measured and sediment samples were collected from surface 0–1 cm by using a core. Benthic diatoms which were separated from sediment samples were identified at genus level and counted to calculate the cell density. The average of the cell densities of benthic diatoms at Stn A (estuary site) and Stn C (inner site) were 7.8×10^5 cells/g and 4.8×10^5 cells/g, respectively. These values were larger than those of planktonic diatoms in typical tidal flats. The value of chl *a* conc. in the sediment, representing biomass of benthic diatoms, was 10^3 times larger than that in the water column. Seasonal change in the cell density of benthic diatoms differed between the two sites. Stn A showed a clear seasonal change that decreased in summer, while no clear change was observed at Stn C. The $\delta^{13}C$ analysis in the sediment at Stn A showed higher value of terrestrial materials than Stn C. So, this difference of seasonal change in cell densities may be associated with inflow of water from the land. The benthic diatom community was dominated by the genera *Navicula*, *Cymbella* and *Amphora* throughout the year and its structure was stable. Further investigation is expected to reveal the relationships between benthic diatoms and their predators.

Keywords: benthic diatoms, lagoon, seasonal change, chlorophyll *a*, stable isotope ratio

The importance of habitat diversity for biodiversity of benthic macrofaunal species in a semi-enclosed coastal sea

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In coastal marine zones, diverse habitats are closely formed. However, natural habitats have been lost or altered to habitats with artificial structures by human activities. Although recent studies show that habitat loss leads to the increasing in the risk of species loss and accelerating deterioration of ecosystem functions, the impact of decreasing habitat diversity on the biological community has not been concretely investigated. In this study, we show the interrelationships based on species commonality between four different types of habitats for benthic macrofaunal species (eelgrass bed, muddy bottom, tidal flat, and harbor breakwater) in Matsunaga Bay, western Japan. Furthermore, we compared the functional compositions of benthic macrofaunal communities focusing on primary feeding modes and common life forms to detect the differences of ecosystem functions driven by benthic macrofaunal species among the habitats.

We conducted field surveys in September (summer) in 2016 and in January (winter) in 2017. We collected benthic macrofaunal species with sediments using a Smith–McIntyre grab sampler in eelgrass bed, muddy bottom, and tidal flat. In eelgrass bed, eelgrass-associated species were collected with eelgrass shoots using mesh bags and quadrates. Because the benthic macrofaunal community was composed mainly of sessile species on harbor breakwater, we used scraper blades, mesh bags, and quadrates. After identification and counting of all the species, we compared the species compositions, the community compositions, and the functional compositions by multivariate analyses.

Our results showed that the interrelationships of habitats for benthic macrofaunal species were strong between eelgrass bed, muddy bottom, and tidal flat. About 25-37% of species were shared in each set. For the benthic macrofaunal community on harbor breakwater, the number of collected species was the highest, but the community characteristics were unique. Functional compositions of benthic macrofaunal communities were different among the four habitats.

In conclusion, habitat diversity is deeply related to species and functional structures of biological communities. Our results suggest that habitat characteristics and connectivity should be considered for effective management and conservation of biodiversity and ecosystem services at local scales.

Keywords: Macrobenthos, Species diversity, Habitat loss, Seascape, Coastal development, Biodiversity, Ecosystem function, Habitat connectivity, Functional trait

Vertical distribution of the introduced Invasive smooth cordgrass, *Spartina alterniflora* in the West Coast of Korea

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Since the invasion of smooth codgrass, *Spartina alterniflora* was reported in 2015, its distribution has spread rapidly on the west coasts of Korea. This study was performed to examine vertical distribution of the cordgrass and identify competition with native salt marsh plants.

In 2015, field surveys were conducted on Dongmak and nearby Buno in Ganghwa-do (6 m in mean tidal range), and Jindo (2 m in mean tidal range). Belt transects of 15 m in width, including *Spartina* patches and native salt marshes, were carried out with 5 in Dongmak, 2 in Buno and 5 in Jindo respectively. In addition, vegetation type, tidal elevation and vegetation coverage were measured.

Spartina in Ganghwa was mainly distributed between MHW and MHWN. However, the main patches in Jindo grow from MHW to near MSL, much lower than that of Ganghwa and the lowest patch was found below MSL. Common reed marsh, *Phragmites australis* was present in the upper part of the tidal flats together with the *Spartina* marsh in the study areas. The vertical distribution ranges of *Spartina* were much larger than those of all native salt marshes studied. In Dongmak area, *Spartina* coinhabit and spatially compete with *Suaeda japonica*. Compared to the vertical distribution of *Spartina* in their native habitats on the east coast of the America, the pattern seems similar and the same is true of the tidal flats in the Yangtze Estuary, China. Therefore, *Spartina* marsh also compete with the common reed marsh at the upper limit of their distribution, and it out competes the native *S. japonica* marsh in middle tidal flat.

Finally, *Spartina* become rapidly abundant and established at mid to high tidal elevations, where it will soon displace the native salt marshes. Therefore, this invasion will change the coastal landscape in the near future, so that the traditional ecosystem services will be on the decline.

Keywords: Cordgrass, Halophyte, Invasive species, Korean tideland, Salt marsh, *Spartina*, Tidal elevation, Tidal flat

Denitrification activities in coastal mangrove soils of Taiwan

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Mangrove soils have important roles in biogeochemical cycling of nitrogen. In this study, we analyzed the activity of denitrification, an essential process of nitrogen cycle, and the abundances of genes (*nirS* and *nirK*) encode enzymes involved in denitrification of mangrove soils under *Kandelia candel* and *Avicennia marina* in Taiwan. The denitrification activity was measured in seven-day incubation with nitrate, and the abundances of *nirS* and *nirK* were assessed using real-time quantitative polymerase chain reaction. The soil pH values ranged from 6.0 to 7.5, while the amount of organic carbon in *Kandelia* soils was significantly higher than that in *Avicennia* soils. In general, the maximum denitrification activity was recorded at the third day of incubation in *Kandelia* soils and at the second day in *Avicennia* soils. The abundance of *nirS* gene was up to 10^9-10^{10} copies per gram soil, while the *nirK* gene was only about 10^5 copies per gram soil. The highest gene copy number occurred in the second or third day of incubation in both soils, which was associated with the depletion of added nitrate. The denitrification rate and abundance of *nirS* were positively correlated with soil organic carbon content ($P <$ 0.05). These results suggest that the differences in denitrification between variant mangrove vegetations could result from soil characteristics, which were directly or indirectly influenced by vegetation.

Keywords: denitrification, mangrove, *nirS*, *nirK*

The role of crabs having cellulose digestion ability in mangrove organic carbon processing

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Brachyuran crabs have been recognized as an important functional component in mangrove ecosystems, particularly in terms of trophic linkages between producers and higher consumers and organic carbon processing through their feeding activities. The crabs are generally surface-deposit feeders ingesting sediment organic matter which primarily comprises detritus originated from leaf litter (mangrove detritus). Several studies based on direct observations of food habits of crabs (e.g., stomach content analysis) have shown that mangrove detritus and/or leaf litter significantly contribute to their diets, especially sesarmids. Nevertheless, the isotopic studies have suggested a greater contribution of nutritious and easily degradable microphytobenthos as a carbon source for many crab species rather than that of mangrove materials, probably because the latter mainly comprise indigestible carbohydrates, such as cellulose. The simple ingestion of mangrove materials does not necessarily indicate any direct assimilation of the materials, and thus implicitly role of crabs in acting as initial processors of mangrove organic carbon has been questioned.

Recent studies using stable isotope techniques and digestive enzyme assays, however, have revealed that some macrobenthos in temperate estuaries possess cellulase enzymes enabling them to efficiently digest and assimilate cellulose-rich plant detritus. Accordingly, it is inferred that some crabs in mangrove estuaries also assimilate refractory mangrove materials using the enzymes, resulting in key role in initial decomposition of the materials and driving the detritus-based food chain in mangrove ecosystems. In order to clarify the role of crabs with the ability to digest cellulose in carbon processing, we investigated 1) cellulase enzyme activities of crabs and their assimilating of refractory mangrove materials, 2) how the crabs contribute to the decomposition of leaf litter as an initial processor, and 3) whether the crabs link mangrove organic matter to higher trophic levels.

Dual stable isotopes (δ13C and δ15N) analysis and cellulase enzyme assays were performed toward the six dominant crab species inhabiting three microhabitats (i.e., mangrove forests, bare sandy flat and muddy flat) in a subtropical mangrove estuary on northern Iriomote Island, southern Japan. The results showed that most dominant crab species, such as the soldier crab Mictyris guinotae on the sandy flat and fiddler crab Gelasimus jocelynae on the muddy flat, have low cellulase activity and essentially depend upon microphytobenthos, whereas Parasesarma bidens inside the mangrove forest with the highest cellulase activity assimilate mangrove detritus and leaf litter. Based on the results, we conducted a field experiment to assess the contribution of P. bidens to the decomposition of leaf litter. Leaf litter consumption by P. bidens, determined using field cages, demonstrated that a single crab consumed 1.5 g/week, the estimated annual consumption under natural crab density (8 individuals/m2) being 626 g/m2 (86% of total litterfall amount). Furthermore, gut content and stable isotope analyses of the dominant fishes in the study estuary, such as the snapper Lutjanus argentimaculatus and grunt Pomadasys argenteus, showed that the snappers feed primarily on crabs inside the mangrove forests, particularly P. bidens, while the crabs assimilating microphytobenthos

Bioturbation of Sesarmid crab Chiromantes dehaani at reed marsh in Yodo river estuary, Japan

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The objective of this research is to reveal the burrow structure and habitat of *Chiromantes dehaani*. The investigation was carried out on a Yodo river reed marsh (ca 1800 m^2) where about 8 km upstream from river mouth in Osaka prefecture, Japan. Burrow structure of *C. dehaani* was investigated using in situ polyester resin casting. Sampling was conducted in May 2017, and a total of 22 burrow casts were obtained. The maximum measured burrow volume was 384 cm^3 and wall surface area was 480 cm^2, while maximum burrow length and depth were 28 cm and 15 cm, respectively. Burrow volume and surface area were recognized statistically significant correlation with carapace width of *C. dehaani*. It was estimated burrow volume 3.89% for salt marsh in investigation area and the area increases 77.2% (1118.9 m^2) due to *C. dehaani* dig out 10.3 kg sediment when sediment depth affected by *C. dehaani* assumed 10 cm. It indicated increasing surface area enhance aerobic environment in sediment by burrows of *C. dehaani*.

Habitat of *C. dehaani* was investigated 29 station in reed marsh in May 2017. We measured particle size composition, water content, AVS, IL, ground height and reed density and sediment penetration. 3 sediment groups were classified by cluster analysis. The sediment environment of the group with many burrows of *C. dehaani* was the sediment environment with high ground height, low water content and high penetration in reed marsh. There is no statistically significant correlation between the number of *C. dehaani* captured using pitfall traps and the number of burrows in each stations. In addition, the activity of *C. dehaani* was measured using pitfall traps, many crabs were collected in September, suggesting high activity associated with movement in summer.

Keywords: Chiromantes dehaani, reed marsh, burrow, sediment

Parmales abundance and species composition in the waters surrounding Hokkaido, North Japan

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The abundance and species composition of Parmales (Bolidophyceae), a siliceous marine phytoplankton, were investigated in the waters surrounding Hokkaido, North Japan. In the Pacific Ocean, high Parmales abundances were observed in the Oyashio region (84.9–95.2 cells mL–1), in the surrounding area of the cold Oyashio Current, and in the Coastal Oyashio Water (35.1–41.4 cells mL–1) being low temperature and salinity in spring. In the Okhotsk Sea, Parmales abundance was moderate (>5 cells mL–1) in the Intermediate Cold Water, which is formed by convective mixing under the pack ice. On the other hand, their abundance was quite low in warm water masses, such as the Tsushima Warm Current in the Sea of Japan and the Soya Warm Current in the Okhotsk Sea. Parmales cells were also found in the sea ice in the Notoro-ko Lagoon connected to the Okhotsk Sea, suggesting that they have an ice algal life cycle. Triparma spp. were almost dominant in the study areas with the occasional contribution of Tetraparma spp. in the Okhotsk Sea. These results indicate that Parmales abundance and species composition are significantly influenced by water currents.

Keywords: Parmales, Distribution, Species composition, Water currents

Species composition and distribution for phytoplankton of Tung Nang Dam estuary in Phang-Nga Province during dry and rainy seasons in 2018-2019

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Phytoplankton are photosynthetic organisms that are the major producers of freshwater and marine ecosystem. Certain species of phytoplankton produce powerful biotoxins, making them responsible for so-called red tides or harmful algal blooms. Based on data collected at 6 stations in Tung Nang Dam river estuary in Phang-Nga Province during cruises of December 2018 (dry season) and May 2019 (rainy season) using 21 micrometer meze size of plankton net, this study examined taxonomic composition, abundance, and spatial distribution of phytoplankton. Results indicated 54 species of phytoplankton in the samples from the dry season, and 62 species in rainy season. Among them, in the dry season , 1 species of cyanobacteria, 25 Species of centric diatom, 15 species of pennate diatom, and 13 species of dinoflagellate were found and in the rainy season, 2 species of cyanobacteria, 33 Species of centric diatom, 17 species of pennate diatom, and 10 species of dinoflagellate were found. The abundance of phytoplankton in the rainy season was higher than that of the dry season, with an average of 208 x 105cells. m-3 and 50 x105cells .m-3, respectively. The dominant phytoplankton species in the dry season was Trichodesmium sp., Amphora sp., Pleurosigma sp., Thalassionema frauenfeldii, Prorocentrum micans and Protoperidinium sp. In the rainy season, Thalassiosira sp., Asterionellopsis gracialis, Thalassionema frauenfeldii, became the key dominant species. Neither marine phytoplankton bloom nor harmful algal bloom were found in this area. Abundance of phytoplankton tended to negatively correlate with salinity and dissolved oxygen of seawater. Range of salinity of sea water was from 32 to 35 ppt in dry season, and from 30 to 36 in rainy season.

Keywords: phytoplankton, estuary, Tung Nang Dam, Phang-Nga Province

Host detection of symbiotic crab Tetralia rubridactyla

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The study of host detection of the coral symbiotic crab *Tetralia rubridactyla* could help explain the relationship, interaction, and importance of symbionts with coral reefs as hosts. Three scleractinian coral were selected for this study: *Acropora hyacinthus* and *A. digitifera* as host corals, and *Stylophora pistillata* as a non-host coral. The study was divided into 2 series of experiments; visual test and chemical test. The visual tests were conduct in a system consist of 3 glass aquaria. The system allowed the crabs to only see the choices but unable to smell them. The chemical tests were conducted in a Y-maze system. The crabs can receive seawater flowing through the various choices, but unable to see any of the choices. In both tests, amount of time that the crab moves from the start point to the half way (Time A) were recorded, along with the time that the crab move from the half way to the either side of the end (Time B). The experimental results from visual and chemical test were analyzed using chi-square tests comparing the observed preference frequencies to an expected frequency of 50:50. Time A and Time B were compared using *t*-test. The results revealed that the crab seems to walk randomly in all treatments of the visual test. On the other hand, the chemical test showed that they can clearly distinguish and trace the coral hosts by detecting smell. In both tests, the reaction times spent by these crabs were extremely varied and no certain pattern. The host detecting experiment demonstrated that the crabs distinguish and trace the coral hosts primarily by using chemical cues from host. Other than chemical cue, the crabs might need tactile sensor and/or visual cue to confirm their hosts' existence. Without these signals, they might be uncertain and continue seeking. This study also revealed that *T. rubridactyla* expresses no preference between *A. hyacinthus* and *A. digitifera*.

Keywords: Symbiosis, Coral, Tetralia rubridactyla, Host detection

Comparative seascape genetics revealed contrasting genetic structure and habitat preferences between co-distributed closely related marine species

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Recent molecular studies have focused on how relationships between physical and ecological factors influence on the marine biogeography. Comparative phylogeography using multiple species is a powerful tool to evaluate the role of ecological traits for shaping genetic patterns of marine species. To uncover the links between ecological traits and genetic structures, closely related and co-distributed species with different habitat preferences is a good model. In the present study, ecological traits and genetic structures of three co-distributed species of the intertidal snail genus Monodonta are compared. We investigated the habitat preference by measuring the degree of coastal exposure and substrate type and estimated the genetic structure and demographic histories. The results showed while M. labio prefers a sheltered habitat, M. perplexa prefers a wave-exposed habitat. In contrast, M. confusa can live in a habitat with a wide range of wave exposure. This indicates that M. labio and M. perplexa is a habitat specialist in tolerance to wave exposure, but M. confusa is a generalist. We found a clear pattern showing distinctive genetic structures and demographies between a habitat specialist and generalist. M. labio and M. perplexa had a lower level of genetic diversities and a higher level of genetic differentiation among populations. However, M. confusa exhibited a high level of genetic diversity and no clear geographical genetic structure. The above findings suggest that ecological specialization is potentially an important process to promote genetic divergence among local populations even in a well-connected marine environment.

Keywords: Phylogeography, Habitat preference, Japanese mainland, Ryukyu Archipelago, Gastropod, Trochidae, Monodonta

Summer variations of macrobenthic community structures in Gwangyang Bay, South Korea

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We investigated the structure change of the macrobenthic community in Gwangyang Bay (Korea) in response to habitat alteration, using the summer fauna data collected between July 2007 and August 2015. The results showed that polychaete worms were the most abundant benthic community faunal group, and polychaetes were richest in species number and density, while mollusks accounted for the highest proportion of the total biomass. There were large variations in species richness and density and the biomass of the macrobenthic faunal communities in Gwangyang Bay that are linked to environmental perturbations that have occurred for more than a decade. There was also a change in the composition of the macrobenthic faunal community, especially in the dominant species. The most dominant benthic fauna were Heteromastus filiformis and Magelona japonica after 2007, and the dominance of Theora fragilis increased after 2008. Scoletoma longifolia dominated from 2009 to 2012, and it was still the dominant species in summer 2015. Analyses based on ANOSIM and nMDS showed significant changes in the benthic community structure during summer periods from 2007 to 2015. In particular, the benthic community in 2015 differed from other summer communities because of the decreased occurrence of T. fragilis. The temporal changes in the faunal composition suggest that the changes were related to long-term changes in habitat conditions brought about by activities such as land reclamation and dredging within the study area that were the result of construction work carried out by the Pohang Steel Company, and the establishment of other industrial facilities.

Keywords: macrozoobenthos, community structure, summer variation, Gwangyang Bay, Korea

Survey of the family Spionidae (Annelida) in Danshuei River and Estuary, north Taiwan

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Spionidae is one of the biggest families in the phylum Annelida and it shows high species diversity and habitat adaptation in marine environments. According to few studies on species identification and habitat condition of the family Spionidae in Taiwan, our purpose is to increase the knowledge of the spionids inhabiting Taiwan especially focusing on the biological characteristics of the so-called polydorid species complex. We conducted the survey in Danshuei River and Estuary, north Taiwan, in February 2018. Environmental factors were measured and water temperature 16–17°C and salinity 7–19.8 were observed during the survey. The worms were collected from the muddy and sandy bottom sediments using Ekman-Birge grab sampler and 1 mm mesh sieve and oysters and pearl oysters were sampled by hands to collect the worms inhabiting the shells. As a result, seven spionid species belonging to seven genera including five newly recorded species from Taiwan were found. *Carazziella spongilla* and *Boccardiella hamata* were extracted for the first time in Taiwan from oyster shells. A large population of *C. spongilla* was observed to inhabit muds in crevices of oyster shells which were distributed along Danshuei River. *Polydora triglanda* was extracted not only from the shells of oysters but also from pearl oysters. Particularly oyster shells were heavily infested by numbers of *P. triglanda*. Other spionid species, *Scolelepis kudenovi*, *Malacoceros* cf. *indicus* and *Rhynchospio* aff. *asiatica sensu* Radashevsky et al., 2014 were collected from sandy beach, mangrove and tidal flat environments, respectively. *Scolelepis kudenov* and *Rhynchospio* aff. *asiatica sensu* Radashevsky et al., 2014 seemed to be new from Taiwan. *Prionospio* cf. *japonica*, which was commonly collected from the sand bottoms of the river, needs further examination for accurate species identification. Next survey is expected to conduct in different waters and seasons to add the spionid species inhabiting Taiwan.

Keywords: Annelida, Spionidae, polydorid species, habitat condition, Danshuei River, estuary, Taiwan

Profiling gene expression responses of the blood clam *Anadara kagoshimensis* to anoxia by *de novo* RNA-Seq analysis

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The blood clam *Anadara kagoshimensis* is one of the commercially important marine bivalves inhabiting East Asian coastal waters. This species has a high tolerance to the anoxic condition, and some studies have reported the metabolic responses to anoxia. However, little is known about their responses to anoxia at the transcriptome level. In the present study, we aim to examine the gene expression responses of the blood clam *Anadara kagoshimensis* to anoxia, by conducting a short-term (24 hours) anoxia exposure experiments and differential expression analysis using a *de novo* assembly of RNA-seq data. *De novo* assembly produced 576,758 transcripts with a mean length of 609 bp. Through a comparison between control and anoxic conditions, 52 significantly differentially expressed genes (DEGs) were detected, including 26 up-regulated DEGs with 7 annotated ones and 26 down-regulated DEGs with 9 annotated ones. One of the most striking results was that genes related to oxygen transport were down-regulated under short-term anoxic conditions. The present study provides valuable insights into the molecular mechanisms of response to anoxia in blood clam *Anadara kagoshimensis* .

Keywords: anoxia, Arcidae, bivalve, de novo assembly, transcriptome

The reef-building coral *Acropora hyacinthus* may use chemical signals to synchronize spawning timing between conspecifics

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Synchronous spawning is a common phenomenon in corals and has been described in the many regions of the world over the last 3 decades. In annual spawning events, multiple coral species spawn together over a couple of nights usually after full moon. Therefore, moonlight and tidal cycles are suggested to play an important role determining coral spawning time, but the actual regulatory mechanism of coral synchronous spawning is still unclear. Accordingly, we examined the effects of moonlight and tidal change on the spawning timing (lunar day) of the reef-building coral *Acropora hyacinthus* in laboratory and field manipulation experiments. In the laboratory experiment, individual coral fragments were kept in separate aquaria and manipulated the moonlight period. In the field experiment, all coral fragments were kept in a small harbor and manipulated the presence/absence of moonlight and tidal change. The experiments were started a few days before the predicted spawning day and continued until spawned in 2015 and 2016. In the laboratory experiment, all the fragments spawned in asynchronous manner, irrespective of different moonlight periods, when moonlight was present, whereas those fragments in no moonlight condition did not spawn during the experimental period. In the field experiment, however, all the fragments spawned together, irrespective of the presence/absence of moonlight and tidal change, on the same night with local *A. hyacinthus* population. The contradictory results between the laboratory and field experiments regarding the response to moonlight and the extent of spawning synchrony, did not deny the effect of those environmental factors, but suggested that *A. hyacinthus* may use other important factors to synchronize their spawning timing between conspecifics, e.g., chemical signals.

Keywords: Corals, Synchronous spawning, Moonlight, Tidal change, Chemical signal

Distribution patterns of some Polychaetes in the intertidal rocky shores in Jeju Island, Korea

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The composition of the benthic community is often used to obtain environmental quality classifications that serve to indicate the health of the environment. This study was focused on the polychaetes associated with some intertidal habitats such as mussel beds and calcareous coralline algae beds in the rocky intertidal of Jeju Island, Korea. Five stations (Biyangdo, Suwolbong, Yeraecheon Estuary, Seobjikoji, Udo) from the rocky shores were selected between the high and low intertidal levels, where qualitative sampling was made by scraping the habitat-forming mussel and algae.

The results showed some typical dominant constituents of these particular habitats as follows;

1) Upper Intertidal Capitulum/Mytilisepta community: *Arabella iricolor, Spirobranchus kraussii, Polydoids, Perinereis mictodonta, Syllids, Perinereis euiini*
2) ;Mid Intertidal Sargassum thunbergii community: *Nereis denhamensis, Syllids*
3) Mid Intertidal coralline algae community: *Polynoids, Syllids, Spirobranchus kraussii, Thelepus hemeinsis*
4) Lower Intertidal coralline algae community: *Polynoids, Syllids, Leodice duplexa*

This study also allowed the classification of the polychaetes into ecological groups, facilitating the calculation of environmental quality indexes.

Keywords: Polychaetes, rocky shore intertidal, Je-ju island

Abandance of macro-invertebrates on shallow reefs flats in the Western Gulf of Thailand

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Coral reefs are the most biologically diverse marine ecosystems, supporting a high diversity of reef-associated organisms. The shallow reef flat is a major zone of coral reefs but its ecological data are relatively limited. This study aimed to examine the composition and abundance of macro-invertebrates in shallow reef flats, less than 1 meter in depth during low tide, in Prachuap Khiri Khan Province, the Western Gulf of Thailand. The field surveys were conducted at five reef sites, namely Ko Sing (northeast), Ko Sing (southeast), Ko Sang, Ko Chan (east) and Ko Chan (west) by using a permanent belt-transect method. The results showed that macro-invertebrates found in the shallow reef flats were polychaetes, particularly *Sabellastarte* sp., bivalves *Pedum spondyloideum*, *Tridacna squamosa*, *Arca ventricosa*, *Beguina semiorbiculata*, *Atrina vexillum*, a sea urchin *Diadema setosum*, sea slugs *Jorunna funebris*, *Phyllidia nigra*, *Phyllidia pustulosa*, *Fryeria picta*, a sea star *Culcita novaguineae* and a sea anemone *Heteractis magnifica*. The highest population density of macro-invertebrates in the shallow reef flats was *D. setosum* at Ko Sang. The population density of *H. magnifica* at Ko Chan (west) was very high. This study highlights the importance of macro-invertebrates in the shallow reef flats and their functions on coral reef ecosystem services.

Keywords: abundance, Gulf of Thailand, macro-invertebrate, population, reef flat

Spatial and temporal distribution of polychaetes in seagrass bed at Kung Krabaen Bay, Chanthaburi Province, Thailand

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This study is about the variability in seagrass-associated polychaetes communities among different positions at seagrass bed area in Kung Krabaen Bay (KKB), Chanthaburi province, Thailand. Field sampling were carried out between January 2017 to January 2018 in 4 sampling areas; 1. *Halodule pinifolia* dominant area (HP), 2. *Enhalus acoroides* dominant area (EA) 3. Mixed area (*H. pinifolia* and *E. acoroides* dominant area) (MIX) and 4. Non seagrass area (NS). At each sampling station, polychaetes were collected during low tide by core sampling with 15 cm deep. Five replicate samples were collected from each station. Results reveal 34 genera and 47 species of the polychaete. Dominant families of the polychaete at the KKB were family Spionidae, *Prionospio* spp. (16%) followed by family Glyceridae, *Glycera* sp. (13%) family Orbiniidae, *Scoloplos* sp. (12%) family Pilargidae, *Sigambra* sp. (9%) and family Capitellidae, *Mediomastus* sp. (8%). Dominant feeding types of the polychaete were surface deposit feeder, carnivore and burrower. High species number and density of polychaete were found at *H. pinifolia* dominant area and mixed area (*H. pinifolia* and *E. acoroides* dominant area). Sediment at the areas are silt-clay. The density, richness index, evenness index and Shannon diversity index of the polychaetes were found at higher values in winter (January 2017, October 2017 and January 2018). These results suggest that the area of seagrass distribution and season may affect the community of polychaetes.

Keywords: Polychaetes, Chanthaburi Province, Kung Krabaen Bay, Spatial and temporal variation, Thailand

On some population characteristics of the parasitic bopyrid isopod Gyge ovalis (Shiino, 1939) in the mud shrimp Upogebia major (de Haan) in Jugyo tidal flat, west coast of Korea

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Many of the bopyrid isopods are parasites of thalassinidean shrimps and they often attach to the gill chamber under the host's carapace. Epicarideans have two hosts during their life cycle and for all epicaridean species that have been investigated, a pelagic calanoid copepod acts as the intermediate host and another crustacean acts as the definitive host (Williams and Boyko, 2012). *Gyge ovalis* is representative parasitic isopod on mud shrimp, *Upogebia major* from Korean Waters. We collected mud shrimps from February 2012 to February 2015 from Jugyo tidal flat (36°21′59.94″N, 126°31′11.74″E) near the mouth of Daecheon River, Boryeong, Chungcheongnam-do, Korea. And we found three bopyrid isopods (*Gyge ovalis*, *Procepon liuruiyui*, *Orthione griffenis*) parasiting on mud shrimps and most of bopyrids was *G. ovalis*. During the study period, 1,937 individuals of *G. ovalis* were collected and they accounted for about 97% of total bopyrid isopods. In this study, we investigate the reproduction and life style of *Gyge ovalis*. The size of *G. ovalis* were correlated with the size of the host shrimp U. major. The growth pattern of *G. ovalis* were observed from May 2012 to Feb 2013. The season that *G. ovalis* brood eggs were from April to October. Especially high brooding ratio of *G. ovalis* was observed in May 2013.

Keywords: Bopyrid isopods, Mud shrimp, Population, *Gyge ovalis*, *Upogebia major*

Community structure of brachyuran crab (Crustacea, Decapoda) among tidal rivers at the Ariake Sea, Kyushu, Japan

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Brachyuran crabs are widely distributed along tidal river courses, and from adjacent terrestrial to seawater environments. Species composition of brachyuran crabs may be primarily regulated by variation of adaptation of each species to physical environments, such as salinity fluctuation involving tidal regimes. However, geographical proximity and/or habitat segregation could also be important for the determination of community structure of brachyuran crabs. We analyzed the presence/absence data of brachyuran crabs in several sites along tidal rivers flowing into the inner area of Ariake Sea, Kyushu, Japan, and evaluated differences in their community structures among rivers. In total, 25 brachyuran crab species were recorded from 396 of 456 sampling sites in 85 rivers. Beta diversity may reflect two different phenomena: nestedness and spatial turnover. Nestedness of species assemblages occurs when the biotas of sites with smaller numbers of species are subsets of the biotas at richer sites, reflecting a non–random process of species loss as a consequence of any factor that promotes the orderly disaggregation of assemblages. Contrary to nestedness, turnover implies the replacement of some species by others as a consequence of environmental sorting or spatial and historical constraints. Variation in species composition of brachyuran crabs could be explained by species turnover rather than nestedness. Community structures were significantly different between the lower and the upper reaches, but not among rivers, indicating that the scale differences in rivers were not attributed to the community differences. Community structures of sampling sites were also separated into several groups based on similarity of species composition. These groups were spatially fragmented, and not geographically continuous. These results suggest that species composition of brachyuran crabs is regulated by not only physical environments but also habitat segregation by crab species.

Keywords: Turnover, nestedness, assembly rule, longitudinal distribution, tidal river

Investigation of marine benthic communities in sandy bed of Fangshan coast near Fenggang harbor

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This study investigated the marine benthic communities in the sandy bed of Fangshan coastal near Fenggang harbor. The sampling site located in the south region of Fenggang harbor was 200 meters far from the coast. Based on the result of the diving observation investigation, the benthic sediment mainly consists of fine sand. In the present study, the benthic organisms were 58 times sampled with Naturalist's anchor dredge (NIEA E103.20C) from April 2017 to December 2018. In the identification of the collected organisms, the 92 families of benthos were found. The richness, abundance, and diversity of marine benthic communities were analyzed. Portunidae, Nereididae, and Penaeidae were the families of dominant benthos in the coastal seabed.

Keywords: sandy bed, Fenggang, benthic organism, dominant benthos

Effect of Spartina anglica and Suaeda japonica vegetation on the macrobenthic community structure of the mud flat in Korea

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The purpose of this study was to observe how Spartina anglica, an exotic species, and Suaeda japonica, an indigenous species, affected the macrobenthic community structure of mud flat in korea. Monthly sampling was conducted on the tidal flat in Donggeom-ri, Ganghwa-do, west coast of Korea, from June to October in 2017 (5 months) and in February, April and August in 2018 (3 months). Sampling station was set up in three different habitats from Spartina anglica, Suaeda japonica vegetations and non-vegetated mud flat (control), respectively. An additional field sampling was conducted in August, 2018, in order to examine the difference between macrobenthic community structures in the inner and outer parts of Spartina anglica vegetation. After aboveground shoot samples equivalent to the surface area of box core (25cm×20cm) were collected five times in Spartina anglica and Suaeda japonica vegetations in each station, sediment samples including roots were also collected in the same way. During the study period, the numbers of macrobenthic taxa in Spartina anglica and Suaeda japonica habitats were recorded 23 and 24 respectively, reaching 189 ind./m2 and 92.3 g/m^2 and 363 ind./m^2 and 188.8 g/m^2 in each habitat. Macrobenthic taxa recorded in the control area were only 35, with 278 ind./m^2 and 97.7 g/m^2. The species diversity showed the lowest level in the Spartina anglica habitat (1.3±0.4 in average) and the highest in the control habitat (1.7±0.5 in average). The polychaete Perinereis aibuhitensis was observed to be the dominant species in the Spartina anglica habitat, while the polychaete Heteromastus filiformis and bivalve Laternula boschasina were shown as the dominant species in the Suaeda japonica and control habitats respectively. The study results revealed that the number of species and abundance of macrobenthos in the Spartina anglica habitat was relatively poorer than those of other habitats. It is considered that this was due to the increase of fibrous roots with Spartina anglica growing.

Keywords: Spartina, Benthic community structure, Korean mud flat, Macrobenthos

Long-term observation of ichthyoplankton community structure and its relation to environmental factors in the Taiwan Strait in winter

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This study provides baseline information about the structure of l ichthyoplankton community structure in the Taiwan Strait (TS), allowing for a better understanding of long-term larval fish dynamics, as well as their relation to environmental fluctuations. The long-term investigations were conducted in the TS during the winters of 2007–2013. The cold, low-salinity China Coastal Current and Mixed China Coastal Water (MCCW) intruded into the TS with annual variations—weakest in 2008-09 but strongest in 2012-13—and impinged with the warm Kuroshio Branch Current (KBC). Consequently, the fluctuations in the strength of cold water masses resulted in the variability of the location of the frontal zones and in the distributions of hydrographic variables and ichthyoplankton community. Cluster analysis showed that the ichthyoplankton community in the Taiwan Strait was mainly structured into two assemblages characterized by differing hydrographic conditions. The composition of the warm KBC assemblage was relatively stable, characterized by Diaphus B and Bregmaceros spp.. By contrast, the cold MCCW assemblage demonstrated considerable variations among years, with Gobiidae spp. considered the most representative, followed by Scorpaenidae spp.. In addition, Benthosema pterotum and Trichiurus spp. were common in both the KBC and MCCW assemblages. KBC assemblage distribution demonstrated sharp boundaries in the frontal zones, whereas the changes in assemblage structure between the frontal zones were gradual for the MCCW assemblages, particularly when demersal taxa were dominant. Sea-surface temperature and salinity were the environmental variables most strongly associated with variability in assemblage structure among the study years in the TS during winter.

Keywords: Ichthyoplankton, community structure, Taiwan Strait

Latitudinal gradient of cold temperature tolerance in an introduced barnacle (Balanus glandula) in Japan

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An intertidal barnacle, *Balanus glandula*, was unintentionary introduced to Pacific coast of Tohoku, Japan from eastern Pacific. This species has expanded its distribution range northward and reached Pacific coast of eastern Hokkaido, Japan in 2000s. Since both air and water temperatures show latitudinal decrease from Tohoku through southern Hokkaido to eastern Hokkaido, selection on cold temperature tolerance may occur during the range expansion. In this study, we tested the cold temperature tolerance of *B. glandula* individuals from these regions.

B. glandula individuals were collected from each three populations in Tohoku, southern Hokkaido, and eastern Hokkaido. They were kept at ca. -5, -10, and -15 °C for 14 hours, and mortalities were calculated. Average mortalities at each temperature treatment were 17.7%, 44.6 %, and 100% in populations of Tohoku; 4.7%, 15.2 %, and 98.8% in populations of southern Hokkaido; 4.4%, 0.7 %, and 93.4% in populations of eastern Hokkaido.

Results suggest that cold temperature tolerance of *B. glandula* is higher in higher latitude. This study suggests that selection on cold temperature tolerance contributed to the range expansion of *B. glandula* from Tohoku to Hokkaido.

Keywords: Barnacle, biological invasion, cold tolerance, selection

Microplastic disturb coral-algae symbiotic relationship

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World production of plastic has dramatically increased from the 1950's and now it reaches approximately 311 million tons per year. The resulting accumulation of small plastic detritus less than 5mm in size, termed “microplastics”, has started threatening the life cycles of marine organisms. Here we show the first evidence that microplastics disturb the initiation of symbiotic relationships in anthozoan-algae symbiosis. We found in both the aposymbiotic sea-anemone Aiptasia sp. and the coral Favites chinensis that the infectivity of symbiotic algae into the host is severely suppressed by microspheres fed either directly or indirectly through microsphere-fed Artemia sp. Similar trends were seen when microplastics collected from commercial facewash were used instead of microspheres. Therefore, ongoing accumulation of microplastics in the ocean might disturb the healthy anthozoan-algae symbiotic relationships, which are cornerstones of the biologically enriched coral reef ecosystem.

Keywords: coral, sea anemone, microplastics, symbiosis, Symbiodiniaceae

Microzooplankton Community Structure in the Northern Andaman Sea, THAILAND

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The potential trophic dynamic is recognized in the area of a coastal zone through the balance of pelagic primary and secondary production. In addition, the main key factor is microzooplankton that transfers the energy from primary producer to higher trophic levels. Not only its abundance but also the complexity of species composition is quite important. This study aimed to investigate a microzooplankton community along the coastal area in Ranong and Phang-nga Province. Microzooplankton was collected by a vertical haul with a plankton net, 125 ■m in mesh sizes and 50 cm. in diameters. The eighteen stations from six different habitats were observed in two seasons; February (dry season) and December (rainy season) in 2018. The environmental parameters were measured in situ. Microzooplankton was recorded in 9 phylum 14 classes 11 orders 23 families 23 genera 28 species 3 groups and 19 larval stages. Small – sized copepodid larvae, Oithona and Oikopleura, dominated along the coastal area in both seasons. The highest dominant species was a neritic copepod (21 species). The minor groups were hydromedusae, ctenophore, cladoceran, pteropod, ostracod, amphipod, decapod, chaetognath and larvacean. Meroplanktonic larvae expressed in a low proportion as 1.6 – 17 % of the total abundance so the majority community was the holoplankton in proportion as 83 – 96.6 % of the total abundance. Average abundance varied in February (9,972 ± 6,461 inds.m-3) and December (7,054 ± 4,596 inds.m-3). These results established that the majority coastal microzooplankton were almost omnivores and detritus feeders while carnivores and predators were the minor group. Moreover, the native neritic species showed the relatively stable components between stations and seasons. So, this area could be expressed as a reference area in term of no environmental contaminant.

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Keywords: Microzooplankton, Coastal ecosystem, The Andaman Sea

Assessing diversity and abundance of scleractinian corals on shallow reef flats in Mu Ko Phangan, the Western Gulf of Thailand

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The reef flat is a large proportion of coral reef areas and it is constituted of shallow and intertidal coral communities. Some corals on the shallow reef flat zone have adapted to a wide range of stressful environmental conditions, particularly exposure during low tides, high temperature and light intensity. Under the global climate change crisis, corals are particularly sensitive to abnormally high seawater temperatures. Therefore, resilient corals are important resources for natural coral recovery and active coral restoration projects. This study aimed to assess diversity and abundance of scleractinian corals on shallow reef flats in the Gulf of Thailand. The field surveys were conducted on shallow reef flats, about 1 m in depth during high tides at six reef sites, namely Ko Kong Than Sadet, Hat Thong Sala, Hat Chalok Lum, Hat Thong Lang, Hat Khom and Hat Mae Hat in Mu Ko Phangan, Surat Thani Province, the Western Gulf of Thailand by using a belt transect method. The highest percentage of live coral cover was recorded at Hat Khom (60.95%) while the lowest one was found at Hat Thong Sala (39.60%). Twenty-five coral species were commonly observed. The dominant corals at all study sites were *Porites lutea*, *Pocillopora* spp., *Acropora* sp., *Pavona decussata* and *P. frondifera*. This research provides important data for coral reef studies in Thailand and can be applied to coral reef conservation and management plans in the Gulf of Thailand.

Keywords: assessment, community, coral, diversity, Gulf of Thailand, reef flat

Long-term monitoring of coral recruitment on settlement panels at Mu Ko Similan, the Andaman Sea after the 2010 coral bleaching event

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Mass coral bleaching events, particularly in the year 2010 have led to a significant reduction of live coral cover in the Andaman Sea. Understanding of coral recruitment at the degraded coral reefs is necessary to predict coral recovery following the impacts of coral bleaching events. This study monitored the recruitment of scleractinian corals following the 2010 coral bleaching event, through settlement panel experiments, at Mu Ko Similan National Park, Phangnga Province, the Andaman Sea. The settlement panels were made of gypsum plates and were submerged following the 2010 coral bleaching event. The panel size was 15 cm x 15 cm. Twelve panels were attached to the iron frames in vertical, horizontal and oblique positions, four panels for each. There were three iron frames for each study site. The settlement panels were collected periodically, labeled and transported back to the laboratory. The highest density of coral recruits on the settlement panels was recorded in the year 2018. The high coral recruitment rates were also found in the years 2013 and 2017. The dominant groups of coral recruits were pocilloporids, acroporids and poritids. The results from this study demonstrate how the 2010 coral bleaching event affected coral communities at Mu Ko Similan and imply coral recovery at several reef sites. However, certain management strategies are still be needed for enhancing coral reef resilience in the Andaman Sea.

Keywords: Andaman Sea, coral bleaching, recovery, recruitment, settlement

The recovery potential of corals at Mu Ko Chang, the Eastern Gulf of Thailand

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Coral recovery after the bleaching events is controlled by available coral larvae, proper substrate, settlement and survival rates of juvenile corals. Connectivity of coral populations is a very important aspect of understanding the recovery potential of corals after the severe disturbances. Coral reef connectivity depends on oceanographic conditions and the sources of coral larvae. This study examined the coral recruitment patterns and their relationships with adult coral communities at six study sites in Mu Ko Chang, Trat Province, the Eastern Gulf of Thailand. Live coral covers were in a range of 25.9-71.2 % while dead coral covers were in a range of 10.8-50.6 %. The live coral covers at Hin Gurk Maa and Ko Thong Lang were significantly higher than those of other reef sites. The low coral recruitment was recorded at Ko Wai, Ko Thong Lang, and Ko Yak Lek. The brooding coral *Pocillopora* spp. at Ko Thian and Ko Yak Lek showed self-seeding. The broadcast spawning coral Poritidae showed high degrees of coral self-seeding at the reef sites. Recruits of *Leptastrea*, *Lithophyllon* and *Psammocora* were frequently found without their parent colonies. The connectivity among reef sites and local coral recruitment are important factors for consideration to provide appropriate management strategies, especially for the designation of marine protected areas and establishing coral reef restoration projects in the Gulf of Thailand.

Keywords: connectivity, coral recruitment, Gulf of Thailand, management, self-seeding

Coral community on an underwater pinnacle at a proposed dive site for marine ecotourism in the Western Gulf of Thailand

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Underwater pinnacles are important marine ecosystems and provide fishery resources as well as important tourist attractions. Several areas in the Gulf of Thailand have coral communities on the underwater pinnacles which harbor diverse reef organisms, particularly corals, soft corals, sea whips, bivalves, echinoderms and fish. However, there are still many underwater pinnacles in the Gulf of Thailand that has not been used due to the unknown location and lack of ecological studies. The objective of this research was to examine the coral community on an underwater pinnacle, Hin Thong Wo to promote and develop as an ecotourism site for SCUBA diving in Chumphon Province, the Western Gulf of Thailand. The field surveys were carried out by using a belt-transect method. The results revealed that Hin Thong Wo pinnacle was about 9-12 m. in depth. The live coral cover was 66.60% with 13 common hard coral species. The dominant corals were *Porites lutea*, *Goniopora columna* and *Favia* sp. Ten species of juvenile corals were observed with the average density of 3.9 colonies/m^2. The dominant juvenile corals were *Porites* spp. and *Goniopora* sp. The dominant reef-associated macrofauna were *Arca ventricosa*, *Diadema setosum* and *Heteractis magnifica*. Thirty-one species of reef fish were commonly found. The dominant reef fish were *Neopomacentrus anabatoides*, *Parioglossus philippinnus* and *Siganus corallines*. The attractive organisms for tourists were the corals *G. columna* and *Pavona decussata*, a sponge *Xestospongia* sp., a sea anemone *Heteractis magnifica* and reef fish *Chaetodon* spp., *Halichoeres* spp., *Lutjanus* spp., *Cephalopholis boenak* and *Siganus corallines*. This study provides an assessment methodology and identifies and underwater pinnacle that is high potential to be promoted and developed for ecotourism sites in Chumphon Province, the Western Gulf of Thailand.

Keywords: coral community, diving, ecotourism, Gulf of Thailand, pinnacle

THE CORRELATION OF MERCURY CONTENT OF THE LIVER AND MUSCLE OF FISHES IN AN ENCLOSED ISAHAYA BAY, KYUSHU, JAPAN

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Abstract

The contents of mercury tend to increase in the body tissues of fish. Conventionally the monitoring investigation of mercury contamination was focused on mercury content in the muscle tissue of fishes. However, the other organs of fishes were deposit different levels of mercury into the tissues. The ratio of mercury content between the liver and muscle of fish were collected in Isahaya Bay, Kyushu, western Japan between 2015 to 2017. Four species of fishes (*Planiliza haematocheila*, *Amblychaeturichthys hexanema*, *Takifugu rubripes*, and *Pseudopleuronectes herzensteini*) show the correlation of mercury content ratio in the liver and muscle higher than 1 that means the mercury content in the liver tissue higher than muscle referring to the liver is the main target to accumulate the mercury as if it's inhabit closed with a location heavily contaminated area. The mercury content ratio between the liver and muscle of *Planiliza haematocheila* shows the highest value as 6 (Liver: 1,974 ng/g d.w, Muscle: 327.9 ng/g d.w) that confirms the correlation of the ratio of their diet, they directly feed on sediment which mainly accumulated with inorganic mercury. These fish species may indicate the location of heavily mercury-contaminated areas. While another group of fish was the ratio of mercury content between liver and muscle lower than 1, refer to their mercury content in muscle more higher than the liver according to they act as a predator accumulating the mercury from their prey.

Keywords: fish, Isahaya Bay, liver and muscle, mercury, ratio

Marine debris and microplastics in the upper Gulf of Thailand

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Marine debris and microplastics along the beach coastlines, Angsila, Bangsaen, Samaesarn, in the eastern coast of Thailand of Thailand were investigated. From the study, coastal debris distribution was related to activities in the areas. Fishery and shell-fish aquaculture activities were primary sources of debris in Angsila while tourism activities were main sources in Bangsaen and Samaesarn. When assessing the microplastic contamination in sessile invertebrates (Rock Oyster: Saccostrea cucullata, Striped Barnacle: Balanus amphitrite, Round Periwinkle: Echinolittorina sp.), the results showed a significant accumulation of microplastics in the intertidal invertebrates at rates of 0.2 – 0.6 counts/g, indicating high pollution levels along the coastline. Filter feeding organisms showed comparatively higher accumulation rates of microplastics. Thus, contaminated bivalves poses potential health risks for seafood consumers. In addition, the plastic pollutant prevalence in sessile communities was corresponded with pollution characteristics of contaminated beach habitats where they live. Site-specific pollution control mechanisms are recommended to reduce public littering. For example, management actions in Angsila should focus on fishery and shell-fish culture practices, while Bangsaen and Samaesarn should be directed toward leisure activities promoting waste management.

Keywords: marine debris, microplastics, Thailand

Effect of Asian Sea Bass (Lates calcarifer) Cage Culture on Benthic Communities in Estuary of the Bang Pakong River Basin at Chachoengsao Province, Thailand.

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The Asian sea bass (Lates calcarifer) is the one of the most economically important fish of Thailand. The national highest quality fish comes from floating cage fish culture from estuary of the Bang Pakong river, eastern part of Thailand. Therefore, this area is containing with high density of Asian sea bass cage farming, according to the fertility of natural biota and suitable environmental conditions. However, this massive of farming activities had prone to accumulation of organic substances and waste production to water bodied and solid surface beneath cages. Thereafter, deterioration on environmental factors and aquatic community must be arise. In order to forecast of environmental degradation and monitoring on changing in aquatic community, studying of benthic animal community might be the easiest way in practice. The objectives of this research were to determine the effect of Asian sea bass cage culture on benthic communities and some environmental parameters. Sampling sites had located on three stations at upper, lower and between the cage, at distance 500 meters along river bank and each station were collected with three replicates. Each station was collected by Ekman's dredge and all benthic organisms were collected with 0.5 mm. mesh size sieve. At the mean time water sample were collected with vertical water sampler. Results had indicated that water quality parameters from three stations such as alkalinity, hardness, nitrite, total ammonia and orthophosphate were classified as normal condition for culturing values. However, we found that nitrite and total ammonia at the cage site was significantly higher than others ($P<0.05$). Meanwhile, sediment property such as wet pH, organic matter (OM) and organic carbon content (OC) were significantly higher than others stations ($P<0.05$). However, sediment texture property from three stations were similar, with sandy clay loam. The diversity of benthic organisms from all station were comprised of 4 Phylum, the Annelida, Nemertea, Arthropoda and Mollusca. Total number of benthos at upper, lower and cage stations were 140±48.83, 161±18.78 and 529±153.72 individual/square meter with 5, 6 and 11 species respectively. The assemblage benthos from every station were similar, in high density of Phylum Mollusca. The dominant specie was Nassarius sp. (Nassa mud snail) which occurring from all stations, especially from Asian sea bass cage culture station. This species had been reported as cosmopolitan distribution but this snail usually prefers to live on mudflats or sand that containing higher organic substance. Our results could be concluded that Asian sea bass cage culture has influenced on water and sediment property in term of organic accumulation which finally effect to benthic community. Especially, cause of abundance of benthic mollusk under Asian sea bass's cage. However, further important study should be focusing on changing of pattern both temporal and spatial distribution of benthic fauna.

Keywords: benthic communities, Bang Pakong river basin, Asian sea bass cage culture

Are in silico endocrine disruption screenings useful for seafood safety predictions for children?

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Chemoinformatics represents a search for chemical information to transform data into information and this into technologies that allow to make decisions faster. In silico (literally Latin for "in silico" related to the bulk use of silica for computer semiconductor) approaches refers to computer application or computer simulation. In silico approaches in environmental health studies can best be understood as chemoinformatics using informational techniques applied to a range of problems in the field of chemistry related to toxicology and the effects of pollutants such as in food safety predictions. We used the VEGA in silico platform to predict acute toxicities with the example “fish” by using three different ecotoxicology in silico models: that is SarPy/IRFMN, KNN/Read-Across and NIC model. For this assessment SMILES of the endocrine disrupting compound tributyltin (TBT) were taken from the PubChem database. By using MarvinSketch 17.6, all chemicals presented in this study are based on PubChem structural data. TBTs fish acute toxicity was predicted by KNN/ Read-Across (Model-1) and NIC (Model-2) model in VEGA. The VEGA in silico prediction Method–1, predicts TBT fish acute toxicity effects at a concentration as low as 0.0276 mg/mL. In silico predictive models provide fast and economic screening tools for desirable and other compound properties. They are less expensive, less time consuming, have a higher reproducibility, and by their replacement reduce the use of animal models or finally humans for testing. Computational approaches as demonstrated here can also prioritize chemicals for their toxicological evaluation in order to reduce the amount of costly in vivo and in vitro toxicological screening and provide early alerts for newly developed substances such as food amendments. Limitations include that ADME aspects (absorption, distribution, metabolism, and excretion – which are basic pharmacokinetic descriptors) are not taken into account, a lack of quality and transparency of the training set of experimental data and the program, the descriptors, and applicabilities are sometimes not clear.

Keywords: in silico, Chemoinformatics

Risk assessment by chemcomputation of biotoxins from marine cyanobacteria

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Cyanobacteria are a phylum of Gram-negative, prokaryotic bacteria that produce several harmful secondary metabolites, called cyanotoxins, causing health hazards to animals and humans. Cyanotoxins are some of the most powerful natural poisons including potent neurotoxins, hepatotoxins, cytotoxins and endotoxins. Some of which result in high mortality and long-term morbidity. Such toxins can provide a serious threat to drinking water, consumption of seafood, aquaculture and recreation. However, less conclusive evidence associates toxins with carcinogenicity and reproductive and developmental toxicity. Therefore, the aim of this study attempts using in silico software to explore other toxin effects or bioactivity to humans. We collected thirteen cyanotoxin isomeric SMILES from PubChem. We predicted human hERG potassium channel blockers and bioactivity potential using software Pre-hERG 4.1 and Molinspiration drug-likeness score online. Results showed that some cyanotoxins have bioactivity. Pred-hERG prediction demonstrated that none of the tested marine bacterial toxins provides a hERG blocker in a multiclass prediction. However, cyanotoxins except Anatoxin-A, BMAA, and Hypoxanthine are hERG blockers, predicted through a Pred-hERG binary prediction. According to in silico results, cyanotoxins might have bioactivity and hERG blocking potentials.

Keywords: Cyanotoxins, in silico

Hypersaline saltpan bacterium Pseudomonas aeruginosa provides antibacterial agents against diabetic wound infections

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In recent years clinically relevant antibiotic drug resistant pathogens are on the rise which is often paralleled by their virulence. Diabetic foot pathogens are causing serious incurable infections among diabetic patients. This study has proven that halophilic bacteria from saltpans could be an effective source for the production of bioactive metabolites against diabetic foot pathogenic bacteria. Saltpan bacteria have been isolated from southern India and their growth was optimized with respect to pH and temperature. Pathogenic strains were isolated from diabetic foot wound patients by plating technique. Strains that were resistant to antibiotics were identified through sequencing based on their resistance to antibiotics. Antibiotic resistance was screened by applying the disc diffusion method with the antibiotics: Diclofloxin, Vancomycin, Neomycin, and Cephalexin. The isolated potent halophilic bacteria showed inhibitory efficiency by the well diffusion assay through its EtOAc (Ethyl acetate) crude extract against drug resistant strains including E. coli and S. aureus. A confocal microscope approach showed the highest lethality of pathogens at the highest concentration of EtOAc extract (160 µL). Damaged membranes of pathogens were observed in treated cells by scanning electron microscopy (SEM). The MIC (minimal inhibition concentration) shows a complete growth reduction at the same concentration of 160 µL for the same pathogens. Based on the 16S rRNA gene sequence, halophilic strain had 100 % homology with Pseudomonas aeruginosa. The FTIR pattern of the EtOAc crude extract had a significant peak including 3388.99 cm-1 showing O-H stretching alcohol that might be the responsible group for its antibacterial activity. The present study discovered a potent compound of the saltpan Pseudomonas aeruginosa against antibacterial resistant clinically relevant bacteria.

Keywords: Antibiotic resistance, Pseudomonas aeruginosa

Hydrothermal vent bacteria from Taiwan provide antibacterials and metalloproteinases

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Thermophilic bacteria and their secondary metabolites provided as yet many industrial and medicinal applications. Thermophiles are extremophiles that can thrive at relatively high temperatures. Since they can adapt to extreme environments, the metabolite extracted from them can withstand harsh treatments and high temperatures and are, therefore, of interest to different applications in industry and research. In this study thermophiles were isolated from hydrothermal vents, using diverse media and incubation conditions since they are adapted to extreme conditions. The isolated strains were identified by 16S rRNA sequencing using the universal bacterial primers 27F and 1492R. A phylo-genetic tree of the different bacterial isolates was constructed using MEGA7 software. For metallo-proteinase activity, a skim milk agar plate assay was done. To check wheter a zinc metalloprotease gene is present and how concentration affects the protease activity, different concentration of ZnCl2 and ZnSO4 were used. The maximum number of different bacterial colonies was observed on modi- fied yeast peptone agar. The results showed that the 23 bacterial genera belonged to the phylum Firmicutes. Two bacterial genera were allocated to the phyla Actinobacteria and Proteobacteria, respectively. Most of the isolates belonged to the genus Bacillus, few belonged to the genus Psychrobacter, one isolate was classified as a member of Staphylococcus, one isolate was classified as Micrococcus, and one belonged to Kocuria. The minimum inhibitory concentration of antibiotics commonly used was calculated for the isolated strains by a resozurin assay. Also a protease assay was done using the skim milk agar method. The result showed that concentrations of more than 1mM of ZnSO4 and ZnCl2 inhibited the protease activity and 50µm–100µm showed maximal activity. Bacteria were isolated using different media, identified and a phylogenetic tree was constructed. Bacillus species were found to be prominent. The metalloproteinase assay using skim milk agar provided bacteria with proteinase activity.

Keywords: Hydrothermal vent, Thermophiles, Bacillus

Bacterial diversity of shallow marine hydrothermal vents at Kueishantao, Taiwan

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Oceanic hydrothermal vents provide particular environments in different marine areas, primarily at deep sea sites such as the Mid-Atlantic Ridge and in the Pacific or Indian oceans but also along the Mid-Atlantic Ridge. In the hydrothermal vents of the deep sea microbial diversity can be substantial, but is little investigated as yet. A group of hydrothermal vents in shallow waters is active at Kueishantao in Taiwan. The shallow locations make them easily accessible by scuba diving. Several samplings from geological and biotic surfaces revealed biofilm forming bacteria of a remarkable systematic biodiversity and biochemical adaptations to the extreme habitat of marine hydrothermal vents at this shallow water location. Microbial communities and their ecology were studied here.

Keywords: Hydrothermal vent, microbial diversity, Kueishantao

Status of ESβL producing bacteria along the southern Indian coast

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Antibiotic resistance provides a serious threat to clinical and environmental backgrounds. Microbial population contain antibiotic resistance and ESβL production can provide an indication for this. This study was carried out at the Gulf of Mannar regions of southern India. The coastal regions of the Gulf of Mannar provides considerable bacterial populations including E. coli, Vibrio spp., Salmonella, Shigella, Pseudomonas spp., Aeromonas spp., Staphylococcus aureus, Listeria, Campylobacter, TVC, and FC. Susceptibility of several antibiotics up to 4th generation were tested by the disc diffusion method in this study. Bacterial cultures were resistant to antibiotics such as Cefotaxime, Ceftazidime, and Cefepime. The resistant selected strains were performed by Kirby Bauer disc diffusion method through an initial ESβL detection kit. The zone of inhibition was observed and noted for the confirmation study and the ESβL production was identified by a double disc combination method, the zone growth inhibition was observed and referred to the ESβL producers E. coli and Staphylococcus aureus. The current study has more significance validation with ESβL production of the strains as E. coli and Staphylococcus aureus and shows its seriousness towards the coastal regions. Our study discusses that, there could be more possibilities for the transformation of genes among bacterial populations.

Keywords: Antibiotic resistance, ESβL

Development of a marine featured curriculum in the coastal elementary school San Gu, Tainan, Taiwan

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Building a school-based curriculum and developing a featured school curriculum is one of the core issues of educational reforms in Taiwan. Its development is based on the different conditions of the individual school, such as the teacher's specific skills or the socioecological and geographical environment of the school. San-Gu elementary school is located in Chi-Gu district situated next to a tidal estuary near the city of Tainan. Chi-Gu has abundant and diverse ecological groups of plants and animals, such as mangrove forest, fishes, crabs, shellfishes, and others. Chi-Gu is also famous for its large areas of salt-harvesting basins. In this paper, we designed a marine featured curriculum based on a thematic approach of curriculum models. The curriculum development makes use of the special and unique geographical and ecological environment of San-Gu elementary school which also provides the first childhood experiences for its students. In recent years, increasing urbanization, child safety concerns, and increased digital media that target children, has prompted a wave of concern that children are spending much less time outdoors and are getting deprived of nature. An important function of natural places that is often overlooked is their educational role. This holds particularly for children who are increasingly alienated from nature. Educational activities were explored that possibly provide a positive context for experiences in nature which may further motivate for environmentally friendly behavior.

Keywords: Chi-Gu, San-Gu elementary school

Seasonal changes of fish biodiversity in Hakodate Bay, Japan, revealed by eDNA metabarcoding technique

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Environmental DNA (eDNA) has been recognized as an alternative method for biodiversity survey in recent years. This study aimed to track the seasonal changes of biodiversity using this new technique in Hakodate Bay, the northern part of Japan. The sampling stations are the river mouth of the Moheji river and approximately 125 m, 500 m, 1000 m and 2000 m to offshore. One liter of water was sampled monthly for eDNA and environmental data (water temperature, salinity, chlorophyll a) were collected as well from April to November 2018. A total of 125 fish species were detected from the eDNA metabarcoding. Biodiversity was lowest in April (45 species), while highest in June (77 species). Only 17 species were occurred in every season. Some fishes showed clear pattern of eDNA detection, according to their life cycles. For example, the chum salmon (*Oncorhynchus keta*) was detected from April to June as juveniles migrated from river to the sea, and from September to November as matured adults came back from ocean to estuaries for spawning. On the other hand, the Japanese amberjack (*Seriola quinqueradiata*) was detected from July to November as they migrate from south to Hokkaido in summer. The biodiversity was higher in offshore (> 50 species) than the river mouth (19 species). Seawater species were dominant in entire season. However, the proportion of seawater species were only 32% in river mouth while it took over 50% in the rest of stations. Also, endemic species (e.g. *Salvelinus leucomaenis leucomanenis*) and endangered species (e.g. *Huso dauricus*) were successfully detected in this study. We concluded the results successfully reflect the ecology of fishes, indicating the eDNA is a powerful and novel method of assessing biodiversity in marine environment.

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Keywords: biodiversity, environmental DNA, Hakodate Bay, metabarcoding, seasonal change

Vertical and horizontal movements of bigeye tuna (*Thunnus obesus*) off southeastern Taiwan

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Understanding the movement ecology for species is important for describing behavioral and habitat relationships between species. To learn more about the movement patterns of bigeye tuna (*Thunnus obesus*) in eastern Taiwan, two pop-up satellite archival tags were deployed. Both PSATs prematurely detached after 47 and 72 days-at-liberty. The former PSAT was physically recovered and provided detailed data in aggregate archiving 47 days-at-liberty. The deepest descent recorded was 1,036 m and the coldest temperature visited was 3°C. Typical of the diel diving patterns displayed by many pelagic apex predators, tagged bigeye tuna dove deeper during daytime than at nighttime and exhibited pronounced crepuscular transitions. During daytime, the tuna spent the majority of its time above 400 m at temperatures from 10 - 24°C. At nighttime, residency was largely confined to the surface mixed-layer to ~150 m. Daytime behavior was characterized by W-shaped vertical movement patterns and fast vertical swimming speeds compared to nighttime. Our data suggest vertical movements traversing through the thermocline during the daytime are based on physiological constraints and/or rapid directional changes that presumably increases the chances of prey encounters. Bigeye tuna appear to follow the diel vertical movements of prey organisms comprising the deep sound scattering layer to exploit them effectively as a resource.

Keywords: mixed-layer, movement patterns, oxygen, residence time, vertical speed

Identification guide to the planktonic larvae of marine annelids in Japan

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Annelida is one of the most speciose and ecologically successful phyla in the invertebrate and the members are often dominant in marine and estuarine macrobenthic communities around the world. Many marine invertebrates including annelids pass through a planktonic larval phase during their early life history. The larvae of marine annelids (mostly polychaetes) are the most common and abundant group in the coastal meroplanktonic community. However, the field study of the larval ecology has been restricted due to the difficulties of larval identification. It has been largely caused by the radical morphological differences between larval and adult stages and lack of information of larval forms of many species as is the case in other marine invertebrates. In the present study, we conducted field investigations of annelid larvae mainly in a coastal station in Onagawa Bay, northeastern Japan during the period from 2007 to 2012. Planktonic larvae of annelids were collected by using a NORPAC net with a mesh size of 110 µm or a simple plankton net with a mesh size of 100 µm and mouth diameter of 30 cm. The morphology of live (anesthetized by magnesium chloride solution) and fixed larvae was observed under a stereomicroscope and light photomicrographs were taken by using digital cameras attached to the microscope. The planktonic larvae of the family Spionidae which appear dominantly were identified by comparing larval and adult gene sequences. Totally, 24 families of annelid larvae and 41 species belonging to 13 genera of the family Spionidae were identified in the present study. The purpose of this presentation is to list the previous records of the larvae of marine annelids from larval development studies and field ecological investigations in Japan and to provide the preliminary identification guide to this taxon for the promotion of larval ecological studies of the marine annelids.

Next-Generation Sequence for Mitochondrial Genome Construction: An Integrated Pipeline, Assembly to Annotation case of Dermatobranchus otome

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Mitochondrial DNA (mtDNA) sequences have been extensively used as molecular markers for studying taxonomy, systematics, and population genetics of animals since the developing of massively parallel sequencing technologies, that known as next-generation sequencing (NGS). In this method, short high-throughput reads sequencing at a relatively acceptable cost. However, there are still major problems in constructing a complete mitochondrial genome according to high frequencies of sequencing errors or genomic repeats. In this study, we addressed the basic framework of next-generation genome sequence data analysis, which divided three stages: pre-processing, construction of the mitochondrial sequence from a seed sequence, and post-processing. Also, common difficulties and overcome methods pointed with the an example of aminid nudibranch *Dermatobranchus otome* mtDNA data analysis.

Keywords: Nudibranchia, NGS, complete mitochondrial genome, Dermatobranchus otome

Marine Mollusk Resource Bank of Korea (MMRBK)

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The Marine Mollusk Resource Bank of Korea (MMRBK) was accredited in 2010 by the Ministry of Oceans and Fisheries of Korea with financial support from the government. The MMRBK houses approximately 700 marine mollusk species collections (wet collections preserved in 70% ethanol) collected from Korean sea coast as well as northwestern Pacific including Japan, and China Sea coasts. Comprehensive inventory information such as GPS data, specimen images, number of specimens are available online and curated under the specimen database system of the MMRBK. Currently the MMRBK has undertaken multiple missions that include (1) research for taxonomy, biodiversity and phylogeny of northwestern Pacific mollusk species, (2) management of mollusk collections and taxonomist education program, and (3) providing taxonomic information and specimen loan to researchers, environmental NGOs, and the general public. The current state (including major tasks) of the MMRBK will be presented in detail in this report.

Keywords: MMRBK, Marine Mollusk, northwestern Pacific mollusk, biodiversity

Morphological characteristics of an undescribed species of gaeticine crab (Crustacea: Brachyura: Varunidae) clinging to mud shrimp abdomen from Japan

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Brachyuran crabs include some symbiotic species that use animal burrows as well as the host bodies of other taxonomic groups, such as cnidarians, mollusks, holothurians, ascidians, and echinoids. The crab genus *Sestrostoma* Davie & N.K. Ng, 2007 includes three species, all of which are known to live in invertebrate burrows; *S. balssi* (Shen, 1932) in the burrows of the annelid *Urechiu unicinctus*, *S. depressum* (Takeda, 1965) in the burrows of *Upogebia issaeffi* and/or *Nihonotrypaea petarula*, and *S. toriumii* (Takeda, 1974) in the burrows of *Upogebia major*,*Upogebia yokoyai*, and *Nihonotrypaea japonica*. In this study, morphological characteristics of an undescribed species (= *Acmaeopleura* sp. sensu Itani (2001), clinging to the abdomen of host *U. major* and the other upogebiid shrimps was shown. The characters of third maxilliped of the undescribed species were mostly agreed with *Sestrostoma*, distinguished well from those of *Acmaeopleura* and *Proexotelson*; thus we refer the undescribed specie as *Sestrostoma* sp. in this paper. *Sestrostoma* sp. was differentiated from the other species of the genus in having small numerous suborbital crests in males (more than 35 in *Sestrostoma* sp., compared with 3 in *S. balssi*, 5~6 in *S. depressum* and 9 in *S. toriumii*. Moreover the tip of the gonopod of *Sestrostoma* sp. was longer and more slender than that of the other species of the genus. The dactylus of 4th pereiopod *Sestrostoma* sp. was strongly curved, which may facilitate to cling to the abdomen of the host upogebiid shrimps.

Keywords: Sestrostoma, Upogebia, symbiosis, burrow

Molecular evidence of two sibling species in "*Perinereis shikueii*" (Annelida: Nereididae) and their distributions in Taiwan and Japan

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Taxonomic reexamination of Japanese populations of the *Perinereis nuntia* species group, which constitutes a major polychaete component in intertidal benthic communities, was carried out by analyzing the mitochondrial 16S rDNA and the nuclear ribosomal ITS sequences in Japan. The Japanese populations of the *P. nuntia* species group could be divided into four genetically different groups, which corresponded morphologically to four nominal species (*P. mictodonta*, *P. wilsoni*, *P. shikueii*, and *P. nuntia*), with some exceptions. The clade containing *P. shikueii* was subdivided into two sister clades (forms A and B), indicating that cryptic speciation has occurred within this clade; form A seems to correspond to *P. shikueii* sensu stricto (Type locality, Taiwan), distributed in Taiwan and Japan (Ariake Sea): form B seems to be the undescribed species, distributed in Japan (Kyushu and Honshu).

We also designed an easy polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) analysis to identify the three morphologically similar nereidid polychaete species *P. mictodonta*, *P. wilsoni* and *P. shikueii* (forms A and B). Restriction digestion analysis of the PCR products of the partial nuclear ribosomal ITS sequence of these three species, using *Alu*I, *Cfr*10I and *Hin*fI endonucleases, generated speciesspecific restriction patterns. The PCR-RFLP method enables easy and accurate identification of these species.

Keywords: 16S rDNA, ITS, PCR-RFLP, taxonomy

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