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2019 Annual Symposium of the Korean Society of Environmental Biology & Harmful Organisms 2019

New Horizons in Harmful Organism Science

April **24** (Wed)~**27** (Sat), 2019
Busan Port International Exhibition & Convention Center, Busan, Korea

ABSTRACT BOOK

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2019
한국환경생물학회 춘계학술대회
HARMFUL ORGANISMS 2019

NEW HORIZONS IN HARMFUL ORGANISM SCIENCE

| 일 자 | 2019년 4월 24일(수) - 27일(토)
| 장 소 | 부산항국제전시컨벤션센터

| 주 최 | 한국환경생물학회, 한국해양과학기술원
| 공동주최 | 한국기초과학지원연구원, 한국생명공학연구원, 해양환경연구소,
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세종대학교, 연세대학교, 한경대학교, 한양대학교 자연과학연구소
| 후 원 | 락앤락, 마린액트, 인트론바이오테크놀로지

Opening remarks

Dear Participants,

I would like to truly thank all delegates, KOSEB members including former presidents and executive directors of KOSEB, despite all of the difficulties.

With great responsibility, I am honored to be president of KOSEB, which has a long history and traditions that goes back near 40 years. KOSEB has offered venues for qualified scientific research and education in the environmental biology. We have put all our effort into developing our research for environmental health and ecological soundness. Additionally, KOSEB will devote its time into enhance its standing, and also strive to attract and successfully host the international conference, SCI entry of our Journal, and establish leading positions of Korean researchers in prominent international associations to carry out leading research with foreign as well as Korean researchers.

In this year, annual spring conference of KOSEB is held together with Harmful Organisms 2019, finding connections between environmental cause and unwanted blooming or outgrowth of certain lives in East Asia. By holding fruitful symposiums we can expand the knowledge for harmful organisms, publish the special journal issue and exchange knowledge with leading international scientists as well as training and educating members.

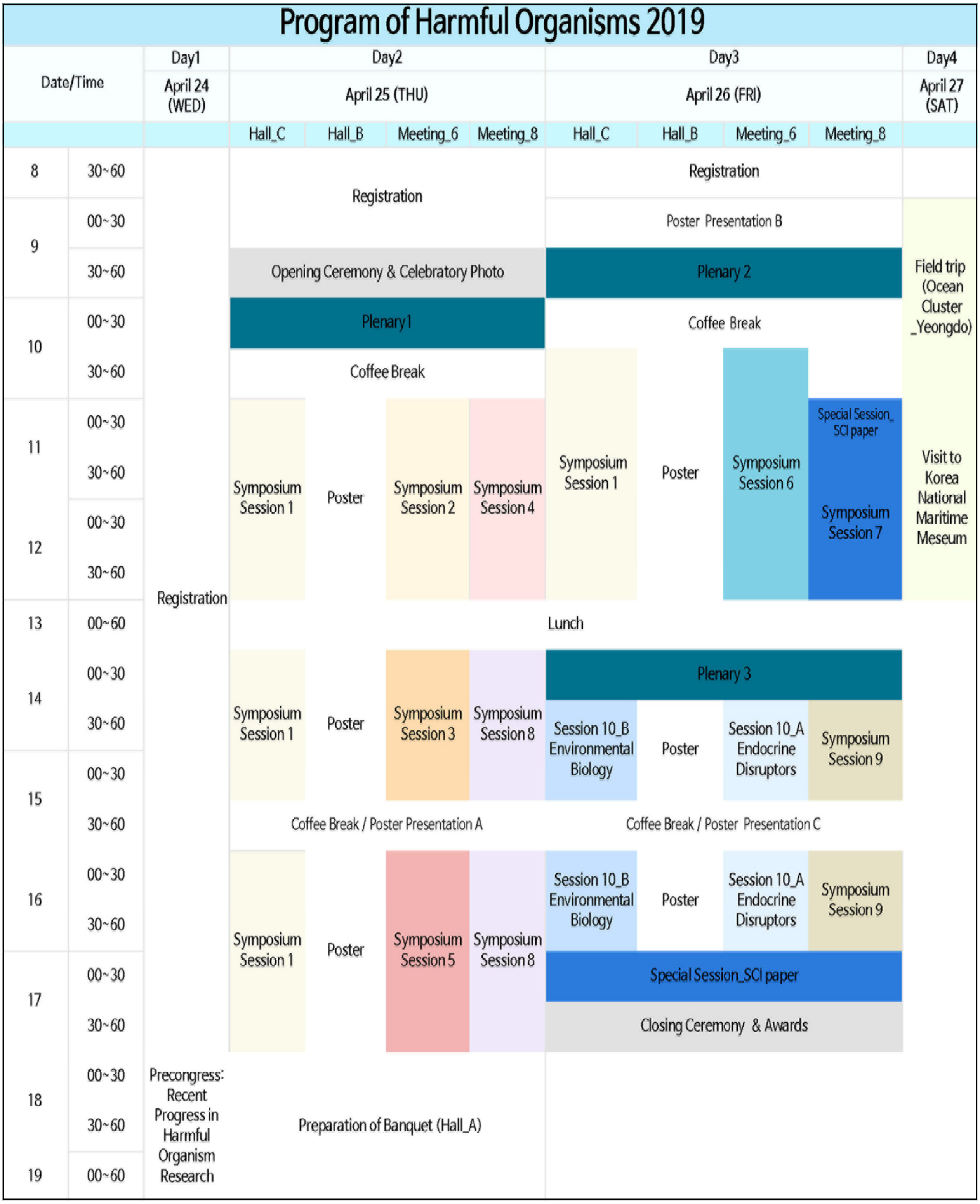
I sincerely thank all the researchers who are willing to take a step forward in treating the harmful organisms and hope to meet you again.

Thank you.

April, 2019

President of Korean Society for Environmental Biology, **Myung Chan Gye**

Program at a Glance



Program of Harmful Organisms 2019

Date/Time		Day1	Day2				Day3				Day4
		April 24 (WED)	April 25 (THU)				April 26 (FRI)				April 27 (SAT)
			Hall_C	Hall_B	Meeting_6	Meeting_8	Hall_C	Hall_B	Meeting_6	Meeting_8	
8	30~60	Registration	Registration				Registration				
9	00~30						Poster Presentation B				Field trip (Ocean Cluster _Yeongdo)
	30~60		Opening Ceremony & Celebratory Photo				Plenary 2				
10	00~30		Plenary1				Coffee Break				
	30~60		Coffee Break				Symposium Session 1	Poster	Symposium Session 6		
11	00~30		Symposium Session 1	Poster	Symposium Session 2	Symposium Session 4				Special Session_ SCI paper	Visit to Korea National Maritime Meseum
	30~60									Symposium Session 7	
12	00~30										
	30~60										
13	00~60		Lunch								
14	00~30		Symposium Session 1	Poster	Symposium Session 3	Symposium Session 8	Plenary 3				
	30~60						Session 10_B Environmental Biology	Poster	Session 10_A Endocrine Disruptors	Symposium Session 9	
15	00~30										
	30~60		Coffee Break / Poster Presentation A				Coffee Break / Poster Presentation C				
16	00~30		Symposium Session 1	Poster	Symposium Session 5	Symposium Session 8	Session 10_B Environmental Biology	Poster	Session 10_A Endocrine Disruptors	Symposium Session 9	
	30~60										
17	00~30						Special Session_SCI paper				
	30~60						Closing Ceremony & Awards				
18	00~30	Precongress: Recent Progress in Harmful Organism Research	Preparation of Banquet (Hall_A)								
	30~60										
19	00~60										

Schedule

April 24 (WED)

16:00~20:00	Precongress : Recent Progress in Harmful Organism Research

April 25 (THU)

9:00~	Registration		
09:30~10:00	Opening Ceremony (Hall_C) Opening address : Myung Chan Gye (President of KOSEB) Congratulatory message : Jin Hwan Lee (Former president of KOSEB)		
	Celebratory Photo		
10:00~10:30	Plenary Lecture 1 **The occurrence mechanism of fish-killing red tides of *Chattonella* (Raphidophyceae) and successful trial of environment-friendly prevention strategies using diatoms** Ichiro Imai (Hokkaido University, Japan) (Hall_C)		
10:30~11:00	Coffee Break		
11:00~13:00	Symposium Session 1 The physiological, biochemical, genetic and behavioral features of harmful algae (Hall_C)	Symposium Session 2 Current status and future research direction of drifting macro-algal blooms (Meeting_6)	Symposium Session 4 Entomological research on harmful organisms in agriculture and vector-borne disease (Meeting_8)
13:00~14:00	Lunch		
14:00~15:30	Symposium Session 1 The physiological, biochemical, genetic and behavioral features of harmful algae (Hall_C)	Symposium Session 3 Jellyfish blooms in the East Asian Seas (Meeting_6)	Symposium Session 8 Application of Integrated Mosquito Management (IMM) in South Korea and southeast Asia (Meeting_8)
15:00~15:30	Coffee Break & Poster Presentation A (Hall_B)		
16:00~18:00	Symposium Session 1 The physiological, biochemical, genetic and behavioral features of harmful algae (Hall_C)	Symposium Session 5 (41th Yonsei Tropical Medicine Symposium) Harmful organism of medical importance (Meeting_6)	Symposium Session 8 Application of Integrated Mosquito Management (IMM) in South Korea and Southeast Asia (Meeting_8)
18:00~20:00	Preparation of Banquet (Hall_A)		

April 26 (FRI)

8:30~	Registration		
09:00~09:30	Poster Presentation B (Hall_B)		
09:30~10:00	Plenary Lecture 2 **A new horizon of cyanobacterial bloom control and its biomass utilization** Hee-Mock Oh (Korea Research Institute of Bioscience & Biotechnology, Korea) (Hall_C)		
10:00~10:30	Coffee Break		
10:30~13:00	Symposium Session 1 The physiological, biochemical, genetic and behavioral features of harmful algae (Hall_C)	Symposium Session 6 Ecological, economic and human health impacts of invasive alien plants (Meeting_6)	Symposium Session 7 Waste to resources: Emergent materials for environmental applications (Meeting_8)
13:00~14:00	Lunch		
14:00~14:30	Plenary Lecture 3 **Harmful jellyfish blooms in the East Asian Seas: Is our ocean more gelatinous?** Shin-ichi Uye (Hiroshima University, Japan) (Hall_C)		
14:00~15:30	Session 10_B Environmental Biology (Hall_C)	Session 10_A Endocrine Disruptors (Meeting_6)	Symposium Session 9 Environmental pollutions and associated microorganisms including harmful organisms (Meeting_8)
15:30~16:00	Coffee Break & Poster Presentation C (Hall_B)		
16:00~17:00	Session 10_B Environmental Biology (Hall_C)	Session 10_A Endocrine Disruptors (Meeting_6)	Symposium Session 9 Environmental pollutions and associated microorganisms including harmful organisms (Meeting_8)
17:00~17:30	Special Session_Special Issue of SCI Journals		
17:30~18:00	Closing Ceremony & Awards		

April 27 (SAT)

09:00~13:00	Field trip (Ocean Cluster _Yeongdo) Visit to Korea National Maritime Meseum

Contents

Plenary

Date & Time : 25 Thu 10:00 - 10:30
Room : Hall C

10:00 - 10:30	Plenary_1	**The occurrence mechanism of fish-killing red tides of *Chattonella* (Raphidophyceae) and successful trial of environment-friendly prevention strategies using diatoms** Ichiro Imai (Hokkaido University, Japan)

Date & Time : 26 Fri 09:30 - 10:00
Room : Hall C

09:30 - 10:00	Plenary_2	**A new horizon of cyanobacterial bloom control and its biomass utilization** Hee-Mock Oh (Korea Research Institute of Bioscience & Biotechnology, Korea)

Date & Time : 26 Fri 14:00 - 14:30
Room : Hall C

14:00 - 14:30	Plenary_3	**Harmful jellyfish blooms in the East Asian Seas: Is our ocean more gelatinous?** Shin-ichi Uye (Graduate School of Biosphere Science, Hiroshima University, Japan)

Plenary_1

The occurrence mechanism of fish-killing red tides of *Chattonella* (Raphidophyceae) and successful trial of environment-friendly prevention strategies using diatoms

Ichiro Imai

Hokkaido University, Professor Emeritus, Hakodate, Hokkaido 041-8611, Japan

Many species of harmful raphidophytes and dinoflagellates have cyst stages in their life cycles. Cysts settle to sea bottom to overwinter and thereby ensure persistent existence in the same area. Consequently, cyst germination provides primary populations for red tides. It is empirically known that flagellate blooms have been observed when diatoms are scarce in water. Diatoms form resting stage cells under nutrient-deficient environments, and rapidly sink to sea bottom. *Chattonella* cysts can germinate in the dark, whereas diatom resting stage cells (DRSCs) require light for germination. Thus predominance of *Chattonella* spp. can be attributed to disappearance of diatoms and subsequent failure of germination of DRSCs under low light environments at sea bottom. Selective germination of cysts at sea bottom is presumably a significant factor for the initiation and success in *Chattonella* red tides. Giving enough light to the abundant DRSCs (usually $>10^5$/g wet sediment) at bottom was expected to enhance DRSCs germination and resultant vegetative cells are expected to proliferate and to overwhelm *Chattonella* populations by exhaustion of nutrient salts. Hence we propose bottom sediment perturbation to lift DRSCs into euphotic layer in coastal areas as environment-friendly HAB strategy. This trial was made using dragnet trawling in the Seto Inland Sea in July 2016. Densities of planktonic diatoms totally increased in water column after the trawling (maximum 1383 cells/mL) and *Chattonella* spp. decreased. The water sample after sediment perturbation was collected and bottle-incubation experiments were conducted in combination with inoculation of *Chattonella antiqua* (200 cells/mL) and strengthening of culture medium. Diatoms always increased and *Chattonella* decreased in all the experimental bottles. We demonstrated a feasibility of control of *Chattonella* with sediment perturbation in coastal sea through artificial induction of phytoplankton flora to diatom dominant communities.

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Plenary_2

A New Horizon of Cyanobacterial Bloom Control and Its Biomass Utilization

Hee-Mock Oh

Principal Research Scientist, Korea Research Institute of Bioscience and Biotechnology (KRIBB)

Microalgae are prokaryotic or eukaryotic photosynthetic microorganisms that can grow rapidly and live in harsh conditions due to their unicellular or simple multicellular structure. Increased cyanobacterial harmful algal blooms (CyanoHABs) are threatening public health and limiting human recreational activities related with freshwater ecosystems. Especially, phosphorus (P) has long been suggested as a critical nutrient for CyanoHABs. Recently, nitrogen (N) has also been highlighted as an impacting nutrient on CyanoHABs. General strategies for CyanoHABs control in lakes and reservoirs include a dual nutrient (N & P) reduction, wastewater collection and treatment, pre-treatment of influent water in buffer zones, etc. In addition, there is a need for sustainable and integrative freshwater algae management, because microalgae including cyanobacteria are not the target organism to be eradicated, but an essential microbial member in the freshwater ecosystem.

On the other hand, microalgal biomass can be used as feedstock for several types of renewable fuels such as biodiesel, methane, hydrogen and ethanol. Biodiesel from microalgae is being recognized as a desirable renewable biofuel with a potential to replace the petroleum-derived transport fuels. In this regard, algae biofuel is thus considered as the 3rd generation bioenergy which will be commercialized in the future. The industrial application of microalgae extends to the production of health foods, antioxidants, vitamins and other valuable materials. Yet, the economic viability of these microalgae-based applications mainly relies on the biomass productivity of microalgae.

Consequently, CyanoHABs in lakes and reservoirs is mainly caused by inflow of wastewater containing high N and P, on the other hand, microalgal cultivation for biomass production needs N and P as major nutrients. Therefore, key nutrients in wastewater can be used for microalgae cultivation which can reduce the concentration of N and P in influent resulting in reduction of CyanoHABs in lakes and reservoirs. Additionally, the cultured microalgal biomass can be used as a feedstock for microalgal biorefinery to produce fuels, foods, feed, cosmetics, pharmaceuticals, pigments, etc. The fundamental mechanism behind the dense and massive growth of CyanoHABs in nature can be applied reversely in order to stimulate the rapid growth of beneficial microalgal species in photobioreactor and raceway pond artificially.

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Plenary_3

Harmful jellyfish blooms in the East Asian Seas: Is our ocean more gelatinous?

Shin-ichi Uye

Graduate School of Biosphere Science, Hiroshima University, 4-4 Kagamiyama 1 Chome,
Higashi-Hiroshima 739-8528, Japan

Human society is largely dependent on a stable supply of marine ecosystem services, including fisheries and aquaculture. Our expectation of stability is usually fulfilled by the intrinsic resiliency of ecosystems to perturbations. However, marine ecosystems are never stable, and sometimes shift drastically from one state to another state if external forcing exceeds a threshold. Under the enhancement of anthropogenic activities, unexpected marine ecosystem changes have happened more frequently than before. Unprecedented increases or outbreaks of jellyfish populations can be one of such cases. Jellyfish are one of the earliest multi-celled animals on earth ca. 500 million years ago, and have adapted to living in various marine environmental conditions from estuaries to deep ocean. In recent decades, jellyfish population outbreaks have been increasingly prominent in many parts of the world ocean, such as the Black Sea, Namibian coastal waters, the Mediterranean Sea and the East Asian Seas. I will overview 1) how the jellyfish populations proliferated, or fluctuated, 2) why they increased in response to global/regional climate changes and anthropogenic impacts, 3) what negative consequences they have for our human wellbeing, and 4) what countermeasures we can take, primarily in cases of the East Asian Seas. Although true causes of jellyfish population outbreaks are still under investigation, they tend to bloom massively where healthy marine ecosystem has been deteriorated by increased anthropogenic impacts (e.g. global warming, eutrophication, over-fishing, increase of man-made structures, translocations by ballast water exchange). Improvement of our understanding of the mechanisms of marine ecosystem responses to natural and/or anthropogenic forcings and finding appropriate ways for the sustainable use of marine ecosystem services are emergent issues in the global change era.

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Mini-Symposium

Session 1

The physiological, biochemical, genetic and behavioral features of harmful algae

Date & Time : 25 Thu 11:00 - 13:00
Room : Hall C

Chair : Dr. Hee-Mock Oh
Korea Research Institute of Bioscience & Biotechnology, Korea

11:00 - 11:30	OS_1_01	**Physiological and toxicity changes in the invasive cyanobacterium *Cylindrospermopsis raciborskii* in response to nitrogen fluctuation** Renhui Li (Institute of Hydrobiology, China)_**Invited speaker**
11:30 - 12:00	OS_1_02	**Linkage between zebra mussel establishment, cyanobacteria community composition and microcystin levels in the United States lakes** Jiyoung Lee (The Ohio State University, USA)_**Invited speaker**
12:00 - 12:20	OS_1_03	**The inhibition and development of harmful alga *Cochlodinium polykrikoides* bloom related with Changjiang River discharge in Korean coastal waters** Seung Ho Baek (Korea Institute of Ocean Science & Technology, Korea)
12:20 - 12:40	OS_1_04	**Microbial interactions during *Cochlodinium polykrikoides* bloom in South Sea, Korea** Chi-Yong Ahn (Korea Research Institute of Bioscience and Biotechnology, Korea)
12:40 - 13:00	OS_1_05	**Early warning of *Cochlodinium polykrikoides* (Dinophyceae) blooms in the South Sea, Korea using real-time PCR** Tae Gyu Park (National Institute of Fisheries Science, Korea)

Chair : Prof. Ichiro Imai
Hokkaido National University, Japan

14:00 - 14:30	OS_1_06	**Toxic HAB species from the Sea of Okhotsk detected by a metagenetic approach** Satoshi Nagai (National Research Institute of Fisheries Science, Japan)**_Invited speaker**
14:30 - 14:50	OS_1_07	**Phytoplankton pigments patterns and environmental factors variations during harmful algal bloom in South-western coast, Korea** Moonho Son (National Institute of Fisheries Science, Korea)
14:50 - 15:10	OS_1_08	**Mating rate and occasion as a sexual reproductive strategy according to growth phase of parent cells of pennate diatom *Pseudo-nitzschia pungens*** Jin Ho Kim (Korea Institute of Ocean Science & Technology, Korea)
15:10 - 15:30	OS_1_09	**Spatio-temporal shifts of microbial communities and their co-occurrence patterns in a dynamic coastal ecosystem** Yingshun Cui (Korea Research Institute of Bioscience & Biotechnology, Korea)

Chair : Dr. Chi-Yong Ahn
Korea Research Institute of Bioscience & Biotechnology, Korea

16:00 - 16:30	OS_1_10	**Homogenizing co-dispersal resulting in an uniform distribution of antibiotic resistance genes in two nearby sub-watersheds, China** Anyi Hu (Institute of Urban Environment, China) **_Invited speaker**
16:30 - 17:00	OS_1_11	**Taxonomy, composition, distribution pattern and toxicity of *Prorocentrum* (Dinophyceae) in the coastal water of China** Pengbin Wang (Ministry of Natural Resources, China) **_Invited speaker**
17:00 - 17:20	OS_1_12	**Invasion of exotic nostocalean cyanobacteria and their toxin production potential in the Nakdong River, Korea** Hae-Kyung Park (Nakdong River Environment Research Center, Korea)
17:20 - 17:40	OS_1_13	**Field application of biologically derived substances (BDSs: naphthoquinone derivative) for eco-friendly mitigation of harmful cyanobacterial blooms** Jae-Hyoung Joo (Hanyang University, Korea)
17:40 - 18:00	OS_1_14	**Interactions of the harmful dinoflagellate *Cochlodinium polykrikoides* and *Alexandrium* sp.: physiological and genomics responses** Jang-Seu Ki (Sangmyung University, Korea)

Date & Time : 26 Fri 10:30 - 13:00
Room : Hall C

Chair : Dr. Seung Ho Baek
Korea Institute of Ocean Science & Technology, Korea
Chair : Dr. Satoshi Nagai
National Research Institute of Fisheries Science, Japan

10:30 - 11:00	OS_1_15	**Environment-friendly prevention strategies for harmful algal blooms using algicidal bacteria associated with seaweeds and seagrasses** Ichiro Imai (Hokkaido University, Japan)_**Invited speaker**
11:00 - 11:20	OS_1_16	**Genetic relatedness of a new Japanese isolates of *Alexandrium ostenfeldii* bloom population with global isolates** Sirje Sildever (National Research Institute of Fisheries Science, Japan)
11:20 - 11:40	OS_1_17	**Remote sensing monitoring of *Margalefidinium polykrikoides* blooms in the South Sea of Korea** Jisun Shin (Korea Institute of Ocean Science & Technology, Korea)
11:40 - 12:00	OS_1_18	**Using network analysis to explore dynamics of *Microcystis* genotypes and other microbial community during cyanoHABs** Seong-Jun Chun (Korea Research Institute of Bioscience & Biotechnology, Korea)
12:00 - 12:20	OS_1_19	**Population development strategy of two dinoflagellates *Cochlodinium polykrikoides* and *Alexandrium affine* during the summer in the coastal environments of the southern sea of Korea** Young Kyun Lim (Korea Institute of Ocean Science & Technology, Korea)
12:20 - 12:40	OS_1_20	**Potential role of oil-degrading bacteria in the formation of a harmful dinoflagellate bloom after the Texas City “Y” Oil Spill: evidence from culture experiments** Bum Soo Park (University of Texas Marine Science Institute, USA)
12:40 - 13:00	OS_1_21	**Transcriptomic responses to nutrient (N, P) and light limitation in pelagophytes** Yoonja Kang (Gwangju Institute of Science and Technology, Korea)

OS_1_01

Physiological and toxicity changes in the invasive cyanobacterium *Cylindrospermopsis raciborskii* in response to nitrogen fluctuation

Renhui Li, Yiming Yang, and Youxin Chen

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The heterocystous cyanobacterium, *Cylindrospermopsis raciborskii* is a cosmopolitan species which thrives in reservoirs, lakes and rivers worldwide. There are increasing researches for the invasiveness potential of *C. raciborskii* in recent years, with the species expanding from tropical to subtropical and temperate zones. Many studies concerned about the role of nutrients in driving *C. raciborskii* blooms, but little is known about the effect of nutrient fluctuations on the physiology and toxicology of this organism. Based on our previous field survey in which *Cylindrospermopsis* species was found to have a high fitness under nitrate concentrations fluctuating from 0.02 mg L^{-1} to 2.90 mg L^{-1} in Chinese freshwater lakes, we here assessed the role of short-term N fluctuations in both toxic and non-toxic *C. raciborskii* strains exposed to a range of N concentrations supplied in two patterns, namely one-time pattern and ten-time pattern in which the equal amount of N was divided into ten-time accretions. The results showed the growth of both strains were not vulnerable to the transient nutrient fluctuations. The toxic strain showed considerable toxicological flexibility with the highest yield of cylindrospermopsin (CYN) obtained in the absence of N and the lowest in full medium. Larger amounts of total CYN were observed at lower N levels, indicating that N deficiency may promote the intracellular accumulation and simultaneously restrained the extracellular release of CYN. Furthermore, CYN production was significantly different in two N supply patterns. The maximum quotas of intracellular and extracellular CYN in one-time pattern were respectively 2.79-3.53 and 3.94-7.20 times higher compared to the ten-time pattern. Such results provided evidence of toxicity variations of *C. raciborskii* to the impermanent N fluctuations, shedding new light on its toxicological plasticity.

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OS_1_02

Linkage between zebra mussel establishment, cyanobacteria community composition and microcystin levels in the United States lakes

Feng Zhang[1], Song Liang[2,3], Ozeas Costa[4] and Jiyoung Lee[1,5,6]

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[2]Department of Environmental and Global Health, University of Florida
[3]Emerging Pathogens Institute, University of Florida
[4]School of Earth Sciences, The Ohio State University at Mansfield
[5]College of Public Health, Division of Environmental Health Sciences, The Ohio State University
[6]Department of Food Science and Technology, The Ohio State University

Zebra mussel invasion in the lakes of the United States lakes during the last century may play an important role in the occurrence of toxic cyanobacteria blooms. Herein, large-scale data from the US Environmental Protection Agency National Lake Assessment (> 1,000 lakes) were used to study the potential linkage between zebra mussels, cyanobacteria community composition, and microcystin (MC) levels in the lakes. ANOVA Based on Dissimilarities tests (Adonis) showed that there was a significant difference in cyanobacterial communities between lakes located in areas with and without established zebra mussel populations. Meanwhile, significantly higher MC levels and cyanobacteria abundance were observed, but lower concentrations of phosphorous in lakes located in areas with established zebra mussels. Structural equation modeling was used to confirm and estimate the effect of zebra mussels on MC concentrations via different pathways. The results suggest three potential pathways whereby zebra mussels influence MC production: 1) altering phosphorous concentration; 2) increasing cyanobacteria abundance; and 3) shifting cyanobacteria community structure. The total net effect of zebra mussel establishment resulted in an overall 1.40 times net increase in MC level. The study suggested the important potential role of zebra mussel invasion in altering cyanobacterial composition and influencing MC levels in the US lakes.

OS_1_03

The inhibition and development of harmful alga *Cochlodinium polykrikoides* bloom related with Changjiang River discharge in Korean coastal waters

Seung Ho Baek[1], Min Ji Lee[1], Young Kyun Lim[1], Jin Ho Kim[1],
Chi-Yong Ahn [2], Bum Soo Park[3]

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[3]Marine Science Institute, University of Texas at Austin, Port Aransas, TX 78373, USA

Over the last three decades, harmful alga *Cochlodinium polykrikoides* bloom have been consistently present along the Korean coastal water but they abruptly disappeared in 2016. Despite extensive studies on this dinoflagellate, the cause of this abrupt decline remains largely unknown. To understand the inhibition and development of harmful alga *Cochlodinium polykrikoides* population related with Changjiang River discharge, physico-chemical and biological data were collected along the south-eastern area of South Sea through a biweekly field survey from June to September. The environmental differences between 2016 and previous years (2012-2015) were investigated. In August, the water temperatures (c.a.,30°C) and the salinity (c.a., 30) were outside the optimum ranges for *C. polykrikoides* growth in the study area. Moreover, the averages of these factors were significantly different from previous years ($p<0.001$). In 2016, the amount of Changjiang River discharge, which can affect coastal environments via ocean currents, was relatively larger than in the past four years, reducing the salinity in August. Increased stratification and diatom dominance, both negatively associated with *C. polykrikoides* growth, were consistently observed during the study period. In the Goheung-Oenarodo area, which is the western part of the southern Korean coastal waters (KCW), *C. polykrikoides* blooms were observed, but they did not expand to the entire southern KCW, unlike in previous years. Therefore, we suggested as the non-outbreak mechanism of *C. polykrikoides* huge bloom in Korean coastal waters related with extension of Changjiang diluted water by large Changjiang River discharge that salinity was relatively kept to low (i.e., 28-30 psu) in the south sea frontal zone including Jeju channel in South Korea.

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OS_1_04

Microbial interactions during *Cochlodinium polykrikoides* bloom in South Sea, Korea

Chi-Yong Ahn[1,2,*], Yingshun Cui[1], Seong-Jun Chun[1,2], Seung Ho Baek[3],
Moonho Son[4], Hee-Mock Oh[1,2]

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[2]Department of Environmental Biotechnology, KRIBB School of Biotechnology, Korea University of Science and Technology (UST), Republic of Korea
[3]South Sea Research Institute, Korea Institute of Ocean Science and Technology (KIOST), Republic of Korea
[4]South Sea Fisheries Research Institute, National Institute of Fisheries Science (NIFS), Republic of Korea

Harmful algal blooms (HABs) by *Cochlodinium polykrikoides* cause huge economic and ecological damages frequently in Korea. Many previous studies revealed that the rise and fall of HABs are closely related to their associated microbes, including bacteria, archaea, and phytoplankton. However, their exact roles in the formation of HABs have not been elucidated. To explore the potential links between *C. polykrikoides* and other microbes, water samples in different size-fractions were collected during *C. polykrikoides* bloom in South Sea, Korea. Bacteria, archaea, and phytoplankton community structures were analyzed using next-generation sequencing. Marine group I (archaea), *Micrococcaceae* and *Piscirickettsiaceae* (bacteria), and *Syndiniales* group I (phytoplankton) were significantly enriched in *C. polykrikoides* bloom samples, compared with the non-bloom ones. Network analysis further showed that microbial compositions were quite different between *C. polykrikoides*–included module and others. It means that specific microbial clusters were more closely related to *C. polykrikoides*. Marine group I is supposed to supply vitamin B_{12}, the essential element for *C. polykrikoides*, while the potential fish pathogens (*Micrococcaceae* and *Piscirickettsiaceae*) could partially contribute to massive fish death. *Syndiniales* group I, a parasite to dinoflagellates, is presumed to induce a sudden collapse of *C. polykrikoides* blooms. In conclusion, a new insight into the microbiological mechanisms of HABs could be derived through the network analysis of microbial interactions.

OS_1_05

Early warning of *Cochlodinium polykrikoides* (Dinophyceae) blooms in the South Sea, Korea using real-time PCR

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Massive *Cochlodinium polykrikoides* blooms-related fish kills have occurred in the South Sea, Korea since 1995. To minimize economic losses of aquaculture farms, the Korean government runs a red tide monitoring program according to notification no. 2008-22. National Institute of Fisheries Science (NIFS) and local governments monitor red tides particularly *C. polykrikoides* in the summer season. Since 2014, NIFS applied molecular approach, real-time PCR, for early detection of *C. polykrikoides* at below cell detection level by microscopic observation. The real-time PCR was developed based on TaqMan method and designed to enumerate *C. polykrikoides* at very low cell densities (up to 1 cell per 10 L) in nature. The real-time PCR successfully enumerated very small amounts of *C. polykrikoides* at detection ranges of 1-14,000 cells per 10 L in June for the last five years. The early detecting areas and ranges in June differed by years during 2014 to 2018. However, *C. polykrikoides* blooms initiated in July or August mostly in the early warning areas measured by real-time PCR.

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OS_1_06

Toxic HAB species from the Sea of Okhotsk detected by a metagenetic approach

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During recent decades, the distribution of harmful algal bloom (HAB) species has expanded worldwide together with the increase of blooms and toxicity events. In this study, the presence of toxic HAB species in the Sea of Okhotsk was investigated based on metagenetic data collected during 6 years of weekly monitoring. OTUs associated with the toxic HAB species were detected based on amplifying 18S V7-V9 and 28S D1-D2 rRNA gene regions. In total, 62 OTUs associated with toxic HAB species were revealed, with 42 of those previously not reported from the Sea of Okhotsk. More OTUs belonging to dinoflagellates were detected by 18S, whereas almost equal number of OTUs associated with dinoflagellates and diatoms were detected by targeting the 28S region. Species belonging to genera *Alexandrium*, *Karenia* and *Prorocentrum* were mainly associated with OTUs under Dinophyceae and species belonging to genus Pseudo-nitzschia were the most dominant contributors to OTUs associated with Bacillariophyceae. From the detected OTUs, 22 showed a clear seasonal pattern with majority of those appearing during summer-autumn. For *Alexandrium pacificum*, *Aureochoccus anophagreffens*, *Chattonella marina*, *Pheopolykrikos hartmanii*, and *Pseudo-nitzschia pungens*, the seasonal pattern was detected based on both rRNA regions. Additionally, 16 unique OTUs were detected during all the seasons and 14 OTUs appeared sporadically. OTUs associated with the toxic species had low relative abundances, which together with other factors such as similar and variable morphology as well as usage of fixatives, may explain why those species have previously not been detected by light microscopy. Environmental parameters, especially water temperature, significantly (<0.05) influenced the variability in OTU relative abundances and displayed significant correlations with the unique OTUs. Potential influence of other factors such as low crazing pressure may also explain the variable presence of some OTUs.

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OS_1_07

Phytoplankton pigments patterns and Environmental factors variations during harmful algal bloom in South-western coast, Korea

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Harmful algal blooms(HAB) is frequent occurrence in the southern coast of Korea. So it is important to create an environment that minimize the damage of aquatic organisms to the occurrence of red tides and suppresses of harmful algal blooms. We monitored the marine environment, phytoplankton biomass and community structure on once every two weeks from June to the disappear HAB at 18 stations in South-western coast. We compared the characteristics of pigments distribution and environmental factors in the summer of 2016 and 2018 when the red tide occurred. *Cochlodinium polikrikoides* blooms occurred at the station Y2 near Yeosu (Becya Island) in the middle of August 2016, and *C. polikrikoides* blooms occurred at the station Y3 near the Goheung (Nenaro Island) in late July to August 2018. Water temperature in 2016 and 2018 is in the range of 16 ~ 28 ℃, however, the surface water temperature rapidly increased due to the high water temperature phenomenon in 2018 and red tides was occurred more rapidly than in 2016. Chlorophyll *a* showed 11 $\mu g\ L^{-1}$(2016) and 18.7 $\mu g\ L^{-1}$(2018) at the time of HAB, respectively, which was higher than the chl *a* (1.6 $\mu g\ L^{-1}$) in the South-western sea after the disappearance of HAB, the concentration of chl *a* was decreased rapidly to 0.74 $\mu g\ L^{-1}$(2016) and 1.75 $\mu g\ L^{-1}$(2018). In specially, the number of *C. polikrikoides* was rapidly decreased in 2018 due to the high water temperature of 2~4 °C higher than average temperature, and the occurrence of typhoons. The concentration of Peridinine, the indicator pigment of the Dinoflagellates, is rapidly increased to 2.2 $\mu g\ L^{-1}$ and 3.2 $\mu g\ L^{-1}$ in 2016 and 2018. Understanding of the Dinoflagelltes distribution can be used as important data for guessing and predict red tide occurrence. The community composition of phytoplankton(%) calculated using the CHEMTAX was divided into 8 community. In both of these years, diatoms were predominant group with 75.7% (2016) and 77.6% (2018). In the year 2016, phytoplankton community showed 12.4% of dinoflagellates, 8.3 of prasinophytes 2.8 of cryptophytes. In contrast, in the year 2016, it showed 8.8 of prasinophytes, 6.4% of cryptophytes, 4.9% of dinoflagellate. During HAB occur, phytoplankton community composition was changed by a reduction of diatoms and increases Dinoflagellates. After the end of HAB, in 2016, prasinophytes composition was increased, it is possible related influence of rainfall. On the other hand, in 2018, phytoplankton communities excluding diatoms have decreased rapily, and diatoms was dominented at 99.1% in last survey, another communities were showed for less than 1%. Decrease of diatoms will affect rapid increasing dinoflagellates in the feeding competition for the nutrients as well as water temperature and light conditions in the occurrence of HAB.

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OS_1_08

Mating rate and occasion as a sexual reproductive strategy according to growth phase of parent cells of pennate diatom *Pseudo-nitzschia pungens*

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Sexual reproduction allows the maintenance of genetic diversity and play a fundamental role in establishing the genetic structures of population. Two populations of different two genotypes of *Pseudo-nitzschia pungens* occurred co-bloom in Korean coasts and its genetic polymorphism resulted from sexual reproduction was reported, however the frequency and development of sexual reproduction according to their blooming phase were not investigated. We measured the mating rates and observed the developmental process according to different cell status (or growth phases; log, early stationary, late stationary and death phase) of *P. pungens* using genetically different two strains. In all co-cultivations sexual events were successfully observed, however different sexual reproductive rates were measured according to different growth phases of parents. The co-cultivation of log phase shown higher mating rates and generated higher number of zygotes than the other co-cultivation. The mating rates and number of zygotes were gradually decreased from log to death phase. The maximum zygote number was 1,390 cells per mL and maximum mating rate was 7.1% in co-cultivation of healthy parents cells of log phase, but just 9 cells per mL (mating rate: 0.1%) were observed in co-cultivation of death phase. In all co-cultivation, maximum mating rates were observed inner 10 days. Furthermore, in dark and turbulent condition, it could not make the zygote cell, and nutrient enriched condition rather interfered with the sexual events. Our results suggest that *P. pungens* may have adapted to make the large bloom in coastal areas to increase the sexual reproductive chance.

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OS_1_09

Spatiotemporal shifts of microbial communities and their co-occurrence patterns in a dynamic coastal ecosystem

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To investigate the spatiotemporal shifts of microbial communities and their co-occurrence patterns in relation to the environmental fluctuations, free-living (FL), nanoparticle-associated (NP), and microparticle-associated (MP) microbial community compositions were analysed. A total of 645 environmental samples were collected over a year in three different water depths and six stations in the southern coastal water of Korea. Our results revealed the water-column dependent seasonal variations of microbial community compositions. Multidimentional analysis uncovered that these variations were mostly caused by the abiotic environmental parameters, such as temperature and salinity fluctuations. The co-occurrence patterns of coastal microbial communities in surface and bottom water layers clustered into modules in which the microbial compositions varied considerably. Repeatable correlations between module eigengenes and environmental parameters were observed, indicating rapid and distinct response of tightly coupled bacterial groups in relation to environmental fluctuations. *Verrucomicrobiae* dominated in both surface and bottom spring modules, and correlated to the major phytoplankton groups in this season, suggesting their essential roles in development of spring phytoplankton bloom. *Actinobacteria*, one of dominant group in bottom spring modules, could contribute to degrade the phytoplankton debris that sank into the bottom water layers from surface. The increasing proportions of *Oxyphotobacteria* observed in surface summer module could be related to the higher temperature in this season. Collectively, our results showed new insight into the seasonal transitions of microbial communities and interconnectivities within microbes.

OS_1_10

Homogenizing co-dispersal resulting in an uniform distribution of antibiotic resistance genes in two nearby sub-watersheds, China

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Rivers not only are the most important freshwater resources, but also are a significant reservoir of antibiotic resistance genes (ARGs) due to the effects of intensive anthropogenic disturbances. However, the biogeographic pattern of ARGs and its underlying driving forces remain poorly understood. Here, we investigated the spatio-temporal variation of the abundance and composition of ARGs in surface waters of two nearby sub-watersheds (North River, NR and West River, WR) of Jiulong River, China by using metagenomic approach. The results indicated that bacitracin, multidrug, sulfonamide, tetracycline and aminoglycoside were the most five dominant ARG types, accounting for 22.8%, 20.7%, 15.2%, 10.9% and 9.8% of the total ARGs, respectively. Although there was no significant variation in ARG abundance between NR and WR, ARG during the wet season had significant higher abundance than those during the dry and normal seasons. SourceTracker analysis indicated that sewage treatment plants may be the main source of ARGs in all the samples, while animal feces contributed to the spread of ARGs in the upper area of NR. Random forest and network analyses confirmed that NR rather than WR was under the influence of fecal pollution. PCoA ordination analysis demonstrated that the composition of ARG changed along anthropogenic gradients, while the results of Raup–Crick null model showed that homogenizing dispersal was the main ecological processes controlling the assembly of riverine ARG communities. Structural equation models revealed that Class 1 integron was the major vector that was responsible for the spread of ARGs in Jiulong River, while grassland, total phosphorus, non-antibiotic chemicals and microbial community composition may also play important role in influencing the biogeographic distribution of ARGs, especially for NR. Taken together, our findings provide novel insights into the dissemination of ARGs in river ecosystems experiencing anthropogenic stresses.

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OS_1_11

Taxonomy, composition, distribution pattern and toxicity of *Prorocentrum* (Dinophyceae) in the coastal water of China

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Prorocentrum is a kind of dinoflagellate with cosmopolitan distribution. Many species of *Prorocentrum* can produce the diarrhetic shellfish poison (DSP), which can enter the food web through the prey of fish and shellfish. So far, there are many studies only on serval main species of *Prorocentrum*, such as *Prorocentrum donghaiense* (pelagic) and *Prorocentrum lima* (benthic) in China. To this big genus with about 80 species, it is apparently that there is not sufficient on the study of *Prorocentrum* biodiversity and geographical distribution. Based on our previous work, samples will be taken by collecting the surface water and using vacuum collection, artificial substrates as well as other methods. The targeted species and strains will be isolated and cultured in lab condition. Normal light microscope, laser scanning confocal microscope, SEM and TEM will be used for morphological study. The molecular identification will be also performed by amplifying and sequencing for specific genes. The biogeographic distribution pattern of *Prorocentrum* in typical coastal habitats of China will be constructed, which will also be contributed to improving global distributive pattern of these important species. In addition, it will be beneficial for further study on deep research of marine biotic resources, maintaining marine ecosystem health and monitoring or early warning of HABs.

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OS_1_12

Invasion of exotic nostocalean cyanobacteria and their toxin production potential in the Nakdong River, Korea

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Harmful cyanobacterial blooms (cyanoHABs) are one of the largest global issues regarding the water quality of fresh waters. It has been predicted that the amount and duration of cyanoHABs will increase along with recent climate changes. Moreover, global warming is associated with the apparent spread of some nostocalean cyanobacteria from tropical to temperate latitudes including northern Europe, North America and Asia. The Nakdong River is the second largest river in Korea, serving as the agricultural, industrial water source, and the drinking water source for the 13 million people. After the construction of the eight weirs along the river in 2012, there have been cyanoHAB formations every summer. In addition, cyanoHABs were recently observed to persist even during the winter, and the nostocalean cyanobacteria, *Aphanizomenon* spp., were the most dominant. This expansion of amount and duration of cyanobacterial blooms may indicate the possibility of so-called invasive nostocalean cyanobacteria occurrence in the Nakdong River. To confirm the occurrence and distribution of *Cylindrospermopsis raciborskii* and other nostocalean cyanobacteria in the Nakdong River, weekly monitoring of surface water have performed for morphological identification, along with the isolation of *Cuspidothrix issatschenkoi* and *Sphaerospermopsis aphanizomenoides* strains. The isolates were conducted molecular examination for the phylogenetic analysis and cyanotoxins production potential. Weekly water samples were also conducted molecular examination for the qualitative and quantitative analysis of cyanotoxin biosynthesis genes. *C. raciborskii*, *C. issatschenkoi* and *S. aphanizomenoides* have found in low densities in the Nakdong River chiefly in summer. *S. aphanizomenoides* and *C. issatschenkoi* isolates neither produced microcystins, cylindrospermopsin, saxitoxins and anatoxin-a using ELISA test, nor yielded PCR products using primers of main cyanotoxins biosynthesis genes including *mcyA*, *mcyB*, *cyrA*, *cyrJ*, *sxtA* and *sxt1*.

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OS_1_13

Field application of biologically derived substances (BDSs: naphthoquinone derivative) for eco-friendly mitigation of harmful cyanobacterial blooms

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Microcystis, a genus of Cyanobacteria, has been regarded the most harmful taxon in temperate freshwater ecosystems. To evaluate the possibility of using a naphthoquinone derivate (NQ 40) for the field application, the mesocosm (50 ton) and test-bed (3,000 ton) were conducted. In the mesocosm and test-bed experiments, NQ 40 showed strong and selective algicidal activity against the target cyanobacteria (*Microcystis* sp.). Accordingly, algicidal activity of NQ 40 increased gradually until the 8th and 30th days, and algal biomass decreased by 96.7 and 100%, respectively. Furthermore, the abiotic dynamics (except the pH, DO, and phosphate) showed similar trends in the control and treatment groups of test-bed. The concentrations of phosphates in the treatment group were higher than those in the control were, due to decomposition of dead *Microcystis* sp., whereas DO and pH under the treatment conditions were slightly lower than those in the control were, which was due to increment of organic acids and higher degradation activity. The Shannon-Wiener diversity index of phytoplanktons in the treated test-bed increased significantly after 2, 4 and 6 days. Additionally, because of analyzing the carbon flow in the ecological pyramid, the unbalanced ecological pyramid was restored using NQ 40. Changes in the ecosystem structure were observed in our study on each successive day of the experiments, with reference to control; integrity of the beneficial microalgal populations was not affected, which indicated possible restoration of ecosystem and regain of similar structure. These results suggested that NQ 40 could be promising for use as an eco-friendly algicidal substance to mitigate the harmful cyanobacterial blooms in freshwaters.

OS_1_14

Interactions of the harmful dinoflagellate *Cochlodinium polykrikoides* and *Alexandrium* sp.: physiological and genomics responses

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The harmful dinoflagellate *Cochlodinium polykrikoides* lives with other dinoflagellates while competing, and sometimes it grow rapidly to make algal blooms. However, their biological interaction of *Cochlodinium* and other dinoflagellates were not discovered clearly. In the present study, we performed co-culture experiment of *C. polykrikoides* and *Alexandrium* sp., including the *Alexandrium* filtrates. When the *C. polykrikoides* were cultured together with different initial cell concentrations of *Alexandrium*, the growth of *C. polykrikoides* was significantly decreased when compared to control. In addition, affected by the other species. In addition, cellular ROS increased, and antioxidant genes, *HSP70* and *HSP90*, induced greatly. However, photosynthesis efficiency and photosynthesis-related genes (*psbA, psaB,* and *rbcL*) expression were decreased. Further co-culture experiment of *Cochlodinium* and *Alexandrium* filtrate showed little decrease of cell number; however, photosynthesis and stress genes were not affected by the *Alexandrium* filtrates. These results suggested that shading and/or *Alexandrium*-releasing compounds, like allelochemicals may affect significantly to *Cochlodinium* cell growth and physiology.

OS_1_15

Environment-friendly prevention strategies for harmful algal blooms using algicidal bacteria associated with seaweeds and seagrasses

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There is an urgent need of strategies for bloom mitigation and/or prevention in coastal areas due to heavy fishery damages by harmful algal blooms (HABs). Microorganisms such as bacteria appear to be promising control agents against HAB. Algicidal bacteria have actually been detected and isolated from the HAB-occurring coastal waters. It has gradually been known that algicidal bacteria specifically associate with the occurrence and crash of red tides, and also contributed to the rapid termination of HABs in the coastal waters such as the Seto Inland Sea. It was found that huge numbers of algicidal bacteria inhabited on the surface of seaweeds (million of killer-bacteria per gram wet weight) such as *Ulva* sp. (Chlorophyta), *Gelidium* sp. (Rhodophyta) and Sargassum spp. (Heterokontophyta) without occurrences of any microalgal blooms. And further comparatively abundant existence of algicidal bacteria (ten times or more than seaweeds) including killers for HAB causative microalgae on the surface of leaves of seagrass (*Zostera marina*). And in seawaters in *Zostera* bed and seaweed beds abundant existence of algicidal bacteria were confirmed. The presence of the large number of algicidal bacteria indicates the potential for preventing HAB occurrences. Incubation experiments of HAB species using waters of seagrass beds and seaweed beds demonstrated the actual killing (decrease) of harmful algae by virtue of algicidal activity of bacteria. We here propose new prevention strategies for red tides by polyculture of seaweeds and fishes in aquaculture areas. When the natural seaweed- and seagrass-bed are developed and restored as a part of Sato-Umi initiative, these presumably function to prevent the occurrences of HABs. Furthermore, restored seaweed- and seagrass- beds also serve as nursery grounds for important fisheries resources.

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OS_1_16

Genetic relatedness of a new Japanese isolates of *Alexandrium ostenfeldii* bloom population with global isolates

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In recent years, blooms of toxic *Alexandrium ostenfeldii* strains have been reported from around the world. In 2013, the species formed a red tide in a shallow lagoon in western Japan, which was the first report of the species in the area. To investigate the genetic relatedness of Japanese *A. ostenfeldii* and global isolates, the full-length SSU, ITS and LSU sequences were determined, and phylogenetic analyses were conducted for isolates from western and northern Japan and from the Baltic Sea. Genotyping and microsatellite sequence comparison were performed to estimate the divergence and connectivity between the populations from western Japan and the Baltic Sea. In all phylogenetic analyses, the isolates from western Japan grouped together with global isolates from shallow and low saline areas, such as the Baltic Sea, estuaries on the east coast of U.S.A. and from the Bohai Sea, China. In contrast, the isolates from northern Japan formed a well-supported separate group in the ITS and LSU phylogenies, indicating differentiation between the Japanese

populations. This was further supported by the notable differentiation between the sequences of western and northern Japanese isolates, whereas the lowest differentiation was found between the western Japanese and Chinese isolates. Microsatellite genotyping revealed low genetic diversity in the western Japanese population, possibly explained by a recent introduction to the lagoon from where it was detected. The red tide recorded in the shallow lagoon followed notable changes in the salinity of the waterbody and phytoplankton composition, potentially facilitating the bloom of *A. ostenfeldii*.

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OS_1_17

Remote sensing monitoring of *Margalefidinium polykrikoides* blooms in the South Sea of Korea

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Harmful Margalefidinium polykrikoides blooms has frequently occurred in the South Sea of Korea (SSK) since 1995. In order to cope with this bloom, it is essential to understand spatio-temporal distribution of M. polykrikoides blooms. Compared to traditional field survey method, remote sensing techniques is efficient in periodic and wide red tide detection, which requires fast and accurate monitoring. Until now, satellite-based red tide detection has been mainly performed, but it is difficult to monitor red tide more precisely because of limitation of spatial-spectral resolution. The objective of this study is to identify accurate distribution and extent of M. polykrikoides blooms using remote sensing data, such as optical image of UAV and hyperspectral data. In situ observations of M. polykrikoides blooms were conducted on August 7 and 8, 2018 in the coastal areas in Yeosu. During the field survey, the spectrum of waters and cell abundance of red tide were measured. At the same time to the field survey, UAV optical images were acquired for obtaining precise information of spatial distribution. It shows distinct spatial distribution of red tide blooms through geometric correction. Also, airborne hyperspectral images were acquired for understanding red tide species and cell abundance. As a result of comparing Rrs calculated by atmospheric correction of hyperspectral image and in situ Rrs, the correlation was good (0.7~0.9). The correlation between hyperspectral band and in situ cell abundance was calculated to obtain band ratio having the highest correlation with cell abundance. Cell abundance map showed the detail distribution of red tide blooms. The two images were combined to calculate red tide distribution and extent. Remote sensing monitoring using high spatial-spectral resolution is expected to be an efficient tool for identifying the distribution and extent of blooms.

OS_1_18

Using network analysis to explore dynamic of *Microcystis* genotypes and other microbial community during cyanoHABs

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To elucidate the co-occurrence patterns between producers, consumers, and decomposers in aquatic ecosystem during cyanobacterial harmful algal blooms (cyanoHABs), we investigated diversity and compositions of cyanobacterial (16S), including genotypes of *Microcystis* (cpcBA gene), non-cyanobacterial (16S), and eukaryotic (18S) communities using high-throughput sequencing. Combined these components, we constructed microbial network and identified their distinct modular structure. *Microcystis* blooms were divided into three different types and dominant oligotypes (genotypes) of *Microcystis* were also different. Co-occurrence network analysis revealed that the overall transition of modules that involved in the same phase of CyanoHABs showed similar patterns even in different stations. In addition, the components of the module were clearly classified, while these components were similar across the station. Especially, *Acetobacterales*, *Betaproteobacteriales*, *Flavobacteriales*, and *Frankiales* were involved in mutualistic interactions, while *Pseudanabaena, Vampirovibrionales, Cytophagales*, and *Oligohymenophorea* were involved in parasitism or predation interactions. Importantly, shallow sub-network revealed that major cyanobacteria formed complex network with other microbes and deep sub-network allow us to capture hidden correlation between *Microcystis* genotypes and other microbes. Therefore, to understand complex ecological interactions during cyanoHABs, we should consider their interactions through a network and modular structures based on the *Microcystis* genotypes. Overall, the distinct modular structures and deep network based on *Microcystis* may offer new insight into the dynamic of cyanoHABs.

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OS_1_19

Population development strategy of two dinoflagellates *Cochlodinium polykrikoides* and *Alexandrium affine* during the summer in the coastal environments of the southern sea of Korea

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Marine Harmful alga, the dinoflagellates *Cochlodinium* and *Alexandrium* are known to have serious negative impacts on marine ecosystems and the aquaculture industry. We investigated the appearance and succession patterns of both HAB species in coastal environments of southern Korea and performed a bioassay using *C. polykrikoides* and *A. affine* cultures to evaluate their competitive relationship. Due to the expansion of Changjiang Dillued Water in the summer of 2017, the surface water temperature increased from 17.4°C to 26.8°C, the salinity decreased from 34.15 to 30.8, and strong stratification developed. First, *C. polykrikoides* dominated in July; however, abundance of *A. affine* reached bloom levels in whole study areas in August. The growth experiments were carried out on each species at six water temperature (15, 20, 22.5, 25, 27.5 and 30°C) and six salinity (20, 24, 26, 28, 30 and 32) conditions. In growth experiments, both species did not grow well at 15°C, and the growth rate also increased with water temperature, showing the maximum growth rate at 25°C (*C. polykrikoides*: 0.31 d^{-1}, *A. affine*: 0.43 d^{-1}). However, *C. polykrikoides* did not grow at low salinity of 20 at 25°C and 27.5°C, and A. affine did not show any difference in growth rate by salinity ($p < 0.001$). At 30°C, cultured *C. polykrikoides* cells died within 2 days, while *A. affine* grew well in all salinity conditions. In addition, *A. affine* showed a significantly higher growth rate than *C. polykrikoides* at 20-30°C except for 15°C ($p < 0.001$). In co-cultivation at a 1:1 cell inoculation ratio, *A. affine* had a competitive advantage over *C. polykrikoides* at all temperature; however, when the inoculation ratios were varied, the species with a higher initial cell density showed a competitive advantage at all temperatures except 30°C. Combined the field and bioassay results indicated that *A. affine* may have an advantage over *C. polykrikoides* based on better environmental tolerance and high growth rate, particularly, under higher temperature and lower salinity conditions. This suggests that the difference of physiological characteristics in response to environment may be an important factor of succession between HABs species. As in the case of 2017 from *C. polykrikoides* to *A. affine*.

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OS_1_20

Potential role of oil-degrading bacteria in the formation of a harmful dinoflagellate bloom after the Texas City "Y" Oil Spill: evidence from culture experiments

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The association between phytoplankton blooms and oil spills is still controversial despite numerous studies. Surprisingly, to date, there have been no studies on the effect of bacterial communities exposed to crude oil on phytoplankton growth, even though crude oil leads to variation in bacterial communities, and this variation can affect phytoplankton growth and species composition. In this study, to investigate the impact of altered bacterial communities exposed to crude oil on the growth of dinoflagellate, we exposed free-living bacteria isolated from a *Prorocentrum texanum* culture to crude oil for a month, and then investigated the growth change in *P. texanum* after addition of these oil-treated bacteria. As a result, the growth rate and yield of *P. texanum* in bacterial treatment was clearly enhanced, compared to control. To gain more direct evidence, we isolated oil-degrading bacteria from sediment samples collected from oil-contaminated sites after the Texas City "Y" oil spill, and investigated variation in dinoflagellate growth after co-culture with single bacterial isolates. A total of seven oil-degrading bacterial cultures were established, and two bacterial cultures (C1-T3 and E1-Gal-T2) clearly enhanced the growth rate and yield of six dinoflagellate cultures; axenic *Amphidinium carterae* and *Peridinium sociale*, and xenic *Karenia brevis*, *P. gracile*, *P. minimum*, and *P. texanum*. To determine whether or not these bacteria can enhance dinoflagellate growth by releasing nutrients, nutrient-limited medium was prepared by removing each one of the components (nitrogen, phosphorous, trace metals or vitamins), and C1-T3 and E1-Gal-T2 were inoculated into each nutrient limited media, containing *A. carterae* and *Pe. sociale*. These two bacterial cultures greatly enhanced the growth rate and yield of the two dinoflagellates, regardless of any nutrient-limited media. Together with these findings, oil-degrading bacteria may enhance the growth of dinoflagellates and this growth enhancing activity may not be derived from nutrients released from the bacteria.

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OS_1_21

Transcriptomic responses to nutrient (N, P) and light limitation in pelagophytes

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Pelagophytes are abundant picophytoplankton within open ocean ecosystems and the causative algae of harmful brown tides blooms in estuaries. The physiological pathways facilitating the ecological success of pelagophytes in these diverse ecosystems remain poorly understood. Here, we investigated the transcriptional response of two coastal pelagophytes, Aureococcus anophagefferens and Aureoumbra lagunensis, and two open ocean pelagophytes, Pelagococcus subviridis and Pelagomonas calceolata, to conditions commonly found within the marine ecosystems where they thrive: low concentrations of nitrogen (N), phosphorus (P), or light. OrthoMCL was used to generate a total of 62,653 orthologous groups (OGs) with only a small fraction of these OGs (2,776 or 4.4%) being commonly shared among all four pelagophytes with a range of 13% to 33% in each species. Of the commonly shared OGs, 8% were significantly and differentially abundant under low N, P, or light with the majority being associated with energy and lipid metabolism. Specific OGs that were differentially expressed under low N, P, or light included OGs associated with cleavage of N from organic compounds, intracellular P recycling, lipid hydrolysis, low-light acclimation, and use of selenocysteine-related genes. Distinct responses among pelagophytes included the expression of unique phosphate transporters by Aureococcus in low P, the use of intracellularly recycled phosphate originating from pyrophosphate under low P in Aureococcus and Pelagomonas, the expression of organic nitrogen-degrading enzymes under low N as well as the use of flavodoxins over ferredoxins under low light for Pelagomonas, the increased transcript abundance of lysophospholipase under low light in Pelagococcus, and the differential expression of selenocysteine-related genes in all pelagophytes except Pelagococcus. Collectively, this study demonstrates that coastal and open ocean pelagophytes possess a combination of shared and unique ecophysiological features that likely facilitate their adaptation to distinct environmental conditions.

Session 2

Current status and future research direction of drifting macro-algal blooms

Date & Time : 25 Thu 11:00 - 13:00
Room : Meeting 6

Chair : Prof. Hyuk Je Lee
Sangji University, Korea

Chair : Prof. Sang Rul Park
Jeju National University, Korea

11:00 - 11:10		**Introductory remarks** (Prof. Hyuk Je Lee)
11:10 - 11:30	OS_2_01	***Sargassum horneri*** **golden tide on the rise in Korea: current status and management strategies** Sangil Kim (National Institute of Fisheries Science, Korea)
11:30 - 11:50	OS_2_02	**Current status of macroalgal bloom (golden tides and green tides) in Korea: the magnitude, formation, transport and management** Sang Rul Park (Jeju National University, Korea)
11:50 - 12:10	OS_2_03	**'Golden tide' seaweeds** ***Sargassum horneri*** **in Korean waters: the origin and genetic/genomic comparisons between floating and benthic populations** Hyuk Je Lee (Sangji University, Korea)
12:10 - 12:30	OS_2_04	**Species diversity of green tide forming macroalgae** ***Ulva*** **species in Jeju Island, Korea using DNA-based species delimitation approaches** Ji Hyoun Kang (Korea University, Korea)
12:30 - 12:50	OS_2_05	**Satellite monitoring of green and golden-tide in the eastern Yellow Sea** Keunyong Kim (Korea Institute of Ocean Science & Technology, Korea)
12:50 - 13:00		**Closing remarks** (Prof. Sang Rul Park)

OS_2_01

Sargassum horneri Golden Tide on the rise in Korea: current status and management strategies

Sangil Kim, Hyun-Ju Oh, Seok-Hyun Youn

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In recent years, golden tide of pelagic *Sargassum* have been a recurrent event in Korean coasts, where unprecedented great biomass of this *Sargassum* is washed ashore, resulting has produced a lot of economic and environmental damages. Hence, we have organized the *Sargassum* watch system to predict this event, which is vital for field monitoring and management decisions, as well as fisheries, tourism and other related businesses. The system processes diverse data collected from satellite, drone photographs, aerial and cruise survey, numerical model and many local monitors. The results gives people and decision makers timely information on the drifting *Sargassum* location and scale. We issue a *Sargassum* bloom forecast for potential beach event if necessary. Government and agencies associated with this monitoring system do proper actions to cope with incoming drifting *Sargassum* according to the forecast. Fishermen and travelers can use it in their own plans, like a weather forecast. Ecological monitoring has been incorporated in long-term plans for the monitoring system. To manage drifting *Sargassum* bloom will not only require biological and ecological understanding, but will also need to assess their ecological roles and impacts on the coastal ecosystem and fisheries industry. These should provide valuable information to make a management policy for drifting *Sargassum* bloom.

OS_2_02

Current status of macroalgal bloom (golden tides and green tides) in Korea: the magnitude, formation, transport and management

Sang Rul Park[1], Sangil Kim[2], Hyuk Je Lee[3]

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Macroalgal blooms by the genus *Ulva* and *Sargssum* have been reported regularly all over the world. Green tides (massive green algal blooms) is periodically observed along the coasts of Korean. Since 2015, golden tides by excessive masses of floating *Sargassum horneri* biomass have been introduced through via ocean currents and winds to southern coastline of Korea, including Jeju Island. These events can harm tourism-based economies, smother aquaculture operations, disrupt traditional artisanal fisheries or cause the collapse of marine ecosystem. In this study, we investigated distribution, cause of occurrence, biomass and species composition of green tides in Jeju Island from July 2013 to March 2014 in relation to water column nutrients concentrations. Additionally, population dynamics of *S. horneri* were investigated at Munseom, Jeju Island on the southern coast of Korea monthly from November 2017 to November 2018 to predict the extent and formation of golden tides. Three *Ulva* species (*U. pertusa, U. linza* and *U. ohnoi*) were the main species causing green tides in Jeju Island. In particular, subtropical species *U. ohnoi* dominated at bloom sites all year round. Total area covered by *Ulva* mats was approximately 210 ha. It was speculated that around 17,000 wet tonnes of the biomass of *Ulva* mats was produced in Jeju Island annually. Water column NH_4^+ and PO_4^{3-} concentrations at blooms sites were usually less than 2 μM, respectively while $NO_3^- + NO_2^-$ concentrations in the water column was more than 20 μM during the experimental period. This result implies that the growth of green algae is facilitated not by water column NH_4^+ concentrations but by water column $NO_3^- + NO_2^-$ concentrations. At Munseom, the recruitments of *S. horneri* occurred during October-November and the density gradually declined and completely disappeared in July. The thallus height sharply increased during January-April and mortality density was highest in December-January, 2-3 month following the recruitment. During this period, maximum biomass detached from substrates was 1.5 kg wet weight m^{-2}. This indicated that massive mat would be formed by free floating *S. horneri detached from substrates and observed in the East China Sea and Yellow Sea from December-January.*

OS_2_03

‘Golden tide’ seaweeds *Sargassum horneri* in Korean waters: the origin and genetic/genomic comparisons between floating and benthic populations

Seo Yeon Byeon[1], Sangil Kim[2], Suk Hyun Yun[2], Hyun-Ju Oh[2],
Sang Rul Park[3], Hyuk Je Lee[1]

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In recent years, drifting and inundating brown seaweed (*Sargassum horneri*) biomass, called ‘golden tides’, has frequently drifted and accumulated along the southern coastlines of Korea, causing devastating impacts on the local economy and coastal ecosystems. In this study, based on combined analyses of mitochondrial (mt) DNA *cox3* gene and seven microsatellites, we investigated the genetic makeup of the floating *S. horneri* populations (N=14) in comparison to Korean benthic populations (N=5), and tracked their genetic sources. Given a shared mtDNA haplotype and oceanic circulation systems, the floating populations may have been originated from the southeastern coast of China (e.g. Zhoushan, Zhejiang province). Population structure analyses with microsatellites revealed two distinct genetic clusters, each comprising floating and benthic populations. High levels of inter-population differentiation were detected within Korean benthic samples. The floating populations from the same periods during a 2015-2018 year were genetically more different from one another than those from different periods. These results suggest that the floating populations might be of multiple genetic sources within geographic origin(s). Given insufficient variation observed in the mtDNA *cox3*, we further performed a comparative analysis of the whole organelle genomes of a Korean benthic sample with those of a Chinese sample. We successfully mapped a mitochondrial genome of 34,620 bp and a chloroplast genome of 124,068 bp for the Korean benthic sample. We are currently developing molecular markers that can differentiate between floating and Korean benthic populations by exploring those organelle genomes. The results of our study will inform management efforts including the development of “*S. horneri* blooming forecasting system”, which will assist in mitigating ecological and economic damages on the Korean coastal ecosystems in the future.

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OS_2_04

Species diversity of green tide forming macroalgae *Ulva* species in Jeju Island, Korea using DNA-based species delimitation approaches

Ji Hyoun Kang[1], Ji Eun Jang[2], Jae Hwan Kim[2,3], Seo Yeon Byeon[2], Sangil Kim[4], Sun Kyeong Choi[5], Yun Hee Kang[5], Sang Rul Park[5,*], Hyuk Je Lee[2,*]

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Green macroalgal blooming, called “green tide”, has severe detrimental influences on coastal ecosystems. Green tides caused by *Ulva* species have recently occurred more severely and more frequently all over the world, including Korea, due to anthropogenic pressure, such as coastal eutrophication and climate change. However, which species are responsible for such phenomena, and what and how many species comprise the green-tide assemblages on the Korean coast remain largely unexplored. Using molecular analyses we investigated the species composition, diversity, and distribution of the genus *Ulva* along the entire coast of Jeju Island, off the southern tip of Korea. Species identification was performed for 215 samples collected from 23 sites, based on three different phylogenetic analyses using the sequences of two molecular markers, chloroplast elongation factor Tu (*tuf*A) and nuclear internal transcribed spacer (ITS). We identified 193 specimens as *Ulva* species (nine species), 14 as *Blidingia* spp., and 8 we were unable to determine, based on the combined analysis of *tuf*A and ITS phylogenies. Two other species delimitation approaches (ABGD and GMYC) further supported nine groups of *Ulva* species. Previously documented species complex, such as *U. ohnoi* –*U. spinulosa* and *U. procera* –*U. linza* showed discordant relationships between the two phylogenies. The occurrence of *U. torta*- on Jeju Island was first observed, despite its existence on the mainland previously reported. *Ulva australis* [16 of 23 sites; 34.4% (relative frequency)], *U. ohnoi* (16; 21.9%), and *U. procera* (11; 14%) were found to be the predominant species. Our study highlights that molecular analysis is critical for species delimitation in the genus *Ulva* and provides fundamental information for an understanding of green-tide blooming on the “biological hotspot” coastal ecosystem, Jeju Island in Korea. This study will also help to monitor and manage green tides at the areas that are currently encountering rapid climate changes.

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OS_2_05

Satellite monitoring of Green and Golden-tide in the Eastern Yellow Sea

Keunyong Kim, Jisun Shin, Euihyun Kim, Joo-Hyung Ryu

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In the Yellow Sea, macroalgae bloom of Ulva (also called green tide) have been reported since 2008, and macroalgae bloom of Sargassum (also called golden tide) also observed since 2013. Remote sensing is considered to be a very effective method to monitor the distribution, areal extent and migration of floating macroalgae. However, although a number of studies used remote sensing to estimate their spatial distributions and temporal changes, most studies are focused in the western part of the Yellow Sea (YS), very little information is available in the eastern part. Furthermore, the long-term distribution and migration of floating golden tide is unknown. The aim of this study is to clarify the long-term distribution pattern of green and golden tide in the eastern YS. In addition, we want to analyze the drift characteristic of floating macroalgae using remote sensing data. MODIS, GOCI and Landsat images from 2008 to 2017 were used to demonstrate the long-term distribution of floating macroalgae. The hourly images from GOCI were used to demonstrate the drift characteristic of floating macroalgae. Massive green tide was found in the eastern YS for the first time in 2008, and the satellite image traced back shows that it originated from the western YS. Large mass of green-tide found continuously, and its largest scale of any green-tide has been found in 2011. Floating golden tide was found in the eastern YS since 2013, and the bloom area increased annually. From the result of calculating the drifting velocity at 1-hour intervals, the average drifting velocity of green and golden-tide shows 1.54 km h^{-1} and 1.27 km h^{-1}, respectively.

Session 3

Jellyfish blooms in the East Asian Seas

Date & Time : 25 Thu 14:00 - 15:40
Room : Meeting 6

Chair : Dr. Wonduk Yoon
Human & Marine Ecosystem Research Laboratory, Korea

14:00 - 14:20	OS_3_01	**Distribution of polyps of *Aurelia coerulea*: a compelling evidence of anthropogenic causation of the jellyfish blooms** Jinho Chae (Marine Environmental Research and Information Laboratory, Korea)
14:20 - 14:40	OS_3_02	**Genetic structure and diversity of the jellyfish *Aurelia coerulea* in Korean coastal waters** Jang-Seu Ki (Sangmyung University, Korea)
14:40 - 15:00	OS_3_03	**Comparison of density estimates between scientific echosounder and acoustic camera system for moon jellyfish (*Aurelia coerulea*)** Inwoo Han (Chonnam National University, Korea)
15:00 - 15:20	OS_3_04	**Proteomic approach to examine the cardio toxic effects in H9c2 cells and component identification of *Nemopilema nomurai* venom (NnV)** Ramachandran Loganathan Mohan Prakash (Gyeongsang National University, Korea)
15:20 - 15:40	OS_3_05	**Discovery of anti-cancer effect from *Nemopilema nomurai* jellyfish venom on HepG2 cells and tumor xenograft animal model** Euikyung Kim (Gyeongsang National University, Korea)

OS_3_01

Distribution of polyps of *Aurelia coerulea*: a compelling evidence of anthropogenic causation of the jellyfish blooms

Jinho Chae[1,2], ByeongHo Kim[1], Gunhee Sung[1], Changgyun Yu[1],
Kiyeon Hahn[2], Wonduk Yoon[2]

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We located polyp populations of *Aurelia coerulea* and determined their total amount around Korean coast using underwater photographs collected by SCUBA diving. Diving observation has been made approximately in 1,400 sites, finding important (significantly large) polyp populations from more than 500 sites. Downward-facing surface of floating piers, barges in aqua-farm and marina were the most frequently observed habitats of the jellyfish polyps among variety of artificial structure providing polyps' habitat such as concrete dock walls, dike ripraps, submersing pillars of industrial facilities, abandoned fishnet and artificial reefs. Only a polyp population was found in natural habitat, the bedrock of Manjaseo. These results provide compelling evidence that increase of coastal development and construction is the major causation of the jellyfish blooms. To understand to what extent polyp populations of *A. coerulea* contribute to the jellyfish bloom, we simultaneously determined total amount of polyps, ephyrae liberated from those and young medusa with high frequencies in Gamak Bay; Total amount of polyps was estimated from underwater photographs gained from downside surface of 145 floating piers and barges of 645 in total. Strobili formation and ephyrae liberation were photographed every 30 min with six close-up cameras installed underwater for 37 days, and 10,015 shots of photographs were analyzed. Ephyrae liberated from the polyps and young medusa in the water column were collected with a net at 58 stations for 1 - 7 (generally 3) days intervals. Ephyrae started to be liberated below 5 °C, accelerated with temperature increase and continued for 32 days. Total polyps in Gamak Bay before ephyrae occurred were ca. 516 x 10^6 individuals and expected total ephyrae liberated from the polyps were ca. 4,053 x 10^6 individuals. Total number of ephyrae and metephyrae at the peak in the actual water column were ca. 1,136 x 10^6, corresponding to 28.79 % of the expected total numbers liberated. Young medusae were predominant without possible influx from the outside in 23 Apr, and total numbers were ca. 96 x 10^6 individuals. While the abundance of the young medusae was still at bloom level, it corresponded to only 2.44 % of total amount of ephyrae expected to be liberated, suggesting ephyrae are susceptible stage among the jellyfish life cycle.

OS_3_02

Genetic structure and diversity of the jellyfish *Aurelia coerulea* in Korean coastal waters

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[3]Human and Marine Ecosystem Research Laboratory, Gunpo 15850, Korea

The moon jelly *Aurelia* occurred widely coastal waters in Korea and their dense blooms caused economic loss for fisheries and notorious impacts to environments. All of them were identified as *Aurelia coerulea* (=*Aurelia* sp.1) by morphology and molecular basis; however, their population genetic diversity has not been elucidated clearly. In the present study, we used nuclear ITS rDNA, mitochondrial 16S rDNA and COI to study the genetic structure and diversity of *A. coerulea* in Korean coastal waters. Nuclear ITS rDNA sequences revealed very low levels of genetic diversity in Korean *A. coerulea* populations. However, mitochondrial genes showed relatively high genetic diversity, and COI (20 haplotypes) was much greater genetic diversity than 16S (9 haplotypes) in *A. coerulea*. We analyzed polyp specimens collected from 8 Sts. in Goseong Bay, Korea, and found that single genotype (designated H4) was a dominant population. In addition, it was mostly detected from St. 4. These results suggested that *A. coerulea* medusa may originate from polyp beds at St. 4 in Goseong Bay.

OS_3_03

Comparison of Density Estimates between Scientific echosounder and Acoustic camera system for Moon Jellyfish (*Aurelia coerulea*)

Inwoo Han[1], Euna Yoon[2], Wooseok Oh[1], Geunchang Park[1], Kyounghoon Lee[2]

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[2]School of Marine Technology, Chonnam National University, Yeosu 59626, Rep. of Korea

A moon jellyfish (*Aurelia coerulea*) have recently become one of major issues in the Northeast Asia region due to their fatal damage to fishing industry and power plants near to coastal areas. Therefore it becomes important to quantify the jellyfish's density variation in the survey area in order to prevent jellyfish's blooming from various damages in main season. A moon jellyfish, which is estimated to be developing in inshore sea, gives a fatal damage to Korean and Japanese coastal fisheries and the power plants. It needs to estimate its abundance in the survey when it blooms to prevent from a fatal damage. By the acoustic method, It can be extracted echo signals from the echogram using an echo counting method and be also verified its echo signals mixed by other scatterers using a 2 frequency difference method. A moon jellyfish, which is developed in the coastal area, is relatively small size and has intensive patchiness, so an echo integration method would be more useful and effective than an echo counting method. To extract their echo signals, the 2 frequency characteristics were collected and analyzed by 38 and 120kHz on the basis of sizing estimates using an acoustic camera, and it was also estimated the density in south-western coastal area of Korea, and it was compared the density estimated values acquired from 2 systems. Results can be utilized to forecast and reduce the damages caused by jellyfishes and it can be also effectively used to estimate jellyfish's abundance in coastal areas using the scientific echo sounder and the acoustic camera systems.

OS_3_04

Proteomic approach to examine the cardio toxic effects in H9c2 cells and component identification of *Nemopilema nomurai* venom (NnV)

Indu Choudhary[1], Ramachandran Loganathan Mohan Prakash[1], Du Hyeon Hwang[2],
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Nemopilema nomurai is one of the giant jellyfish that blooms in East Asian seas. In recent times, it has been symbolized from toxicological and pharmacological perspective. In our study, we discussed about components identification and cardio toxic effects of *Nemopilema nomurai* venom (NnV) in H9c2 (rat cardiomyocytes). The IC_{50} value of H9c2 cells of NnV is about 3 μg/ml and it showed limited viability at different time intervals (6 & 12 hrs.). The proteomic analysis of differentially abundant proteins in H9C2 cells and the cardiac protein regulations were identified in 2D gel electrophoresis followed by (matrix-assisted laser desorption/ionization time of flight mass spectrometry) MALDI-TOF and western blotting respectively. The proteomic results revealed that, totally 34 proteins were identified; 25 proteins with amplified abundance and 9 proteins were reduced abundance. The proteomic analysis were validated by western blotting in H9C2 cells treated with NnV. The protein blot results confessed that calumelin, annexin, SOCS1 and aldose reductase were upregulated in NnV treated H9C2 cells in a time dependent manner. The other objective of identifying the components in NnV were also performed as a next step. The components of NnV has been validated by 2D gel electrophoresis followed by MALDI-TOF and 150 proteins were identified. The analysis of 2D gels were done by progenesis same spots software. Henceforth, our study deals about the components identification and also the cardio toxic effects of NnV.

OS_3_05

Discovery of anti-cancer effect from *Nemopilema nomurai* jellyfish venom on HepG2 cells and tumor xenograft animal model

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Various kinds of animal venoms and their components have been widely studied for potential therapeutic applications. This study was evaluated whether *Nemopilema nomurai* jellyfish venom (NnV) potentiates anti-cancer activity. Among several cancer cells, NnV strongly induced cytotoxicity of HepG2 cells through apoptotic cell death, demonstrated by alteration of chromatic morphology, activation of procaspase-3 and increasing Bax/Bcl-2 ratio. Furthermore, NnV inhibited the phosphorylations of PI3K, PDK1, Akt, mTOR, p70S6K and 4EBP1, whereas enhanced the expression of p-PTEN. Interestingly, NnV also inactivated negative feedback loops of Akt activation demonstrated as down-regulation of Akt at Ser473 and mTOR at Ser2481. The anti-cancer effect of NnV was significantly distinct in HepG2 xenogragft mice model with no obvious toxicity. As a result of purification using DEAE ion exchange chromatography, metalloprotease in NnV is closely related with anti-cancer effect in HepG2 cells. Therefore, this study demonstrate, for the first time, NnV exerts highly selective cytotoxicity in HepG2 cells via dual inhibition of Akt and mTOR signaling pathways, but not in normal cells.

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Session 4

Entomological research on harmful organisms in agriculture and vector-borne disease

Date & Time : 25 Thu 11:00 - 13:30
Room : Meeting 8

Chair : Dr. Doo-Hyung Lee
Gachon University, Korea

11:00 - 11:10		**Introductory remark**
11:10 - 11:40	OS_4_01	**The bean bug *Riptortus pedestris* and its *Burkholderia* symbiont** Yoshitomo Kikuchi (AIST, Japan)_Invited speaker
11:40 - 12:00	OS_4_02	**Abundance and diversity of gut-symbiotic Bacteria, the genus *Burkholderia* in overwintering *Riptortus pedestris* populations and soil in South Korea** Minhyung Jung (Gachon University, Korea)
12:00 - 12:20	OS_4_03	**Investigating different patterns of plant virus spread respective to type of plant viruses using an individual based model** Jung-Wook Kho (Gachon University, Korea)
12:20 - 12:40	OS_4_04	**Development of species distribution model for migratory insect pests under climate change scenario** Jung-Joon Park (Gyeongsang National University, Korea)
12:40 - 13:00	OS_4_05	**Survey of ticks based on epidemiological investigation of severe fever with thrombocytopenia syndrome (SFTS) patients in South Korea** Jong Yul Roh (Korea Center for Disease Control and Prevention, Korea)
13:00 - 13:20	OS_4_06	**Regulation of osmoregulatory organ in hard ticks** Donghun Kim (Kyungpook National University, Korea)
13:20 - 13:30		**Closing remark**

OS_4_01

The bean bug *Riptortus pedestris* and its *Burkholderia* symbiont

Yoshitomo Kikuchi[1]

[1]Bioprocess Institute, AIST, Japan

A number of animals and plants possess symbiotic microorganisms inside their body, wherein intimate interactions occur between the partners. Owing to technological advancement and a growing body of recent studies, now we know the general importance of microbial symbiosis in the organismal evolution. Insects, which feed exclusively on nutritionally-poor food sources, such as plant sap, vertebrate blood, or woody materials, commonly harbor endosymbiotic microorganisms inside the gut lumen, body cavity, and/or specific cells called bacteriocytes. These symbionts are known to be important for host survival, whereas molecular mechanisms underpinning symbiotic interactions remain poorly understood, because many insect-microbe symbioses are not easily accessible for functional analyses. The bean bug *Riptortus pedestris*, a notorious pest of leguminous crops in East Asia, develops symbiotic crypts in a posterior region of the midgut, wherein specific bacterial symbionts of the genus *Burkholderia* populate densely. Unlike previously well-studied insect symbionts, the *Burkholderia* symbiont is easily culturable and genetically manipulatable. In addition, the insect is amenable to reverse genetic techniques like RNAi. These features of the *Riptortus-Burkholderia* model system provide an unprecedented opportunity to elucidate the molecular basis of insect-microbe symbioses. In this presentation, I review recent findings in the *Riptortus-Burkholderia* model system, mainly focusing on the molecular basis underpinning the host-symbiont specificity.

OS_4_02

Abundance and Diversity of Gut-symbiotic Bacteria, the genus *Burkholderia* in Overwintering *Riptortus pedestris* Populations and Soil in South Korea

Minhyung Jung, Jung-Wook Kho, Soowan Kim, Donghyun Lim and Doo-Hyung Lee*

[1]Department of Life Sciences, Gachon University, Seongnam-si, 13120, South Korea

Riptortus pedestris (Hemiptera: Alydidae) is a major agricultural pest on leguminous plants in South Korea and Japan. Recent studies have revealed that *R. pedestris* can form facultative insect-microbe symbiosis with bacteria belonging to genus *Burkholderia* acquired from soil newly for every generation. Although their physiological interactions are relatively well-understood, field infection rate of *Burkholderia* in *R. pedestris* and abundance of the *Burkholderia* in natural conditions remain unknown. Therefore, the objective of this study was to characterize *Burkholderia* infection dynamics of overwintering *R. pedestris* populations as well as prevalence and diversity of the genus *Burkholderia* in soil by conducting a two-year field survey. From the field survey, we found 29 overwintering *R. pedestris* adults in forested areas nearby soybean fields. Diagnostic PCR analysis revealed that overall infection rate of the symbiotic *Burkholderia* was 93.1 % from overwintering adults. Among the Burkholderia-infected *R. pedestris*, 70.4 % of individuals harbored unclassified *Burkholderia* clades whereas 22.2 % and 7.4 % of *R. pedestris* harbor stinkbug-associated beneficial and environmental (SBE) group and *Burkholderia cepacia* and complex (BCC), respectively. All *R. pedestris* were infected with a single clade of *Burkholderia*. In soil, 56.2 % of soil samples harbored *Burkholderia*, and unlike *R. pedestris*, 62.2 % of the samples were infected with multiple *Burkholderia* clades. Clade composition of the genus Burkholderia in the samples with the bacteria was 91.1 %, 60.0 %, 31.1 % and 8.8 % for plant-associated beneficial and environment (PBE), BCC, SBE and unclassified clade, respectively. Our study can serve as basis to improve pest management against *R. pedestris* by characterizing risk levels of pest populations based on the size of overwintering populations and their symbiont-associated fitness levels.

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OS_4_03

Investigating different patterns of plant virus spread respective to type of plant viruses using an individual based model

Jung-Wook Kho[1], Joo-Young Kim[1], Hyunsung Song[1], Doo-Hyung Lee[1]

[1]Department of Life Sciences, Gachon University, Seongnam 13120, S. Korea

In our study, to look into how different types of plant viruses, non-persistent virus (NPV) and persistent virus (PV) differ in their spread pattern with respective to distinct effects they have on the host plant and insect vectors, we built a spatially-explicit individual-based model. Our probability-based model considered how biological traits of insect vectors including longevity and reproduction and behavioral factors such as interplant movement and feeding are affected by plant virus infection and nutrition status of host plant an individual level and estimated how local spread of plant virus is shaped at a population level. Especially, we mainly focused on 1) how NPV and PV differ in their spread when they are singularly present in a crop field (singular infection scenario), 2) how NPV and PV spread when they are both present in a field (multiple infection scenario) while infecting either same host plants (mixed-infection condition) or separate host (co-habitation condition), and 3) how singular infection scenario is compared to multiple infection scenarios. In case of singular infection, PV resulted in a more severe damage to the crops, spreading faster and forming a larger aggregated patch. Similar results were observed in multiple infection scenarios, where PV-infection dominated the crop field in both mixed-infection and co-habitation conditions. Finally, when comparing singular infection scenario with multiple infection scenarios, spread of PV was rarely affected by presence of NPV, yielding similar number of PV-infected host plants. On the other hand, in mixed-infection condition, less number of NPV-infected host plants was observed compared to scenario with singular infection of NPV, suggesting potential interaction of the two plant viruses. To conclude, the results of our model address how different interactions affect transmission of plant viruses shape the overall spread, which can be critical in formulating an effective virus management program.

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OS_4_04

Development of species distribution model for migratory insect pests under climate change scenario

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Gyeongsang National University

Migratory insect pest populations migrate from southern China to Korea through jet streams. In Korea, three migratory planthoppers are important in relation to damage to the major crop, rice: *Nilaparvata lugens*, *Sogatella furcifera* and *Laodelphax striatellus*. Sampling insect pest population is often a necessary component of a proposed pest management strategy. Insect populations are poikilothermic animal and readily applied to model systems in several ways. When insect population intrude into new possible habitats, they should be related with biotic and abiotic environments for survive and settle down. Based on climate change scenario, invasive insect species would be overcome its geographical limitation as well as local distribution of well-known species should be changed in near future. In this study, species distribution model of migratory insect pests were developed, compared and discussed sampling and management strategies for migratory insect pests under climate change scenario.

OS_4_05

Survey of ticks based on epidemiological investigation of severe fever with thrombocytopenia syndrome (SFTS) patients in South Korea

Seong Yoon Kim, Bong Goo Song, Hyung Woo Lim, Tae-Kyu Kim, Hee Il Lee,
Shin-Hyeong Cho, Jong Yul Roh

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The tick survey based on the epidemiological investigation of SFTS patients was performed to find encounter/contact environments between patients and ticks. The predictable environments were categorized 3 groups as flatland, mountain-side hill and mountain according to their characteristics of landform. The category of survey area was divided by 13 sub-categories according to their status and usage (such as residence, family garden, field, paddy field and so on). In 2018, we surveyed ticks and their SFTS virus at 74 environments of 20 SFTS case regions including Jeju islands. Prior to tick survey, through analysis of the epidemiological researches and interviews, mountain-side hill (n=47) was pointed out most visiting place by patients (in detail, grassland, field and family garden in mountain side hill). We compared the tick density (flag index) at each environment and investigated SFTS virus in ticks. A total of 8,344 ticks were collected by flaggings and dry-ice bait traps. *Haemaphysalis longicornis* (Asian tick) was predominant species as 95.9% and nymphal stage ticks were collected by 74.4%. Tick density (flag index) at mountain-side hill (6.2) was higher than those at flatland (1.7) and mountain (0.9). In detail, at grassland (17.0) and residence (9.8) of mountain-side hill and copse (4.7) of flatland were higher than other environments. In the view of plant traits, tick density was higher at ankle high-plants and at bracken inhabitation. The existence of sheds and grazing livestock increased tick density but weeding and chemical controlling decreased. In conclusion, the results suggested that a typical environment at which SFTS patients encounter ticks might be an ankle height grassland of mountain-side hill. Tick controls including weeding on restricted area might be effective to decrease tick population and designate 'tick safety zone'.

OS_4_06

Regulation of osmoregulatory organ in hard ticks

Donghun Kim[1]

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Ticks are obligatory hematophagous ectoparasites, which can transmit various pathogens including bacteria, protozoa, and viruses via salivary secretion during feeding. Dopamine is known to be the most potent molecule for tick salivary secretion during blood feeding. Two dopamine receptors were recently characterized in tick salivary glands: dopamine receptor (D1) and invertebrate specific D1-like dopamine receptor (InvD1L). Dopamine's action controlls the salivary glands by two distinct physiological actions: 1) inward fluid transport into the lumen of salivary glands acini via D1 receptor, 2) emptying lumen solute into salivary duct by pumping and gating via InvD1L. Between blood feeding, ticks can survive long period of time without blood feeding because of their highly developed osmoregulatory mechanisms. Off host ticks can maintain water balance by obtaining atmospheric water vapor via salivary glands. Understanding osmoregulation in ticks is crucial for the development of novel methods to prevent tick-borne disease transmission.

Session 5

(41th Yonsei Tropical Medicine Symposium) Harmful organism of medical importance

Date & Time : 25 Thu 16:00 - 18:00
Room : Meeting 6

Chair : Prof. Tai-Soon Yong
Department of Environmental Medical Biology, Institute of Tropical Medicine,
Yonsei University College of Medicine, Korea

16:00 - 16:20	OS_5_01	***Acanthamoeba*** **spp. in Korea** Hyun-Hee Kong (Donga University College of Medicine, Korea)
16:20 - 16:40	OS_5_02	**The mechanism of inflammation via degranulation of human mast cells induced by *Trichomonas vaginalis*-derived LTB4** Arim Min (Yonsei University College of Medicine, Korea)
16:40 - 17:00	OS_5_03	**Introduction of *Acanthamoeba* as a new allergen** Hak Sun Yu (Pusan National University, Korea)
17:00 - 17:20	OS_5_04	**Factors underlying the spread of *Echinococcosis* in Central Asia** Zafar Sadikov Yusufovich (Isaev Research Institute of Medical Parasitology, Uzbekistan)
17:20 - 17:40	OS_5_05	**Species diversity of mosquito-carriers *leishmaniasis* in the modern ecosystem of Uzbekistan** Olesya Achilova Djurabayevna (Isaev Research Institute of Medical Parasitology, Uzbekistan)
17:40 - 18:00	OS_5_06	**Allergy related intestinal microbiome profiling from house dust mite using next generation sequencing** Ju Yeong Kim (Yonsei University College of Medicine, Korea)

OS_5_01

Acanthamoeba spp. in Korea

Hyun-Hee Kong[1]

[1]Department of Parasitology, Donga University College of Medicine

The genus *Acanthamoeba*, one of the amphizoic protozoa has ubiquitous distribution in the human environment. Some species of the amoeba can cause sight-threatening keratitis or life-threatening granulomatous encephalitis. In Korea, 2 strains of *Acanthamoeba*, YM-2 and YM-3, were first isolated from the environment in 1974. However, phylogenetic identification of Korean *Acanthamoeba* isolates from human infections or the environment were tried from the late 1990s. The isolates of *Acanthamoeba* from soil, contact lens storage cases, and infected eye in korea were subjected to 18s rDNA analysis for species identification. First of all, the phylogenetic tree based on comparison of 18s rDNA sequences among reference species distinguished the 3 morphological groups of *Acanthamoeba* and divided them into 12 unique sequence types (T1-T12 genotypes). Most clinical and environmental isolates from Korea belonged to the morphological group II and the genotype T4. Sequence analysis of 18s rDNA revealed that almost clinical isolates including the one from a suspicious granulomatous amebic encephalitis patient belonged to the genotype T4. A large number of environmental isolates from contact lens storage cases, tapped water, and ocean sediments also belonged to the genotype T4. Almost identical strain characteristics, such as Mt DNA RFLP pattern of environmental isolates, with the clinical isolates could make a simple conclusion that most environmental isolates might be a potential *keratopathogen*.

OS_5_02

The mechanism of inflammation via degranulation of human mast cells induced by *Trichomonas vaginalis*-derived LTB4

Arim Min, Myeong Heon Shin

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Trichomonas vaginalis is a sexually transmitted parasite that causes vaginitis in women and itself secretes lipid mediator LTB_4. Mast cells are important effector cells of tissue inflammation during infection with parasites. Membrane-bridging SNARE (Soluble N-ethylmaleimide-sensitive factor attachment protein (SNAP) receptors) complexes are critical for fusion during exocytosis. Although *T. vaginalis*-derived secretory products (TvSP) have been shown to induce exocytosis in mast cells, information regarding the signaling mechanisms between mast cell activation and TvSP is limited. Herein, we found that stimulation with TvSP induced exocytotic in human mast cells via BLT1 receptor. TvSP induced trafficking of BLT1 from the cytosol to the plasma membrane. Next, we found that knockdown of SNAP23 abrogated TvSP-induced exocytosis and surface trafficking of BLT1 in HMC-1 cells. Indeed, there was a physical interaction between BLT1 and SNAP23 by co-IP assay, suggesting that there may be a crosstalk between BLT1 and SNAP23 in TvSP-stimulated HMC-1 cells. Our data collectively demonstrate a novel regulatory mechanism for SNAP23-dependent mast cell activation to *T. vaginalis*-secreted LTB_4 involving surface trafficking of BLT1. These results can help to explain how the cross talk mechanism between parasite and host can govern deliberately tissue inflammatory responses.

OS_5_03

Introduction of *Acanthamoeba* as a new allergen

Hak Sun YU

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We introduce a new allergen, .*Acanthamoeba* which is a free-living amoeba commonly present in the environment and often found in human airway cavities. In order to check the aeroallergenicity of *Acanthamoeba,* we repeatedly inoculated mice with *Acanthamoeba* trophozoites or excretory-secretory (ES) proteins intra-nasally and evaluated symptoms and airway immune responses. *Acanthamoeba* trophozoites or ES proteins elicited immune responses in mice that resembled allergic airway inflammation. ES proteins had strong protease activity and activated the expression of several chemokine genes (CCL11, CCL17, CCL22, TSLP, and IL-25) in mouse lung epithelial cells. ES proteins also stimulated dendritic cells and enhanced the differentiation of naive T cells into IL-4-secreting T cells. Furthermore, asthma patients had higher *Acanthamoeba*-specific IgE titers than healthy controls. Additionally, patients with common antibodies reacted to the 13–15 kDa *Acanthamoeba* unknown allergen. We examined whether profilin of *Acanthamoeba* is a human airway allergic agent because of its molecular weight. We expressed recombinant Ac-PF (rAc-PF) protein using an *Escherichia coli* expression system and evaluated whether Ac-PF is an airway allergic agent using an allergic airway inflammation animal model. Airway hyperresponsiveness was increased in rAc-PF-inoculated mice. The number of eosinophils and levels of Th2 cytokines, interleukin (IL)-4, IL-5, and IL-13 were increased in the bronchial alveolar lavage fluid of rAc-PF-treated mice. Our findings suggest that *Acanthamoeba* elicits allergic airway symptoms in mice via a protease allergen, and the rAc-PF may be one of the allergens in *Acanthamoeba.*

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OS_5_04

Factors underlying the spread of Echinococcosis in Central Asia

Zafar Sadikov Yusufovich[1], Tai-Soon Yong[2], Hak Sun Yu[3],
Uktamjon Suvonkulov Toirovich[1], Sattarova Khulkar Gayratovna[1]

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Within the framework of the project for the study of echinococcosis in Samarkand region (Republic of Uzbekistan), which was conducted by the scientists of Isaev Research Institute of Medical Parasitology, together with Samarkand State Medical Institute and the Veterinary Research Institute, in collaboration with leading professors of Yonsei University and under the support of KOICA, studies have been carried out and main local epidemiological aspects were established. Genotyping of *Echinococcus granulosus (EG)* from humans' cystic fluids showed that G1, G2, G3 strains are common in Uzbekistan, and strain G5 is less found. Initially, the fact of human infection with G4 genotype (*E. equinus*), which until now was considered as an atypical for humans, was revealed. Investigation of family dogs showed that 8 out of 471 pets were infected by EG. Parasitological study of wild animals (foxes, jackals) and stray dogs showed the presence of EG tapeworms in 4 cases out of 31. Soil investigation on the territory of residential yards, farms, orchards, crop fields, pastures showed contamination (5 samples of 110) with eggs. In addition, uncontrolled cattle slaughtering also serves as one of crucial factors of spreading EG. A study among the population revealed slight knowledge of echinococcosis and was only about 5%.

Thus, the problem of echinococcosis is complex and requires the involvement of many organizations in the fight against this disease: practical public health services, sanitary and epidemiological services, veterinary services.

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OS_5_05

Species diversity of mosquito-carriers leishmaniasis in the modern ecosystem of Uzbekistan

Olesya Achilova Djurabayevna[1], Tai-SoonYong[2], Uktamjon Suvonkulov Toirovich[1], Timur Muratov Ibragimovich[1], Gafur Usarov Xusanovich[1]

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Uzbekistan is an endemic territory regarding leishmaniasis. There are two types of leishmaniasis in the republic: visceral leishmaniasis (the pathogen - *Leishmania infantum*), cutaneous leishmaniasis (*Leishmania tropica and Leishmania major*). There are 12 species of mosquitoes on the territory of Uzbekistan, which belong to two genera - *Phlebotomus* and *Sergentomie*.

Since 1960s to the middle of 1990s was conducted extensive defoliation of agricultural fields on the territory of Uzbekistan which contributed to reducing the number of mosquitoes. However, after cessation of wide application of insecticides, number of mosquitoes began to increase and number of patients with leishmaniasis rose correspondingly among the population.

Data obtained by our institute, considering climate change from 1988 to 2018, showed that mosquito population increased significantly. Thus population of Ph. papatasi increased 3.5 times, Ph. caucasicus - 2.8 and Ph. sergenti - 5.5. Since 2010, annual monitoring of the species and population of mosquitoes is conducting in the Isaev Research Institute of Medical Parasitology. Molecular biological methods (PCR) in foci of zoonotic cutaneous leishmaniasis (Mubarek district) identified, besides *Leishmania major*, previously unregistered in this area *Leishmania tropica* and entomological studies revealed the prevalence of *Phlebotomus sergenti*.

Changes in agriculture sector, climate change, have affected to increase in population and changes in species of mosquitoes. Studies show an increased risk of the incidence of leishmaniasis in areas where this disease has been previously forgotten. Regularly entomological monitoring, implementation of molecular diagnostics and predictive model of morbidity is important and relevant.

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OS_5_06

Potential immunomodulatory effect of the house dust mite microbiome

Ju Yeong Kim[1,2], Myung-hee Yi[1], Jinyoung Lee[1], In-Yong Lee[1], Tai-Soon Yong[1]

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Background

The HDM microbiome might have an immunomodulatory role in allergic diseases owing to its ability to generate microbial-associated molecules, such as lipopolysaccharides and lipoteichoic acid. In this study, a 16S rRNA amplicon analysis using high-throughput sequencing technology was performed to determine the microbiome of *Dermatophagoides farinae*.

Methods

Mites were cultivated for 6 weeks with or without ampicillin powder. 16S rRNA amplicon (V3_V4) analysis using high-throughput sequencing technology was performed with Miseq (Illumina). 16S rRNA cloning, bacterial culture of mite homogenates, and several stains were performed.

Result

Over 99% of reads were assigned to *Bartonella* and *Enterococcus*. This finding was supported by 16S rRNA cloning, culture of mite homogenates. *Enterococcus faecalis* were distributed throughout the intestine of *D. farinae* and were densely gathered in the stool at the hindgut region. *Bartonella* spp. were detected in the hemocoel. Antibiotics were applied to the mites to determine if the microbiome of them affects the allergy induction. The amount of total bacteria and the endotoxin concentration in mites were reduced. However, allergen (Der f1) concentration was not changed by antibiotics treatment. When the extract of antibiotics-treated mites was administered to the human bronchial epithelial cell line (BEAS-2B), the secretion of IL-6 and IL-8 was significantly decreased.

Conclusion

We found that *Enterococcus* and *Bartonella* are the core microbiome of *D. farinae* and that a change in the microbiome could affect the ability of the mite to induce allergic diseases.

Session 6

Ecological, economic and human health impacts of invasive alien plants

Date & Time : 26 Fri 10:30 - 13:00
Room : Meeting 6

Chair : Prof. Sun-Hee Hong
Hankyong National University, Korea

10:30 - 11:00	OS_6_01	**Prioritizing weeds as targets for biological control: a consultative and transparent framework for investing limited resources for weed management** Raghu Sathamurthy (CSIRO, Australia)_**Invited speaker**
11:00 - 11:30	OS_6_02	**Predicting non-target attacks of biological control in invasive plant management: Insect host recognition** Ikju Park (New Mexico State University, USA)_Invited speaker
11:30 - 12:00	OS_6_03	**Plant Growth Inhibition by Natural Chemicals from Native and Alien Plants in Korea** Songmun Kim (Kangwon National University, Korea)
12:00 - 12:30	OS_6_04	**Physical control technology based on soil-stored seedbank management of invasive alien species.** Sun Hee Hong (Hankyong National University, Korea)

OS_6_01

Prioritizing weeds as targets for biological control: a consultative and transparent framework for investing limited resources for weed management

S. Raghu[1,2], Matthew Purcell[1,2], Louise Morin[1]

[1]CSIRO, Health & Biosecurity, Australia
[2]USDA-ARS Australian Biological Control Laboratory, Australia

Invasive weeds represent significant threats and costs to production (rangelands, croplands) and natural landscapes. Classical biological control programs can yield substantial benefits in the management of invasive weeds and historical programs have high benefit-cost ratios. However, these programs are typically long-term investments with significant up-front costs to develop safe agents, the efficacy of which can be uncertain. Given that resources to manage weeds in any jurisdiction are often limited, there is a need to better prioritize weed targets for biological control to facilitate their management in the most cost-effective manner possible. Improving on previous prioritization processes developed and applied for weed classical biological control, we have developed a two-stage, structured framework that achieves this in a consultative and transparent manner. The first stage elicits, captures and characterizes the relative importance of a weed, its impacts and desirable management goals. This stage captures the knowledge of weed scientists and land managers to ensure that those investigating and managing impacts on the ground arrive at a list of weeds for which biological control may be desirable. The second stage subsequently assesses the feasibility of biological control and the likelihood of achieving the desired management goals for these weeds. This stage takes advantage of the collective experience of biological control scientists and practitioners to classify the prospects of biological control contributing to successfully achieving the management goals. Using examples from our recent work undertaken on prioritizing weeds of both natural and agricultural systems in Australia and the USA, we illustrate the strengths and utility of this approach.

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OS_6_02

Predicting non-target attacks of biological control in invasive plant management: Insect host recognition

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One of the main criticisms of classical biological control is that biological control agents cannot be recalled once they are released in nature. While more than 99% of released biological control agents do not impact native plant populations, direct non-target attacks on native plants still raise potential concerns in classical biological weed control programs. Since insects exploit signals produced from plants before landing on them for sustained feeding and oviposition, examining the signals used by insects may enhance the prediction of potential non-target attacks by both potential and released biological control agents on native plants. Two different study systems were investigated from the United States: the potential biological control agent (*Mogulones borraginis* F.) for houndstongue (*Cynoglossum officinale* L.) and the released biological control agent (*Rhinocyllus conicus* Frölich) for musk thistle (*Carduus nutans* L.). To investigate the foraging behavior of female weevils, volatile organic compounds (VOCs) emitted from invasive plants and native threatened plants were examined using a dynamic headspace volatile collection system and gas chromatography-mass spectrometry. Both weevils reacted to electrophysiologically active VOCs in electrophysiological experiments. In behavioral bioassays, *M. borraginis* distinguished *C. officinale* from native threatened plants while *R. conicus* did not differ between *C. nutans* and a native threatened plant. It is consistent with the results of pre-release host specificity tests of *M. borraginis in-situ* and non-target attacks of *R. conicus in-situ* and *ex-situ*. Therefore, investigating signals during the initial host recognition of potential and released biological control agents may open new opportunities to reduce non-target attacks on native plants for invasive plant management.

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OS_6_03

Plant Growth Inhibition by Natural Chemicals from Native and Alien Plants in Korea

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Allelopathy is the growth inhibitory effect of one plant on another through the production of chemicals that are released into the environment. The allelopathy is important to understand the crop and weed competition in agricultural environment where weeds are one of the major problems causing enormous losses in crop yields. A total of 900 native and alien plants were collected in Korea based on random, ethnobotanical and biochemical knowledge. To screen the allelopathic activity, the methanol extracts obtained from these plants were used against the seedling growth of *Brassica napus* L. (rapeseed) and determined their GR_{50} values. Compounds with the potent allelopathic activity were isolated by using bioassay-guided isolation and identified using GC-MS, ^{1}H-NMR and ^{13}C-NMR. Among 900 plants, GR_{50} values of *Asarum sieboldii*, *Epimedium koreanum*, *Pulsatilla koreana*, *Rumex acetosella*, and *Rumex crispus* were < 1,000 microgram per gram extract. Elemicin and asarone from *Asarum sieboldii*, methyl-p-hydroxybenzoate from *Epimedium koreanum*, anemonin and 5,6,7-trimethoxycoumarin from *Pulsatilla koreana*, chrysophanic acid from *Rumex acetosella*, and angelicin from *Rumex crispus* were identified as effective allelopathic compounds. In these, chrysophanic acid from *Rumex acetosella* showed a strong plant growth-inhibiting activity under greenhouse as well as field conditions. These allelopathic compounds could be used as natural herbicides for the management of weeds in the production of crops.

OS_6_04

Physical control technology based on soil-stored seedbank management of invasive alien species

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The invasive alien species(IAS) greatly lowers local biodiversity. In general, physical control techniques are particularly effective at the beginning of the invasion. However, it is impossible or very difficult to control them by physical control if the populations of invading species are large and reach the dominant stage. Therefore, it is known that the application of biological control is effective in this case. In the meantime, we have focused on the removal of above-aerial part of IAS. In addition, there was virtually no way to manage underground parts(seeds, roots, etc.). Thus, it was difficult to expect the effects of physical control if seeds rain were not effectively prevented. Therefore, this study aims to analyze the ratio and amount of seeds in the soil between the dominant and the non-dominant ragweed(*Ambrosia artemisiifolia*), which are exotic weeds in Korea, and propose some methods to control physically them effectively.

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Session 7

Waste to resources: Emergent materials for environmental applications

Date & Time : 26 Fri 11:00 - 13:00
Room : Meeting 8

Chair : Prof. Yong Sik Ok
Korea University, Korea

11:00 - 11:20		**Special Session_SCI paper**
11:20 - 11:45	OS_7_01	**Evaluation of Potential Environmental Risks of Waste Compounds Using Ecotoxicological Tests** Felizitas Boie (University of Wuppertal, Germany) **_Invited speaker**
11:45 - 12:10	OS_7_02	**Biochar as a Sustainable Adsorbent for Capturing Carbon Dioxide: A Critical Review** D.M.P.D. Dissanayake (Korea University, Korea)
12:10 - 12:35	OS_7_03	**Biochar Mediated Soil Microbial Community Change in Soils: A Review** Kumuduni Niroshika Palansooriya (Korea University, Korea)
12:35 - 13:00	OS_7_04	**Cost of 'Recycle'** Hyoungwoo Benny Kim (Feople, Korea)

OS_7_01

Evaluation of Potential Environmental Risks of Waste Compounds Using Ecotoxicological Tests

Felizitas Boie[1], Lisa Duchscherer[1] and Jörg Rinklebe[1]

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Increasing awareness of environmental pollution and shortage of resources leads to enhanced processing and re-use of waste materials in waste-to-resource or waste-to-energy pathways as well as the application of solid wastes as biochar for soil fertility or decontamination/contaminant-binding. Beside these application possibilities the question of environmental health issues due to toxic waste compounds, especially on soil biota and aqueous organisms, is not yet fully answered. Accordingly, for future engineers dealing with industrial or municipal waste materials it is essential to consider possible impacts on terrestrial and aqueous ecosystems. During a lab rotation project several engineering students from the University of Wuppertal performed ecotoxicological tests to examine the avoidance behaviour of earthworms due to cadmium (Cd) sulfate and the effect of dichlorophenol (DCP), a compound in herbicides, on the globally spread water plant *Lemna minor*. The earthworm avoidance test was performed with *Eisenia Hortensis* in a vessel with uncontaminated soil (control) and Cd-contaminated soil in increasing concentrations. After three days the vessels were checked for how many earthworms avoided the contaminated soil and actively moved to the control soil. An avoidance of 80 % declares a limitation of the habitat function. The avoidance test, being a sensitive indicator in many former toxicity studies, gave no clear results considering the hypothesis of increasing avoidance with increasing contaminant concentration. The ecotoxicological test with Lemna minor focused on the growth rate repression considering the weight, the leaf size and the chlorophyll content due to an increasing dichlorophenol concentration. With increasing concentration of DCP the growth rate of *Lemna minor* decreased in comparison to the control sample, except for the lowest DCP-concentration which could be explained by repression of a resource-competing fungi.

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OS_7_02

Biochar as a Sustainable Adsorbent for Capturing Carbon Dioxide: A Critical Review

D.M.P.D. Dissanayake[1], Yong Sik Ok[1,*]

[1]Korea Biochar Research Center, O-Jeong Eco-Resilience Institute (OJERI) & Division of Environmental Science and Ecological Engineering, Korea University, Seoul, Korea

At present global warming has become a major concern due to its tremendous negative impacts for terrestrial ecosystems. Carbon dioxide is considered as the main contributor for global warming. Therefore, development of carbon dioxide capturing technologies for combating global warming has gained more attention among the scientific community. Even though several technologies have been adopted for capturing CO_2, they have several drawbacks such as use of high energy, release of hazardous byproducts and high cost. Biochar, a porous carbonaceous material produced through thermochemical conversion of organic materials, might be a cost effective, less energy consuming and sustainable tool for capturing CO_2. Feedstock type, production conditions and biochar properties may play a vital role in CO_2 adsorption. At present, engineered/ designer biochar is produced with different surface properties and novel structures which can also be used to enhance CO_2 capturing capacity. This review summarizes and evaluates the potential of using pristine and engineered biochar as a CO_2 capturing strategy, factors influencing CO_2 adsorption capacity of biochar and current challenges against practical applications of biochar based CO_2 adsorbents. However, further studies should be conducted to develop cost effective and sustainable biochar-based composites for capturing CO_2 in large scale.

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OS_7_03

Biochar Mediated Soil Microbial Community Change in Soils: A Review

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Biochar exhibits a range of physicochemical properties depending on the type of feedstock, pyrolysis condition, and modification technique, such as activation. Application of biochar to soils changes soil physicochemical properties and stimulates the activities of soil microorganisms that influence soil quality and plant performance. Studying the response of soil microbial communities in biochar amended soils is important for better understanding their interactions with soil as well as plants. However, the influences of biochar on soil microorganisms have received less attention than its effects on soil physicochemical properties. In this review, the effects of biochar on soil microbial activities, in particular soil carbon mineralization, nutrient cycling, enzyme activities as well as microbial response in biochar amended contaminated soil are discussed. Many studies have shown that application of biochar enhances the microbial biomass with substantial changes in microbial community composition. Changes in microbial habitats, direct or indirect effects on microbial metabolic activities lead to modify the soil microbial community structure in terms of activity, diversity and abundance in biochar amended soils. However, chemical properties of biochar, especially pH and nutrient content, and physical properties such as porous structure and surface area play significant roles in determining efficacy of biochar on microbial performance. The mode of action of biochar leading to stimulate of microorganisms is complex being influenced by the nature of biochar as well as the soil type.

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OS_7_04

Cost of ‘Recycle’

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Worldwide, remodeling market in architecture and Interior, including new build, is getting bigger. As, especially, people in China and India caring of the quality of their daily life, it becomes one of the most fast-growing market. It is simply believed that the world would be better place than before, if people are willing to improve their town and home and to concern more about the quality of the life. Truth, however, is not. Whenever a new building or a new fancy cafe emerges in a town, almost same height of waste from construction site has been buried on the ground. Almost all scrapped parts from old building and interior decoration have been called ‘industrial waste’, not recycled, but dumped. It becomes quite crucial matters for countries with small land surface, and it becomes diplomatic matter between governments ex) Chinese government refused to import waste plastics from other countries including South Korea 2018. And the government decision shook fast-food market in South Korea as chain reaction.

‘Recycle’ dose not only, mean to use high-recycle-rate products. We’ve watched how the most recyclable material, plastic, polluted our ocean. It is more related to ’process’. And the process of recycling is costly. The labour costs to classify wastes are major expenses of recycling process. As inflation of labour costs in many countries, the wastes are put into containers and sent to the third world countries, where labour costs are low. The products that are reproduced as usually handled as second class on market, like paper pipes for roll toilet papers, even though its costly reproducing process. Errors occur because we sell expensive goods too cheap. In this sense, it is necessary to review the current recycling policy of each business group and governments.

Session 8

Application of Integrated Mosquito Management (IMM) in South Korea and southeast Asia

Date & Time : 25 Thu 14:00 - 16:30
Room : Meeting 8

Chair : Prof. Yeon Jae Bae
Korea University, Korea

14:00 - 14:30	OS_8_01	**Past, Present and Future of Mosquito Control Project in Chiang Mai, Thailand** Chitchol Phalaraksh (Chiang Mai University, Thailand)
14:30 - 15:00	OS_8_02	**Dengue vectors in Vietnam and their control approaches** Van Vinh Nguyen (VNU University of Science, Vietnam)
15:00 - 15:30	OS_8_03	**Study of the mosquito population prediction model** Dong Gun Kim (Sahmyook University, Korea)
16:00 - 16:30	OS_8_04	**Vector control management system with Geographical Information System (GIS)** Hee Il Lee (Korea Center for Disease Control and Prevention, Korea)

OS_8_01

Past, Present and Future of Mosquito Control Project in Chiang Mai, Thailand

Chitchol Phalaraksh[1]

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Chiang Mai 50200, Thailand

Over 3,520 mosquito species that recognized in the world and 459 species in Thailand. In each year, the accumulation numbers of mosquitoes borne disease patients are increasing. In 2016, 1,550 dengue patients occurred in 1.7 million of Chiang Mai population. Unfortunately, dengue vaccine is not popular, expensive and not included in health care policy of Thailand. Main strategy of mosquito vector control in Thailand is chemical control. The significant problem of using chemical control is the accumulation of toxicants in other living organisms and in environment, chemical resistance gene and high cost for running. Chiang Mai University collaborate with Korea University has applied the alternative strategy for controlling of the mosquito vector called "Integrated Mosquito Management" (IMM). The IMM project was established 3 years ago. For first year in 2016, high efficiencies of mosquito control agents were selected and tested the mass production rearing system. In the year 2017 and 2018, experiment of efficiency of using IMM method was conducted in the Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai, Thailand. The Digital Mosquito Monitoring System (DMS) was introduced to monitor the mosquito population during experiment. The significant decreasing of mosquito population showed high efficiency of using the IMM method to control the vector mosquitoes. In the year 2019, the first implementation of IMM method will be introduced to high accumulated number of dengue patient villages. The aim of this year project is to reduce the number of dengue patients of prototype village by using the IMM method. Moreover, understanding of using *in situ* IMM would be expected to improve the mosquito management for Chiang Mai City in the future.

OS_8_02

Dengue vectors in Vietnam and their control approaches

Van Vinh Nguyen

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In Vietnam, Dengue fever is a very serious public health problem and one of the most infectious diseases with the highest incidence and mortality rates. Dengue fever cases are recorded throughout Vietnam, from urban to rural areas. It is estimated that about 70 million Vietnamese are living in areas with circulating Dengue fever and are at risk of being infected. Although there has been a national anti-Dengue fever program established in 1999 and the number of illnesses and deaths has decreased, the average number of cases is still very high, about 70,000 - 100,000 cases with hundreds of deaths. It's a common knowledge that Dengue fever is transmitted by mosquitoes. In Viet Nam, there are two important mosquito species that transmit diseases called *Aedes aegypti* and *Ae. albopictus*, in which *Ae. aegypti* is the main vector. The capital Hanoi, in recent years, also continuously recorded epidemics with high numbers of diseases. The city was also identified as the most important area about Dengue fever in northern Vietnam.

Currently, the prevention of dengue fever in Vietnam in general and in Hanoi in particular is extremely difficult because there is neither vaccination nor specific treatment medicine. In general, the most effective preventive is to rely on controlling the vector of disease transmission. The vector control approaches in Vietnam could be divided into three general categories: chemical control, biological control, and environmental management, regardless of the pathogens to be targeted. All control strategies share a common goal of reducing the size of vector populations.

From 2018 until now, the VNU University of Science, in collaboration with the Korea University, has implemented the project: "Development and application of integrated management (IMM) techniques as a localized customized technology in Vietnam" with the goal: an eco-friendly, safe and sustainable approach is expected to be carried out to reduce human-vector contact in Vietnam.

The main research results achieved so far are:

1) Investigate mosquito and their predators in the field, identify habitats of mosquito larvae and check the population of mosquito in Hanoi; **2)** Set up DMS machines in Hanoi in order to assess the mosquito population dynamic and then do predaceous experiment to choose predator under the laboratory condition. 3) Set up mass rearing system in the Laboratory, VNU University of Science.

In this report, we also discuss the research plan in the future to achieve the project's objectives.

OS_8_03

Study of the mosquito population prediction model

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The various physical and biological systems are transforming worldwide due to climate change, and the changes observed particularly in temperature, humidity, and precipitation are fueling the spatial expansion of disease vectors including mosquitos. An accurate understanding and prediction of mosquito population dynamics are needed to identify areas where there is a high risk of mosquito mediated disease spread and persistence.

The most earlier mosquito prediction models generally focus on analyzing the correlation between environmental factors including temperature, humidity, and precipitation, and the occurrence of adult mosquitos or their blood-sucking activity. However, the occurrence of mosquitos in natural ecosystems is closely associated not only with environmental factors, but also with the biological environment of the larval habitats.

In this context, this study analyzes the relationship between the biological environment of the natural and artificial habitats of mosquito larva and its occurrence, and develops a prediction model in order to identify the optimal sites for application of biological mosquito prevention methods, the best time of application, and the quantity to be applied. Hence, we assumed various model types using species richness and OCH-groups (Odonata, Coleoptera, Hemiptera- groups) individual ratio as a main factor and evaluated the suitability of those models.

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OS_8_04

Vector control management system with Geographical Information System (GIS)

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Hyun Woo Kim, Shin Hyeng Cho

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Mosquito is the deadliest animal to transmit several diseases, like as Malaria, Dengue Fever, Japanese Encephalitis and etc. Integrated mosquito management (IMM) is the best way to control of mosquitoes and mosquito borne diseases. In Korea, mosquito control was responsible for the Public Health Center in each County. To achieve IMM, we need to find the location of vector, understand their ecological character, and know several ways of vector control methods including physical, biological and chemical control methods. So capacity building of people to charge of vector control is very important. However, we cannot make sustainable developing of their ability in Korea because their position has been rotated with several years. So we need to make database with vector control information including larval habitat, civil complaint, types of chemical use, who and when they control, and other miscellaneous events. This system was based on Geographical Information System and set up about 60 public health centers in 2018. Through this system, Korea CDC and other local government can monitor the condition of vector control. To effective vector control result with small amount of chemical, we need to know the mosquito density and the location of hot spot. Through the historical surveillance system, we can know the mosquito density at least one week later because collect and identification need several days with specialists. So this kind of information cannot use the planning of vector control. Se we also invent mosquito counter and transfer the information by network. The accuracy of this counter is about 90% depends on the collection sites. To merge Vector control management system and Mosquito counting information, public health center can easily decide the location of vector control in every morning. So we can effectively use of our resource and achieve to control of mosquito borne diseases in Korea.

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Session 9

Environmental pollutions and associated microorganisms including harmful organisms

Date & Time : 26 Fri 14:00 - 17:00
Room : Meeting 8

Chair : Prof. Yoon-E Choi
Korea University, Korea

Chair : Dr. Kwi-Nam Han
Korea Basic Science Institute, Korea

14:30 - 14:45	OS_9_01	**Biogeochemical investigation of arsenic dynamics in wetland microcosm systems** Young-Soo Han (Korea Institute of Geoscience and Mineral Resource, Korea)
14:45 - 15:00	OS_9_02	**Application of ureolytic bacteria to remediate heavy metal contaminated mine soils** In_Hyun Nam (Korea Institute of Geoscience and Mineral Resource, Korea)
15:00 - 15:15	OS_9_03	**Arsenic stabilization mechanism in mine waste by basic oxygen furnace slag** Seulki Jeong (Korea Basic Science Institute, Korea)
15:30 - 15:45	OS_9_04	**Copper recovery from wood preservative effluent using bacterial waste-based adsorbents** Sok Kim (Korea University, Korea)
16:00 - 16:15	OS_9_05	**Meta-omic analysis reveals carbon remineralization by bacteria in Phaeocystis bloom in the Amundsen Sea polynya** So-Jeong Kim (Korea Institute of Geoscience and Mineral Resources, Korea)
16:30 - 16:45	OS_9_06	**Environmental sensing platform for the determination of trace heavy metal ions** Kwi-Nam Han (Korea Basic Science Institute, Korea)
16:45 - 17:00	OS_9_07	**Investigation of novel bacteriophages and their application on on-site applicable biosensor method** Mi-Kyung Park (Kyungpook National University, Korea)

OS_9_01

Biogeochemical investigation of arsenic dynamics in wetland microcosm systems

Young-Soo Han, So-jeong Kim, In-Hyun Nam, and Jungho Ryu

Geologic Environment Division, Korea Institute of Geoscience and Mineral Resources (KIGAM)

Wetland sediment has been considered as a good scavenger of toxic heavy metal contaminants like arsenic (As). It has been known that the microbial reactions in the geochemical reaction of As in wetland sediment are mainly responsible for controlling oxidation, reduction, methylation and demethylation, and that the geochemical reactions are closely related to adsorption and dissolution/precipitation mechanisms. In the present study, the relatively large-scale laboratory microcosm experiment was conducted to simulate a natural wetland system contaminated with dimethyl arsenate, DMAs(V). Two-month monitoring of As distribution in the aqueous and solid phases demonstrated that the spiked DMAs(V) was completely removed from the aqueous phase after 23 days and most of the As species associated with sediment were identified as inorganic As(V). These results imply that demethylation occurs at the interface between sediment and water, and the transformation of As speciation may be attributable to the microbial activity. The demethylated As(V) seemed to be adsorbed on wetland sediments, and the As(V) was reduced to As(III) in the deeper layers of the wetland sediment with predominantly reducing conditions. The mass balance of As in the microcosm was also calculated based on the total concentration of As measured in water, sediments, and plant biomass, demonstrating an important role of wetland sediment as an efficient sink of As.

OS_9_02

Application of ureolytic bacteria to remediate heavy metal contaminated mine soils

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Three bacterial strains able to produce urease were isolated in the heavy metal highly contaminated mine soils. Each bacterial strain was characterized with respect to morphology, growth conditions, 16S rRNA gene sequence identity and the urease specific activity each isolate was measured. All isolates were identified *Sporosarcina pasteurii* with more than 98% of similarity, therefore they were named *Sporosarcina* sp. KM-01, KM-07, and KM-12. The heavy metals were detected from the collected mine soils containing bacterial isolates as Mn(170.50 mg/kg), As(114.05 mg/kg), Zn(92.07 mg/kg), Cu(62.44 mg/kg), and Pb(40.29 mg/kg), respectively. Isolated bacterial strains KM-01, KM-07, and KM-12 were shown to be able to precipitate calcium carbonate using urea amended with calcium chloride. Scanning Electron Microscope (SEM)-Energy Dispersive Spectrometer (EDS) analytical results showed that calcium carbonate was successfully produced and increased with incubation time in the presence of isolates. In order to confirm the calcium carbonate precipitation ability, urease specific activity and precipitate weight were measured and compared in the present study. It makes the field application of biomineralization process based on stimulation of urea hydrolysis possible and potentially useful for a variety of soil bioremediation applications. Considering the strains isolated area, these results also demonstrate that all isolated bacterial strains could potentially be used in the bioremediation of acidic and heavy metal contaminated mine soils.

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OS_9_03

Arsenic stabilization mechanism in mine waste by basic oxygen furnace slag

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This study investigated stabilization mechanism of arsenic (As) in mine waste using basic oxygen furnace (BOF) slag. Because BOF slags have high Fe_2O_3 and CaO contents, it can be used for stabilization agent of heavy metals. A lab-scale batch test was carried out to stabilize As in the mine waste samples under different condition such as BOF slag content and water to mine waste (L/S) ratio. The efficiency of stabilization was assessed by TCLP method, and X-ray photoelectron spectroscopy (XPS) was used to identify the stabilization mechanism. As BOF slag contents increased (3, 5, 10 wt% BOF slags), As stabilization efficiency increased up to 92%. The water contents had no significant effects to As stabilization with high BOF slag contents of 10 wt%. Interestingly, the increase in water contents (from 0.05 to 1.0 L/kg) decreased As stabilization efficiency from 78 to 22%, when 3 wt% BOF slags were added. XPS result showed that $Ca(OH)_2$ are precipitated on the surface of BOF slags when excess water was added, thus can inhibiting Ca^{2+} bridging and blocking the As adsorption sites. This interruption also occurred when high BOF slag contents were used, however, it might more favorable condition for precipitation such as calcium arsenate formation rather than adsorption onto BOF slag surface, thus remaining high stabilization efficiency. The findings will helpful to find the optimum condition for As stabilization and contribute to As contaminated soil management.

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OS_9_04

Copper recovery from wood preservative effluent using bacterial waste-based adsorbents

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The metal resources including copper are extensively applied in various industrial areas such as metallurgy, mining, electroplating, electronics, and chemicals. Copper-based wood preservatives like alkaline copper quat (ACQ) are highly commercialized for the protection of wood in residential applications. In the case of ACQ treatment of wood, it has been considered as a low health affecting method compared to the chromated copper arsenate (CCA) treatment. However, high amount of copper can be released from ACQ-treated woods and ACQ-waste effluents. The high concentrations of copper become toxic to environments due to their accumulative and non-degradable properties. Therefore, in industrial and environmental viewpoints, released copper in the ACQ effluent should be recovered. In the present study, to recover copper from ACQ effluent, we investigated adsorption-based method using the bacterial wastes generated from fermentation industry as a biosorbents. To fabricate biosorbents for copper recovery, the bacterial wastes were immobilized as fiber forms using various bio and synthetic polymers including alginate and polysulfone. In addition, to improve copper sorption efficiency of sorbents, the surface of sorbents was modified using ionic polymer, poly (acrylic acid) (PAA). The copper-sorption performances of sorbents were tested and compared through various batch sorption experiments like isotherm, kinetic, and sorption/desorption. Also, to understand sorption properties of developed sorbents, surface characteristics of sorbent (morphologies and functional groups) were determined using FT-IR, XPS, and SEM analyses.

OS_9_05

Meta-omic analysis reveals carbon remineralization by bacteria in Phaeocystis bloom in the Amundsen Sea polynya

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[2]Department of Microbiology, Chungbuk National University

Phaeocystis antarctica is the primary producer in Amundsen Sea Polynya. We identified key bacteria active during the peak and decline phases of blooms in western Antarctic waters in 2011-2014. Genome and metatranscriptome analyses revealed that Polaribacter (Bacteroidetes) and Ant4D3 (Gammaproteobacteria) were dominant in the peak phase and exhibited high transcriptional activities. Two dominant Polaribacter had the potential to utilize major polymers in P. antarctica. In the decline phase, Gammaproteobacteria (Ant4D3, SUP05, and SAR92) utilizing low-molecular-weight dissolved organic matter (LMW-DOM) and compatible solutes increased. The versatility of Gammaproteobacteria may contribute to their dominance in eutrophic polynya waters. The potential utilization of both polysaccharides and LMW-DOM explains the abundance of the SAR92 clade in both the peak and decline phases. This characterization of the metabolic potential of abundant bacteria at a fine taxonomic scale provides insight into bacterial community succession and carbon remineralization during phytoplankton blooms.

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OS_9_06

Environmental sensing platform for the determination of trace heavy metal ions

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A wide range of environmental contaminants, especially heavy metals, in water-and ground-system, have posed a significant threat to public health and ecosystem, and has become a critical issue worldwide. Heavy metals can accumulate in vital organs and tissues to damage the central nervous system and other organs. There are increasing interests in dealing with heavy metal pollution. Many efforts has been made to develop rapid and reliable analytical methods for the detection of heavy metal ions. However, these methods usually rely on high-tech equipment and thus are limited in onsite applications due to the expensive cost, large amounts of sample and reagents, and labor-intensive operations.

In order to overcome the difficulties of field application, we proposed nanomaterial-based environmental sensing platform using colorimetric and electrochemical techniques. Colorimetric techniques has been recognized as one of promising methods for on-site heavy metal analysis due to its rapid, simple, inexpensive, intuitive and portable features. Electrochemical techniques also provide advantages over conventional methods with regard to simplicity, sensitivity, portability, and a wide detection range. Based on two techniques, nanomaterials, such as CNT and Gold, were utilized as a signal transducer which can afford the visualization or amplification of detection results owing to theirs outstanding chemical and physical properties. Sensitive and selective on-site analysis of heavy metal ions (e.g. lead, copper, cadmium, mercury, arsenic) was successfully performed on several types of optical and electrochemical environmental sensor with the incorporation of nanomaterials. We believe that the proposed devices are capable of facilitating sensitive, and selective detection of heavy metal ions and being an alternative approach to onsite monitoring of environmental pollution in aqueous environments.

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OS_9_07

Investigation of novel bacteriophages and their application on on-site applicable biosensor method

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Currently used rapid detection methods are still impractical for being used as on-site applicable method due to time-consumption, expensiveness, and inefficient sample preparation procedures. The final goal of the study was to develop a novel on-site applicable detection method for the rapid detection of target pathogens. Novel bacteriophages (phages) against foodborne pathogens (*Salmonella* spp, *Escherichia coli* O157:H7, *Shigella*, *Listeria monocytogenes*, *Bacillus cereus*, and *Staphylococcus aureus*) were isolated and purified as optimum, specific and efficient bio-recognition elements. These phages were successfully immobilized on an oscillating sensor and an automatic surface-scanning system was able to detect target pathogens on foods directly. More than one hundred phages were isolated from slaughter houses, poultry plant processing plants and the environmental samples. Among them, five specific phages against *Salmonella* Enteritidis, *S.* Typhimurium, *Yersinia enterocolitica*, *Escherichia coli* O157:H7, and *Shigella sonnei* were further purified with a final concentration range of 10^{10}-10^{12} PFU/mL. The applicability of those purified phages as a bio-recognition element was investigated with regard to temperature, pH, bacterial reduction assay, one-step growth curve, and immobilization efficiency. The oscillating sensor under magnetic field was successfully fabricated with excellent sensitivity and economic fabrication cost. Then, the phage-immobilized sensor was employed into an automatic detection system for measuring subtle sensitive vibrational changes of the sensor as a result of binding with target pathogens on foods. Therefore, this study demonstrated the successful possibility of environmental phages as a novel bio-recognition element for on-site applicable biosensor method with direct, rapid (within 30 min), economic and convenient manner.

Session 10_A

Endocrine Disruptors

Date & Time : 26 Fri 14:30 - 17:00
Room : Meeting 6

Chair : Prof. In Cheol Shin
Hanyang University, Korea

14:30 - 15:00	OS_10_A01	**4-octylphenol induces craniofacial defect via deregulation of neural crest cells in *Bombina orientalis* embryos** Myung Chan Gye (Hanyang University, Korea)
15:00 - 15:30	OS_10_A02	**Development of personalized risk assessment platform for the use of consumer chemical products** Young Joo Lee (Sejong University, Korea)
16:00 - 16:30	OS_10_A03	**Fluorocolorimetric Analysis of Endocrine Disruptors Using Aptamer-Facilitated Gold Nanoparticles** Young Pil Kim (Hanyang University, Korea)
16:30 - 17:00	OS_10_A04	**Contamination and fate of plastic debris associated chemicals** Won Joon Shim (Korea Institute of Ocean Science & Technology, Korea)

OS_10_A01

4-octylphenol induces craniofacial defect via deregulation of neural crest cells in *Bombina orientalis* embryos

Myung Chan Gye and Yang Xu

Department of Life Science, Hanyang University

4-octylphenol (OP) is an intermediate in the production of phenol and formaldehyde resins. OP reached into the environment via waste waters may be toxic to aquatic animals. We examined the developmental toxicity of OP based on the frog embryo teratogenesis assay. In *Bombina orientalis* embryos, the 23°C-144-hours LC_{50} and the 26°C-96-hours LC_{50} of OP were 12.5 μM and 15.0 μM, respectively. The 23°C-144-hours EC_{50} and the 26°C-96-hours EC_{50} of OP were 1.0 μM and 3.1 μM, respectively. Abnormalities such as head malformation, gut malformation, bent trunks, ventral blisters and abnormal tails were significantly increased by 1 μM OP. The 23°C-144-hours and the 26°C-96-hours teratogenic index (LC_{50}/EC_{50}) of OP were calculated to be 12.5 and 15.0, respectively, indicative of teratogenic potential of OP. In the 23°C-144-hours exposure, the total length, body length, tail length, interorbital width, eye-mouth distance and the eye-nostril distance of stage 45 tadpoles were significantly decreased by 5 μM OP. In the 26°C-96-hours exposure, total length, tail length, body length eye-mouth distance and eye-nostril distance of stage 45 tadpoles were significantly decreased at 10 ~ 25 μM OP. In stage 45 tadpoles treated with 10 μM OP head bones were frequently missed together with decrease in *col2a1* mRNA in head, indicative of deregulation of chondrogenesis. In stage 22 embryos treated wiyj 10 μM OP at 23°C *sox10* and *slug* mRNA markers for neural crest cells (NCCs) were significantly increased and SOX10 (+) cells were visibly increased in the endoderm beside normal moving path of NCCs, indicative of deregulation of NCCs. In tadpole heads, lipid hydroperoxide levels were significantly increased at 23 °C 1 μM OP but not at 26°C. *atf4* and spliced *xbp1* mRNA markers for endoplasmic reticulum stress were significantly increased by 5 ~ 10 μM OP at 23°C while *bcl-2* mRNA was significantly decreased together with increase in DNA fragmentation and cleaved caspase-3 at 23°C and 26°C. Together, OP induced head dysgenesis via oxidative stress, ER stress, apoptosis, and deregulation of NCCs, and which was potentiated following longer exposure at low temperature in *B. orientalis* embryos. This is the first report on the developmental toxicity of OP on chondrogenesis from NCCs in amphibian embryos.

OS_10_A02

Fluorocolorimetric Analysis of Endocrine Disruptors Using Aptamer-Facilitated Gold Nanoparticles

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Endocrine disruptors (EDCs), as xenoestrogens, have been suspected to be associated with reproductive dysfunction and physiological abnormality in human. Among EDCs, bisphenol A (BPA), phthalate, and nonylphenol (NP) are of major concern, due to their environmental or human exposure from plastics and detergents. For vulnerable people, a rapid and simple detection of EDCs is highly demanded. Here we report a simple EDC assay using aptamer-facilitated gold nanoparticles (AuNPs). SELEX-derived anti-EDC aptamers triggered self-assembly of unmodified AuNPs (citrate-stabilized AuNPs) in the presence of EDCs, leading to a color change in the AuNP solution from reddish to purple upon the addition of high salt. We combined fluorescence measurement by SYBR Green with the AuNP colorimetry to enhance detection sensitivity. In BPA, the detection sensitivity was achieved as low as 1 ppb, which was greater than those of other reported methods. This method also enabled a selective and sensitive detection of BPA from real samples including thermal papers or food cans. Furthermore, multiple AuNP-based colorimetry using three EDC aptamers resulted in a rapid determination of BPA, phthalate, and NP with high selectivity. We suggest that this aptamer-facilitated AuNPs will offer many applications in the field of environmental science.

OS_10_A03

Contamination and fate of plastic debris associated chemicals

Sang Hee Hong[1,2], Mi Jang[1,2], Youna Cho[1,2], Won Joon Shim[1,2]

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Microplastics are widely distributed, from lakes to the open ocean, in surface water and deep sea sediments and in various organisms through the trophic levels. As large items fragment into microplastics the abundance of litter increases, and this effectively increases their availability to wildlife. Plastic debris have both absorbed chemicals from the surrounding environments and chemicals added during manufacturing process. Increased surface area increases the potential for leaching or desorption of additive or adsorbed chemicals to an organisms upon ingestion. Non-target screening of various plastic debris from a Korean beach detected over 200 man-made chemicals. A variety of legacy and emerging organic pollutants were detected from microplastics in Korean coastal environments. An flame retardant additive, HBCDs, in expanded polystyrene (EPS) bead leached out in seawater. HBCD was transferred to the mussels attached to EPS debris by ingestion and through water by leaching. Chemical transfer from the ingested plastics and to the organisms depends on concentration gradient between them. Based on model and field studies demonstrated that more attention should be paid to additive chemicals. In some laboratory studies, additive leachate from the plastic purchased from market cause toxic effects on barnacle survival and larvae settlement. In addition, there have been indirect evidences that PBDEs or phthalate in the ingested plastics were transferred to seabird tissues.

OS_10_A04

Development of personalized risk assessment platform for the use of consumer chemical products

Young Joo Lee

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This presentation will introduce our progress in developing a public platform for providing safety information as increasing consumer products. This public platform will provide safety information of aggregate exposure from using mixed chemical products. The contents of our platform includes Development of aggregate exposure and risk intelligent evaluation technology when using mixed chemical products; Development of personalized safe consumption information for the safe use of life chemical products by using personal risk assessment results; Development of behavior guidelines based on personalized risk analysis and verification of behavior guidelines; Building citizen participation/intelligent platform to provide personalized risk information according to complex use of life chemical products. This platform will provide individual risk information due to the hazardous chemicals that are exposed to the body of harmful chemicals in using products or food consumption and it provides a reasonable and safe product consumption and behavior guidelines based on Individuals can manage the risks they receive from harmful chemicals during their daily lives. It can also be extended to personalized disease management platform to integrate information and information for individual diseases.

Session 10_B

Environmental Biology

Date & Time : 26 Fri 14:30 - 17:00
Room : Hall C

Chair : Dr. Jin Kyu Kim

14:30 - 14:45	OS_10_B01	**Temporal changes in the community structure of macrobenthos in the Bongam tidal flat of Masan Bay, Korea** Jeong Hyeon Kim (Korea Institute of Ocean Science & Technology, Korea)
14:45 - 15:00	OS_10_B02	**Population genetic structure of chum salmon, *Oncorhynchus keta* from South Korea: identification of management units for its conservation** Ji Eun Jang (Sangji University, Korea)
15:00 - 15:15	OS_10_B03	**Studies on ecological stability of artificially and naturally restored streams in time and space using a network approach: Case studies of Cheonggye and Jungrang streams** Minyoung Lee (Korea University, Korea)
15:15 - 15:30	OS_10_B04	**Pearson correlation analysis between land use and the population of *Brachymystax lenok*** Min Seop Ko (Sangji University, Korea)
16:00 - 16:15	OS_10_B05	**Comparison of mosquito larvae control techniques using natural enemy and BTI (*Bacillus thuringiensis israekensis*)** Jung Soo Han (Sangji University, Korea)
16:15 - 16:30	OS_10_B06	**4-octylphenol induces developmental abnormalities via deregulation of neural crest cells in *Xenopus laevis* embryos** Yang Xu (Hanyang University, Korea)
16:30 - 16:45	OS_10_B07	**Marine litter on the continental shelf and slope/floor in Ulleung Basin of East Sea (Sea of Japan)** Won-Gi Min (Korea Institute of Ocean Science & Technology, Korea)
16:45 - 17:00	OS_10_B08	**Community characteristics analysis of the Aquatic Oligochaeta according to the installation of weir in four major rivers in South Korea** Ju Hyoun Wang (Sangji University, Korea)

OS_10_B01

Temporal changes in the community structure of macrobenthos in the Bongam tidal flat of Masan Bay, Korea

Jeong Hyeon Kim, Jin Young Seo, Jin Woo Choi

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Geoje 53201, Republic of Korea

This study was conducted to detect annual changes in the community structure of macrozoobenthos in response to the fluctuating benthic habitat conditions in the Bongam tidal flat of Masan Bay, Korea. Faunal samples were collected by monthly from March, 2014 to April, 2016, and from October 2017 to October 2018. At each sampling time, we used box core samples (0.025 m^2) and collected four times per site during low tide period. As a results of sedimentation analysis and benthic community structures, the Bongam tidal flat was a typical sandy bottoms with a contents of 80% or more except May and June 2015. The total organic carbon (TOC) content increased up to 1.7% in May and June 2015, but the mean TOC was less than 1% during most of the study period. The number of species ranged from 6 to 16 during the study period. The density was lower in the summer season of 2014 compared to other study period. Polychaetes accounted for more than 80% of the total density. The maximum biomass ranged from 58.7 to 2,662.8 g wt/m^2 in 2018, because of the mass appearance of bivalve, *Laternula marilina*. The major dominant species were four deposit feeders such as *Heteromastus filiformis*, *Prionospio japonica*, *Simplisetia erythraeensis*, *Hediste diadroma* and a filter feeder, *L. marilina* in the Bongam tidal flat. There was little annual change in the composition of dominant species during the study period. The most dominant species was *H. filiformis* in the Bongam tidal flat. The density of *P. japonicus* showed the highest in April 2014, but its density rapidly decreased in winter 2015. Two deposit feeding nereidid polychaetes, *S. erthraeensis* and *H. diadroma* showed negatively correlated in their densities. *H. diadroma* has the largest density in 2015 and has continued to decline until 2018. On the other hand, *S. erthraeensis* showed a tendency to increase after 2015. After the temporal change of sedimentation in the Bongam tidal flat in 2015, the density of *H. diadroma* temporally increased while, that of *P. japonica* decreased since the winter of 2015.

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OS_10_B02

Population genetic structure of chum salmon, *Oncorhynchus keta* from South Korea: identification of management units for its conservation

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The chum salmon (*Oncorhynchus keta*), known as a Pacific salmon, is widely distributed from the Far East to North America along the Pacific Rim. This species is an important fisheries resource with a high economic and commercial value. They have an anadromous life style where they hatch in freshwater and migrate to the sea for growth, then return to their natal rivers to reproduce. Their homing behavior sometimes lead to decrease within-population genetic diversity resulting from limited gene flow occurring among geographically disconnected populations, elevating the risk of local extinction. As an effective application of genetic data to the fisheries management, elucidating the population genetic structure of the chum salmon using molecular markers will assist in determining its management units. Using mtDNA control region sequences and eight nuclear microsatellite loci, we assessed the current population status of *O. keta* in South Korea by estimating the level of genetic diversity and genetic structure for 16 populations (including ten wild and six hatcheries) from 11 tributaries within major returning river basins. The analyses showed the similar level of genetic diversity between wild and hatchery populations with a total of seven mtDNA haplotypes and 25.4 alleles per microsatellite. Both markers revealed that genetic differentiation (F_{ST}) between populations tend to be low, suggesting a moderate level of gene flow taking place among those populations. For future conservation, we suggest that the Korean salmon population can be considered as a single stock for its management unit. Nonetheless, we should make an effort to preserve the unique haplotypes only detected in particular populations.

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OS_10_B03

Studies on ecological stability of artificially and naturally restored streams in time and space using a network approach: Case studies of Cheonggye and Jungrang streams

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Urban streams are an important component of the natural landscape of urban areas, as they transport water, sediments, nutrient, and organic matter, supporting diverse aquatic species, being closely related to humans. Domestic ecological river restoration projects in Korea have been carried out focusing on urban streams. It is important for understanding the ecological stability of the restored urban streams as new types of ecosystem in terms of man's own survival and their sustainable use. The purpose of this study is to investigate the ecological stability of restored streams in time and space using a network approach. Cheonggyecheon stream (CG) and Jungrangcheon stream (JR), which are the representative of artificially and naturally regulated restored stream in Seoul city, respectively, have been selected as the study sites. CG and JR food-webs were constructed based on biological monitoring data (2008-2017) and global biotic interactions (GloBI) database, being quantified using biomass flow. We analyzed ecological stability in time by measuring total system throughput (TST) and robustness and in space by measuring dissimilarity of pairwise networks with geographic distances. The result showed that both streams were quite robust to the disturbance and JR had higher TST than that of CG over time. In space, the network dissimilarity in both streams increased when two networks are far apart and that of CG tended to increase more rapidly than that of JR, indicating that CG has low longitudinal connectivity. We found the naturally restored stream, JR, is still ecologically more stable than CG in time and space, but also the artificially controlled stream, CG, is quite robust and a well-operated stream.

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OS_10_B04

Pearson correlation analysis between land use and the population of *Brachymystax lenok*

Min Seop Ko[1], Jung Soo Han[1], Won Sub Choi[1], Jun Kil Choi[1], Hwang Goo Lee[1]

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The purpose of this study is to provide the basic data for the conservation of *Brachymystax lenok* habitat through the growth status of the *B. lenok* and the Pearson Correlation Analysis (PCA) between the population of *B. lenok* and the land use of the around the river. Sampling was conducted twice in July and September 2018. A total of 67 individuals of *B. lenok* was collected. The result of the length-weight relationship in the population of *B. lenok* was analyzed with a regression coefficient b value of 3.0132 and a condition factor value of 0.00007, therefore the growth condition of *B. lenok* was regarded to be a good condition. Also, the PCA reveals that the number of populations of *B. lenok* was abundant in forest area (r = 0.562**) and agricultural area (r = -0.576**) and urbanization (r = - 0.136) is a disturbance factor in the distribution of the species. As a result of the population of *B. lenok* was influenced by the disturbance factors around the habitat.

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OS_10_B05

Comparison of mosquito larvae control techniques using natural enemy and BTI(*Bacillus thuringiensis israekensis*)

Jung Soo Han[1], Chae Hui An[1], Jun Kil Choi[1], Hwang Goo Lee[1]

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Wonju 26339, S. Korea

In the past, chemical insecticides were used to control mosquito. However, in recent years, various studies have been conducted to control mosquito larvae using biological control techniques. In this study, we apply natural enemy techniques using *Hydrochara affinis* and *Bacillus thuringiensis israekensis* (H-14 type).

The study site was located at the camping area in the Hwarang amusement park in Danwon-gu, Ansan-si, where there were many complaints regarding mosquitoes. The study period was conducted from July 13 to August 01, 2018 for four times a week. Control site, natural enemy site, and BTI sites were selected. Species composition was similar between control and natural enemy sites, but BTI site showed that species diversity and individual ratio decreased after BTI application. The number of individuals Odonata, Hemiptera and Coleoptera were highest in natural enemy site and decreased after injection of BTI at BTI site. As a result of water quality analysis, mosquito larvae were significantly correlated with temperature and water temperature, and pH showed negative tendency. Most of the dominant species were *Austropeplea ollula* and *Physa acuta*, and it was analyzed that they show unstable communities at the BTI site compared to the control and natural enemy site. The results of Self-organizing map (SOM) were analyzed as three groups. The 1st period of the BTI site is a result of similar communities and species composition of the control site and natural enemy site.

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OS_10_B06

4-octylphenol induces developmental abnormalities via deregulation of neural crest cells in *Xenopus laevis* embryos

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4-octylphenol (OP) reached into the environment via waste waters may be toxic to aquatic animals. We examined the developmental toxicity of OP based on the frog embryo teratogenesis assay *Xenopus* (FETAX). In *X. laevis* embryos, the LC_{50} and EC_{50} of OP were calculated to be 9.9 μM and 10.9 μM, respectively. Abnormalities such as head malformation and abnormal tails were significantly increased by 10 μM OP. The teratogenic index (LC_{50}/EC_{50}) of OP was calculated to be 0.91. In the OP exposure, the body length and total length were significantly increased by 5 μM and decreased by 10 μM OP. The tail length of tadpoles was significantly increased by 1 μM and decreased by 10 μM OP. In tadpoles treated with 10 μM OP head bones were frequently missed together with decrease in *col2a1* mRNA in head, indicative of chondrogenic defect. Of note, melanocytes were frequently underdeveloped in the tadpole skin. OP at 10 μM significantly increased *sox10* mRNA marker for neural crest cells (NCCs) in stage 22 embryo in which SOX10 (+) cells were visibly increased in the endoderm beside normal moving path of NCCs. Together, OP may deregulate the migration and differentiation of NCCs into chondrocytes and melanocytes. In tadpole heads, lipid hydroperoxide levels were significantly increased at 10 μM OP. The spliced *xbp1* mRNA, markers for endoplasmic reticulum (ER) stress were significantly increased by 1 μM OP and decreased by 10 μM OP. *bcl-2* mRNA was significantly decreased together with increase in *bax* mRNA, DNA fragmentation and cleaved caspase-3. Together, OP induced head dysgenesis via oxidative stress, ER stress, apoptosis, and chondrogenic defect via deregulation of NCCs in *X. laevis* embryos.

OS_10_B07

Marine litter on the continental shelf and slope/floor in Ulleung Basin of East Sea (Sea of Japan)

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Marine debris is a recognized global ecological concern. Little is known about the extent of the problem in the East Sea regarding litter distribution and its influence on deep-sea habitats. A quantitative assessment of debris present in the deep seafloor was carried out around the slopes of the Hupo Bank and the Ulleung Basin in the East Sea in June 2015 using the 6,000-meter-class ROV 'HEMIRE'. We first carried out deep-seabed exploration over two weeks, a total of 9 dives were made from a support ship, the R/V Onnuri, at eight stations with water depth ranging between 194 and 2,080 m. The dive times ranged from 1 to 6 hours, depending on the operating conditions. The objectives of this study were to investigate and discuss: (i) litter density, (ii) the kinds of litter, (iii) the influence of environmental factors on the distribution of litter, and (iv) the impact of litter on benthic communities. Litter was found in all 8 sites in 9 dives. The dominant type of debris was represented by Vinyl materials, fishing gears, plastic objects, cans and glass bottles. Over fifty percent of the recorded debris directly impacted benthic organisms. This work provides a first insight on the impact of marine debris in the East Sea deep ecosystems and a valuable baseline for future comparisons.

OS_10_B08

Community characteristics analysis of the Aquatic Oligochaeta according to the installation of weir in four major rivers in South Korea

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The pollution the organic accumulation and water occurs with water velocity decrease caused by constructed weir in the four major rivers in South Korea. Water quality deterioration increased the number of individuals of Aquatic Oligochaeta which is the water contamination indicator species in the benthic macroinvertebrates. It is generally known that Tubificidae spp. have the wide range of pollution tolerance, even if the water environment deteriorates. This study investigated the characteristics of distribution according to the physical and chemical habitat of Aquatic Oligochaeta in Ipoh weir, Sejong weir, Juksan weir, Gangjeong-Goryeong weir and Dalseong weir.

The study investigation was conducted 10 times from March to October, 2018. A total of 18 species and 35,390 ind./m^2 number of individuals were observed. The highest number of species identified was in Dalseong weir consisting of 13 species. The highest, relative number of individuals identified was in Sejoeng weir consisting of 11,280 ind./m^2. *Limnodrilus hoffmeisteri* was found to be the dominant species which is also the dominant species in all the sites while *Branchiura sowerbyi* was the subdominant species. A total of 32.418 g/m^2 was measured as a result of the dry weight analysis and the measured 16.194 g/m^2 from Han river was the highest. The number of individuals showed to be correlated with sediment depth, clay, silt, sand, cobble, pebble, pH and TOC mg/L ($p<0.05$, $p<0.01$). The analysis the relationship of the number of individuals with clay ratio and sediment depth showed a clay ratio and sediment depth increases of number of individuals. Total Organic Carbon (TOC) showed tendency to increase from March to October, and showed a tendency that the number of individuals and dry weight to be decreased.

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Poster Session

Poster Session

Poster Presentation A

Date & Time : 25 Thu 15:30~16:00

PS_1_1	**Toxic HAB species from the Sea of Okhotsk detected by a metagenetic approach** Satoshi Nagai (National Research Institute of Fisheries Science, Japan)
PS_1_2	**Morphology, phylogeny and life cycle of *Fragilidium mexicanum* Balech (Gonyaulacales, Dinophyceae)** Zhun Li (Korea Institute of Ocean Science & Technology, Korea)
PS_1_3	***Prorocentrum shikokuense* Hada and *P. donghaiense* Lu are the synonym of *P. obtusidens* Schiller (Prorocentrales, Dinophyceae)** Hyeon Ho Shin (Korea Institute of Ocean Science & Technology, Korea)
PS_1_4	**Changes in cytoplasmic organelles characteristics by chemical algicidal substance for dinoflagellate *Cochlodinium polykrikoides* and *Heterocapsa circularisquama*** Se Yun Jin (South Sea Fisheries Research Institute, National Institute of Fisheries Science, Korea)
PS_1_5	**Growth change in three harmful algal blooming species by addition of bacterial communities exposed to dissolved organic matter derived from *Heterosigma akashiwo* (Raphidophyceae)** Ro Young Park (Hanyang University, Korea)
PS_1_6	**Evaluation of algicidal substances as a candidate for the control of dinoflagellates *Cochlodinium polykrikoides* and *Heterocapsa circularisquama*** Se Yun Jin (South Sea Fisheries Research Institute, National Institute of Fisheries Science, Korea)
PS_1_7	**Harmful algal blooms by dinoflagellates are related with specific bacteria** Hui Wang (Sangmyung University, Korea)
PS_1_8	**Remote sensing monitoring of *Margalefidinium polykrikoides* blooms in the South Sea of Korea** Joo-Hyung Ryu (Korea Institute of Ocean Science and Technology, Korea)
PS_1_9	**Evaluation of freshness quality of strawberries fruit produced in the biochar mixed hydroponic culture using photochemical reaction and thermal image methods** Tae-Wan Kim (Hankyong National University, Korea)
PS_1_10	**Evaluation of photochemical reactions for shikimic acid accumulation in Burcucumber (*Sicyos angulatus* L.) treated with glyphosate** Tae-Wan Kim (Hankyong National University, Korea)
PS_2_1	**Red Tide Monitoring by Using Unmanned Aerial Vehicle** Seung Yeol Oh (National Institute of Fisheries Science, Korea)
PS_3_1	**The complete mitochondrial genome comparisons of true jellyfishes Scyphozoans** Mustafa Zafer Karagozlu (Sangmyung University, Korea)
PS_3_2	**Molecular approaches reveal biogeographic separation of the harmful jellies *Aurelia coerulea* and *A. limbata* along the eastern coasts of Korea** Yosep Seo (Sangmyung University, Korea)
PS_3_3	**Three species of family Diphyidae (Hydrozoa: Siphonophorae) in Korean Waters** Nayeon Park (Hanyang University, Korea)

PS_3_4 **Proteomic Investigation to Identify Anticancer Targets of *Nemopilema nomurai* Jellyfish Venom in Human Hepatocarcinoma HepG2 Cells**
Du Hyeon Hwang (Gyeongsang National University, Korea)

PS_3_5 **Feeding behavior of a box jellyfish, *Carybdea brevipedalia***
Jinho Chae (Marine Environmental Research & Information Laboratory (MERIL), Korea)

PS_3_6 **Molecular phylogeny of planthoppers according to mitochondrial protein coding genes**
Hyung-eun An (Sangmyung University, Korea)

PS_7_1 **Fabrication of Novel Chitosan Composited Fibers from Paper Mill Sludge Biochar for Effective Removal of Phosphate**
Kumuduni Niroshika Palansooriya (Korea University, Korea)

PS_7_2 **Effect of Feedstock Type and Modification Method on Carbon Dioxide Adsorption Capacity of Biochar**
D.M.P.D. Dissanayake (Korea University, Korea)

PS_8_1 **Screening aquatic insect predators for biological control of *Aedes aegypti* in Hanoi, Vietnam**
Van Cuong Duong (Korea University, Korea)

PS_8_2 **A new distributional record of the giant water bug *Lethocerus patruelis* (Hemiptera: Belostomatidae) in Thailand with notes on its conservation**
Nattawut Sareein (Korea University, Korea)

Poster Presentation B

Date & Time : 26 Fri 09:00~09:30

PS_10_1 **Temporal changes in the community structure of macrobenthos in the Bongam tidal flat of Masan Bay, Korea**
Jeong Hyeon Kim (Korea Institute of Ocean Science & Technology (KIOST), Korea)

PS_10_2 **Impact of environmental variables on the diversity and distribution of the megabenthos in the South Sea of Korea**
Su Min Kang (Korea Maritime and Ocean University, Korea)

PS_10_3 **Species composition and distribution of hull-fouling macrozoobenthos differs among research vessel navigation areas**
Hyung Gon Lee (Korea Institute of Ocean Science & Technology, Korea)

PS_10_4 **Species composition and community structure of the soft-bottom macrobenthos at the coastal and its adjacent areas of Dokdo, the East Sea of Korea**
Ok Hwan Yu (Korea Institute of Ocean Science & Technology, Korea)

PS_10_5 **Fluorocolorimetric Detection of Endocrine Disruptors Using Aptamer-Facilitated Gold Nanoparticles**
Eun-Song Lee (Hanyang University, Korea)

PS_10_6 **Impacts of a massive aquaculture of Manila Clam (*Ruditapes philippinarum*) on the macrobenthic communities in a tidal ecosystem in Korea**
Sang Lyeol Kim (Korea Institute of Ocean Science & Technology, Korea)

PS_10_7 **Effects of booster biocides and by-products from vessels on embryo test of a sea urchin, *Mesocentrotus nudus***
Jin Young Seo (Korea Institute of Ocean Science & Technology, Korea)

PS_10_8 **Seasonal phytoplankton community using microscopic and Chemotax pigment analysis in Seomjin River Estuary, Korea**
Minji Lee (Korea Institute of Ocean Science & Technology, Korea)

PS_10_9 **Environmental factors affecting dynamics of phytoplankton community in port baseline surveys in Korea**
Oh Youn Kwon (Korea Institute of Ocean Science & Technology, Korea)

PS_10_10 **Distribution of mesozooplankton in the deep-sea hydrothermal vent in the Indian Ridge**
Minju Kim (Korea Institute of Ocean Science & Technology, Korea)

PS_10_11 **Population genetic structure of chum salmon, *Oncorhynchus keta* from South Korea: identification of management units for its conservation**
Ji Eun Jang (Sangji University, Korea)

PS_10_12 **Abalone mortality associated with harmful algae *Karenia mikimotoi* and *Cochlodinium polykrikoides***
Sang Jun Lee (Aquaculture Division, South Sea Fisheries Research Institute, NIFS, Korea)

PS_10_13 **Risk assessment of in situ application of microbubble ozonation to cyanobacteria control**
Gwiwoong Nam (Korea University, Korea)

PS_10_14 **A simple and efficient method for removing of ricin B chain from unknown ricin sample**
Sooyong Kim (Chungnam National University, Korea)

PS_10_15 **A rapid immunochromatographic testing strip using catalytic nanomaterials for highly sensitive point of care test**
Soo Hyeon Kim (Korea Basic Science Institute, Korea)

PS_10_16 **Green Light as Supplementary Light for Enhancing Biomass Production of *Ettlia* sp. and Preventing Population Invasion from Other Microalgae**
Ankita Srivastava (Korea Research Institute of Bioscience Biotechnology (KRIBB), Korea)

PS_10_17 **Algicidal effects of *Pseudoruegeria* sp. M32A2M against toxic dinoflagellate *Alexandrium tamarense***
So-Ra Ko (Korea Research Institute of Bioscience Biotechnology (KRIBB), Korea)

PS_10_18 **Specific oceanographic characteristics and phytoplankton responses influencing the primary production around the Ulleung Basin area in spring**
Minji Lee (Korea Institute of Ocean Science & Technology, Korea)

Poster Presentation C

Date & Time : 26 Fri 15:30~16:00

PS_10_19 **Morphological changes of a psychrotrophic *Pseudoalteromonas* species after exposure to sublethal concentrations of vancomycin**
Hyunjun Kim(Yonsei University, Korea)

PS_10_20 **Accumulation of micoplastics in sheepshead minnow (*Cyprinodon variegatus*)**
Youn-Joo Jung (Korea Institute of Toxicology (KIT), Korea)

PS_10_21 **Developmental toxicity of Bisphenol A and their structural analogues in *Xenopus laevis* embryos**
Yang Xu (Hanyang University, Korea)

PS_10_22 **Development and Application of synthetic polymer based bio-sorbents to Control Harmful Alga, *Microcystis aeruginosa***
Ho Seon Kim (Korea University, Korea)

PS_10_23 **Control of harmful alga, *Microcystis aeruginosa,* using adsorptive technique by chitosan sorbents.**
Yun Hwan Park (Korea University, Korea)

PS_10_24 **The identification of IgE binding proteins in non-biting midges (*Cricotopus bicinctus),* potentially potent producers of allergens around the river**
Myunghee Yi (Yonsei University, Korea)

PS_10_25 **Spatial characteristics of microplastics and mesozooplankton in the surface mixed layer of South Sea of Korea and Northern East China Sea**
Jung-Hoon Kang (Korea Institute of Ocean Science & Technology, Korea)

PS_10_26 **Metabarcoding Analysis of Red-Tide Waters in Goeje (South Korea)**
Hye-Eun Kang (Pukyong National University, Korea)

PS_10_27 **Predicting the potential habitat and risk assessment of *Aster subulatus* var. *sandwicensis* using MaxEnt**
Yong Ho Lee (Institute for Future Environmental Ecology Co., Ltd, Korea)

PS_10_28 **The Evaluation of invasive species in Soyang Lake, using AS-ISK (Aquatic Species Invasiveness Screening Kit)**
Un Hwa Heo (Sangji University, Korea)

PS_10_29 **Pyrosequencing and morphological analyses reveal high diversity of freshwater phytoplankton in Paldang reservoir (Korea)**
Hansol Kim (Sangmyung University, Korea)

PS_10_30 **Diversity and seasonal changes of cyanobacteria in Paldang reservoir (Korea) explored by 16S rDNA metagenomcis**
Yosep Seo (Sangmyung University, Korea)

PS_10_31 **A Case Report on the Introduced Species, *Chelydra serpentina,* found in the wild of South Korea.**
Kyo Soung Koo (Chonnam National University, Korea)

PS_10_32 **Survey on Invasive Amphibians and Reptiles Traded Online in South Korea**
Hye Rin Park (Chonnam National University, Korea)

PS_10_33 **Distribution of Exotic Turtles and Comparison with Red-Eared Turtles in Korea**
Jae Hyeok Choi (Chonnam National University, Korea)

PS_10_34 **A study on planting combination methods for considering plant invasiveness to urban vegetation communities**
Seung Won Han (National Institute of Horticultural and Herbal Science, RDA, Korea)

PS_10_35 **Bisphenol A and their structural analogues induces neural tube deformities during *Xenopus laevis* embryos development**
Ji Hyun Jang (Hanyang University, Korea)

PS_10_36 **Effect of the microplastic on meiofauna and nematodes**
Teawook Kang (Korea Institute of Ocean Science & Technology, Korea)

PS_10_37 **Development of diagnosis model of six invasive Convolvulaceae plant seeds by lipid analysis using Matrix assisted Laser Desorption Ionization Time-of-flight Mass spectrometry (MALDI TOF MS)**
Yong Ho Lee (Hankyong National University)

PS_10_38 **A Large-scale production and microwave-assisted extraction of shikimic acid from the aerial parts of *Sicyos angulatus* (Cucurbitaceae) in Korea**
Sun Hee Hong (Hankyong National University)

PS_1_1

Toxic HAB species from the Sea of Okhotsk detected by a metagenetic approach

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Hiromi Kasai[3], Akihiro Shiomoto[4], Seiji Katakura[5]

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During recent decades, the distribution of harmful algal bloom (HAB) species has expanded worldwide together with the increase of blooms and toxicity events. In this study, the presence of toxic HAB species in the Sea of Okhotsk was investigated based on metagenetic data collected during 6 years of weekly monitoring. OTUs associated with the toxic HAB species were detected based on amplifying 18S V7-V9 and 28S D1-D2 rRNA gene regions. In total, 62 OTUs associated with toxic HAB species were revealed, with 42 of those previously not reported from the Sea of Okhotsk. More OTUs belonging to dinoflagellates were detected by 18S, whereas almost equal number of OTUs associated with dinoflagellates and diatoms were detected by targeting the 28S region. Species belonging to genera *Alexandrium*, *Karenia* and *Prorocentrum* were mainly associated with OTUs under Dinophyceae and species belonging to genus Pseudo-nitzschia were the most dominant contributors to OTUs associated with Bacillariophyceae. From the detected OTUs, 22 showed a clear seasonal pattern with majority of those appearing during summer-autumn. For *Alexandrium pacificum*, *Aureochoccus anophagreffens*, *Chattonella marina, Pheopolykrikos hartmanii*, and *Pseudo-nitzschia pungens*, the seasonal pattern was detected based on both rRNA regions. Additionally, 16 unique OTUs were detected during all the seasons and 14 OTUs appeared sporadically. OTUs associated with the toxic species had low relative abundances, which together with other factors such as similar and variable morphology as well as usage of fixatives, may explain why those species have previously not been detected by light microscopy. Environmental parameters, especially water temperature, significantly (<0.05) influenced the variability in OTU relative abundances and displayed significant correlations with the unique OTUs. Potential influence of other factors such as low crazing pressure may also explain the variable presence of some OTUs.

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PS_1_2

Morphology, phylogeny and life cycle of *Fragilidium mexicanum* Balech (Gonyaulacales, Dinophyceae)

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The dinoflagellate genus *Fragilidium* has rarely been reported in taxonomic checklists. We describe the life cycle, morphology and molecular phylogenetic position of *F. mexicanum*, based on vegetative cells established by incubation of resting cysts isolated from sediment trap samples collected at Jinhae-Masan Bay, South Korea. Resting cysts of *F. mexicanum* are spherical and surrounded by transparent mucilage, similar to other *Fragilidium* species. Germinated vegetative cells were identified as *F. mexicanum* based on thecal morphology and tabulation; the plate formula was Po, Pc, 4', 8", 10c, 6s, 7"', 1p, 2"". Molecular phylogenetic analyses of sequences data for small and large subunits of ribosomal DNA genes (SSU and LSU rDNA) revealed that *Fragilidium* species were monophyletic with high supports and that *F. mexicanum* formed a separate clade with *Fragilidium* sp. (JQ317599). Time-lapse photography was used to clarify the life history. Isolated resting cysts germinated into an unarmored planomeiocyte and directly formed the pellicle cyst, with armoured planomeiocyte emerging from the pellicle cyst. The armored planomeiocyte underwent ecdysis and formed a coccoid meiocyte, with a two-celled chain emerging from the coccoid meiocyte. Like the armoured planomeicyte, vegetative cells also underwent ecdysis (asexual coccoid stage) and then divided into two daughter cells that eventually emerged as motile vegetative cells. The life-cycle of *F. mexicanum* has non-motile life-history stages that regularly alternate with motile stages. The non-motile stage consists of five forms: resting cyst, pellicle cyst, asexual coccoid stage and coccoid meiocyte and zygote. The motile stage also has five forms: unarmoured and armored planomeiocyte, planozygote, gamete and vegetative cell.

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PS_1_3

Prorocentrum shikokuense Hada and *P. donghaiense* Lu are the synonym of *P. obtusidens* Schiller (Prorocentrales, Dinophyceae)

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In Japanese, Chinese and Korean coastal waters, a small thecate *Prorocentrium* species has been recognized as the bloom forming species. However, the species has been called as *P. shikokuense*, *P. donghaiense* and *P. dentatum*, respectively, despite their morphological similarity and identical rDNA sequences. To resolve the confusion, we examined the morphological features including architectural details of the periflagellar area and molecular phylogeny of the isolates collected from East China Sea and Korean coast, and reviewed the taxonomic descriptions of the confused species and the related species and its historical records. Morphology and phylogeny based on SSU, ITS region and LSU rDNA sequences revealed that the confused species and our isolates are conspecific and morphological features of *P. dentatum* recorded in the phylogenetic trees does not coincide with those of the originally described *P. dentatum*. Dodge (1975) included *P. veloi, P. monacens* and *P. obtusidens* to *P. dentatum* as synonyms, however the literature review revealed that the morphological features of his specimens were closer to those of *P. obtusidens* in the original description, rather than those of originally described *P. dentatum* and that *P. obtusidens* is distinguished from *P. dentatum* by relatively small size, the parallel sides toward the anterior, blunt anterior extension on one side and probably location of nucleus. This indicates that *P. obtusidens* cannot be assigned to the synonym of *P. dentatum* and should be regarded as an independent species. In addition, the historical records on the description of *P. obtusidens* and the related species allowed us to make a conclusion that *P. shikokuense*, *P. donghaiense*, *P. dentatem* and our isolates, which share identical rDNA sequences, morphologically coincide with *P. obtusidens.* Therefore, we propose that *P. shikokuense* and *P. donghaiense* should be regarded as the synonym of *P. obtusidens,* and based on the literature review and morphological data, *P. obtusidens* can be defined as an independent species characterized by 18-36 μm in length and 7-20 μm in width, parallel sides toward the anterior, blunt extension at one side, presence of valve pore and knob-like spines on the surface of thecal plates, chloroplasts distributed on the surface and the margins of cell, a round nucleus located in the posterior region of the cell, V-shaped periflagellar area and 5 platelets with collar-like projections in the periflagellar area.

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PS_1_4

Changes in cytoplasmic organelles characteristics by chemical algicidal substance for dinoflagellate *Cochlodinium polykrikoides and Heterocapsa circularisquama*

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Most of the chemical algicidal substance studies used to effectively control HABs(Harmful Algal Blooms) have been used extensively because of their potency, although they are potentially negative for other groups in the aquatic system. In this study, the effects of photosynthetic activity, cell wall damage, and enzyme activity on the cytoplasmic organelles were investigated in order to deduce the extinction mechanism of dinoflagellate *C. polykrikoides* and *H. circularisquama* cells as HABs organisms. As a result, chlorophyll concentration of *H. circularisquama* did not show a significant difference in chlorophyll concentration after chemical treatment, but the chlorophyll concentration averaged 14.2 ± 0.4 ㎍ L^{-1} of $CuSo_4$ treatment, NaClO treatment was 16.3 ± 3.6 ㎍ L^{-1}, TD49 treatment was 6.3 ± 1.0 ㎍ L^{-1} at 72 hours. In contrast, $CuSo_4$ was reduced to 9.3 ± 0.2 ㎍ L^{-1} for *C. polykrikoides*, while NaClO was increased to 25.6 ± 2.1 ㎍ L^{-1}. Results of testing the effects of chemical algicidal substance within the cytoplasmic organelles in accordance with the exposure time $CuSo_4$ gave a high effect on the enzymatic activity of *H. circularisquama*. Photosynthetic activity and cell wall damage were reduced to 5.7% and 11.5%, respectively, compared to the control during the treatment period, but the enzyme activity was 64.7% higher than that of the control after 3 hours. 3 hours after the photosynthetic activity of *C. polykrikoides* showed the inhibition rate of 40.8% when compared to the control average, the cell wall damage 54.9%, 89.2% enzyme activity. NaClO after treatment photosynthetic activity of *H. circularisquama* has elapsed after 3 hours compared to the control average of 10.6%, the cell wall damage is 13.2%, the enzyme activity, respectively showed inhibition rate of 20.4%. The photosynthetic activity of *C. polykrykoides* showed a high rate of 81.7% on average over the control, whereas cell wall damage showed an average effect of 32.5% over the control, while enzyme activity was not affected against the same time. Immediately after TD49 treatment photosynthetic activity of *H. circularisquama* and *C. polykrikoides* was 77.0% and 85.6% compared to the control. On the other hand, the enzyme activity after 3 hours after TD49 treatment increased *H. circularisquama* compared with the control, while *C. polykrikoides* showed a tendency to decrease. Overall, compared with the same time elapsed, TD49 showed the highest photosynthetic inhibition rate compared with the treatment with $CuSO_4$ and NaClO, suggesting that

TD49 penetrates into the cells immediately after treatment and affects photosynthetic activity. In this study, it is considered to be a substance that affects HABs by detecting the difference of cytoplasmic organelles changes due to chemical algicidal substance, but it will be usefully used as basic data for HABs control after risk assessment for marine ecosystem.

PS_1_5

Growth change in three harmful algal blooming species by addition of bacterial communities exposed to dissolved organic matter derived from *Heterosigma akashiwo* (Raphidophyceae)

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In marine environment, phytoplankton blooms induce to increase DOC concentration which is major carbon source in bacterial community. Due to difference in DOC consumption depending on bacterial species, this increase in DOC level can lead to variation in bacterial community structure (BCS). Interestingly, variation in BCS can affect phytoplankton growth and species composition. However, the effect of this variation on phytoplankton community is greatly unknown. In this study, we investigated variation in BCS according to addition of DOC released from *Heterosigma akashiwo*, and examined effect of this treated BCS on the growth of phytoplankton which is dinoflagellate *Prorocentrum minimum,* diatom *Skeletonema costatum,* and raphidophyte *Chattonella marina*. The BCS was isolated from field sample (Masan Bay, South Korea) when blooms of *H. akashiwo* were generated, and incubated for 3 days after addition of DOC from *H. akashiwo* culture at a final concentration of 10 mg L^{-1}. Then, the treated BCS was inoculated into three algal species. As a results, the growth of *P. minimum* (76 to 220%) and *C. marina* (158 to 1230%) in bacterial treatments was clearly enhanced. Whereas, the growth of *S. costatum* was suppressed (-24 to -28%). The data indicate variation in BCS induced by *H. akashiwo*-elicited DOC may affect distinctly depending on phytoplankton species.

PS_1_6

Evaluation of algicidal substances as a candidate for the control of dinoflagellates *Cochlodinium polykrikoides* and *Heterocapsa circularisquama*

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Chemical algicidal substances are useful for controlling HABs (Harmful Algal Blooms) and thus have been used for the species control although they have negative potentials to aquatic lives, damaging photosynthetic activity, cell wall, and enzyme activity of the cytoplasmic organelles. We investigated availability of the chemical for the control of two dinoflagellate *Cochlodinium polykrikoides* and *Heterocapsa circularisquama*, key HAB species in the Korean waters. The chemical treatment did not influence initial chlorophyll concentration of *H. circularisquama* but reduced the concentrations with time. The initial concentration, ranging 27.3 ± 0.2 μg L^{-1} to 39.0 ± 0.6 μg L^{-1}, decreased down to 14.2 ± 0.4 μg L^{-1} on average for $CuSO_4$, to 16.3 ± 3.6 μg L^{-1} for NaClO, and 6.3 ± 1.0 μg L^{-1} for TD49 72 hours post the treatment. Similarly, $CuSO_4$ reduced chlorophyll concentration down to 9.3 ± 0.2 μg L^{-1} on average. However, NaClO treatment elevated *C. polykrikoides* concentration of chlorophyll up to 25.6 ± 2.1 μg L^{-1} in the same time frame. $CuSo_4$ also influenced photosynthetic activity and cell wall damage for *C. polykrikoides*, with reduction rates 5.7% and 11.5%, respectively, compared to the control, while the enzyme activity being escalated up to 64.7% 3 hours post treatment. Photosynthetic activity of *C. polykrikoides* was inhibited down to 40.8% on average after 3 hours of the exposure. The treatment also damaged cell wall damage with frequency of 54.9%. NaClO treatment to *H. circularisquama* exhibited reduction in algal photosynthetic activity at the rate of 10.6%, cell wall damage at 13.2%, and the enzyme activity at 20.4% on average 3 hours after the treatment. *H. circularisquama* and *C. polykrikoides* responses to TD49 treatment were immediate and significant in photosynthetic activity with the rates 77.0% for the former and 85.6% for the latter. On the other hand, the enzyme activities of *H. circularisquama* treated with TD49 increasing 3 hours after treatment while those of *C. polykrikoides* showed a tendency to decrease. Overall, TD49 showed higher photosynthetic inhibition over the two chemicals, $CuSO_4$ and NaClO, suggesting that TD49 is more influential for the control of the algae. In conclusion, although algicidal substances might be useful for controlling HABs, it is still suggested that the chemicals need to be evaluated in term of overall damage potential to ecosystem integrity.

PS_1_7

Harmful algal blooms by dinoflagellates are related with specific bacteria

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The marine dinoflagellate algae are eukaryotic protists which exhibit a great diversity of forms, and are the most important primary producer in aquatic environments. However, some species can form harmful algal blooms (HABs; referred to red tide), and even contain biotoxins that affect humans and many other organisms. Recent studies have shown that HAB-forming dinoflagellates may grow in association with co-occurring bacteria as ectosymbiotic, endosymbiotic, and/or free-living forms. Even, many genes coded in the dinoflagellate nuclear genomes were acquired from symbiotic bacteria via horizontal gene transfer (HGT) and/or lateral gene transfer (HGT). In the present study, we examined the bacterial community structures of both free-living bacteria (FLB) and particle-associated bacteria (PAB) from different growth stages of HAB-forming dinoflagellates using pyrosequencing. These metagenomics showed that Roseobacter clades are intimately associated with host dinoflagellate in culture stages and field samples, suggesting they may strongly influence on the host cell growth and HABs in environments. In addition, we explored possible HGT genes using transcriptome libraries of dinoflagellates, and found extraordinary mitochondrial genomes and genes caused by HGT. In addition, we analyzed gene expressional responses of dinoflagellate cells exposed to environmental stressors. This provides molecular understanding genomics structures and responses for the harmful algal blooms.

PS_1_8

Remote sensing monitoring of *Margalefidinium polykrikoides* blooms in the South Sea of Korea

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Harmful Margalefidinium polykrikoides blooms has frequently occurred in the South Sea of Korea (SSK) since 1995. In order to cope with this bloom, it is essential to understand spatio-temporal distribution of M. polykrikoides blooms. Compared to traditional field survey method, remote sensing techniques is efficient in periodic and wide red tide detection, which requires fast and accurate monitoring. Until now, satellite-based red tide detection has been mainly performed, but it is difficult to monitor red tide more precisely because of limitation of spatial-spectral resolution. The objective of this study is to identify accurate distribution and extent of M. polykrikoides blooms using remote sensing data, such as optical image of UAV and hyperspectral data. In situ observations of M. polykrikoides blooms were conducted on August 7 and 8, 2018 in the coastal areas in Yeosu. During the field survey, the spectrum of waters and cell abundance of red tide were measured. At the same time to the field survey, UAV optical images were acquired for obtaining precise information of spatial distribution. It shows distinct spatial distribution of red tide blooms through geometric correction. Also, airborne hyperspectral images were acquired for understanding red tide species and cell abundance. As a result of comparing Rrs calculated by atmospheric correction of hyperspectral image and in situ Rrs, the correlation was good (0.7~0.9). The correlation between hyperspectral band and in situ cell abundance was calculated to obtain band ratio having the highest correlation with cell abundance. Cell abundance map showed the detail distribution of red tide blooms. The two images were combined to calculate red tide distribution and extent. Remote sensing monitoring using high spatial-spectral resolution is expected to be an efficient tool for identifying the distribution and extent of blooms.

PS_1_9

Evaluation of freshness quality of strawberries fruit produced in the biochar mixed hydroponic culture using photochemical reaction and thermal image methods

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Biochar is a pyrogenic carbon derived from carbon-rich biomass, especially agricultural residuals, and is being utilized in various management strategies such as soil chemical and physical improvement, waste management, and crop production. This study was carried out to investigate the effect of biochar application on freshness quality of strawberries fruit after harvest. The strawberries were grown in the conventional hydroponic culture with/without biochar application (manufactured by Nongwoo Bio Co., Ltd.). After harvest the strawberries was storage at room temperature during 7 days. To observe freshness of the harvested strawberries, we applied the analytical methods of photochemical reaction and thermal image at 24 hours interval. As a result of thermal image analysis, the average temperature of strawberries fruits between the conventional hydroponic culture with (CHB) and without biochar application (CH) was not different. Meanwhile, the difference of maximum and minimum temperatures was higher in the CH treatment than in the CHB treatment. The photochemical reaction showed higher maximal chlorophyll fluorescence (Fm) and variable chlorophyll fluorescence (Fv) in the CHB treatment indicating higher light-harvesting efficiency. And the effective quantum yield in PSII (ΦPSII) and chlorophyll fluorescence decrease ratio (Rfd) as a diagnosis tool for freshness quality of fruits were high in the CHB. Therefore, the biochar application improved the freshness of strawberries fruit and increased the storage period.

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PS_1_10

Evaluation of photochemical reactions for shikimic acid accumulation in Burcucumber (*Sicyos angulatus* L.) treated with glyphosate

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Burcucumber (Sicyos angulatus L), at present, was designated as one of the ecological disturbance plants listed by the Ministry of Environment in Korea. Glyphosate (N-phosphonomethyl glycine) is one of the most widely used nonselective herbicides in the world. Particularly, glyphosate inhibits the action of 5-enolpyruvyl shikimate-3-phosphate synthase (EPSPS) in the shikimic acid pathway, increase accumulation of shikimic acid.

The objectives of this study were to determine the optimal method for shikimic acid extraction and to analyze the changes in chlorophyll a fluorescence by different glyphosate concentrations at 24 hours interval. In this study, extraction conditions were determined for mass production of shikimic acid according to different extraction techniques and solvent treatments. As a result of shikimic acid contents in solvent extraction were highly increased at 6 DAT after treatment with 3.075 g.a.i glyphosate. Therefore, glyphosate induced the rapid accumulation of shikimic acid in apical leaves and fruits in burcucumber. The Chl a fluorescence treated with glyphosate in burcucumber leaves seemed to be concentration and DAT dependent inhibition, which was exactly fitted to the Lineweaver-Burk equation at least in J-step($Q_A \rightarrow Q_{B^-}$.) As the glyphosate concentrations increased, the fluorescence was decreased with eventual complete inhibition. The severely inhibitory concentration leading to decreased photochemical reaction was estimated to be 3.075 g.a.i. In conclusion, it could be deduced that the deactivation of Q_B by shikimic acid accumulation resulted in the energy dissipation within RC in PSII and in the inhibition of electron transport to PSI.

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PS_2_1

Red Tide Monitoring by Using Unmanned Aerial Vehicle

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Red tides occur in coastal waters around the world and can cause enormous economic damage. Many attempts have been made to prevent losses from red tides, but no effective method has been established yet. Thus, monitoring and prediction of red tides are considered extremely important. Remote sensing techniques commonly used to monitor red tides have limited accuracy. As an alternative, this study applied monitored the sea surface using an unmanned aerial vehicle (UAV). The target area was the coastal waters of Wando-gun, Jeollanam-do, South Korea. Images were shot by the UAV on September 3 and 10, and October 28, 2015. Using these images, a red tide index was established. Seawater samples were collected in the study area and analyzed to determine the type and quantity of plankton. The results obtained from comparing the quantity of plankton and the red tide index showed a correlation between the quantity of plankton and the index level. The technique proposed in this study is likely to overcome the limitations of existing monitoring methods. If this technique were applied to a seafood farming region, it is likely that accurate information could be promptly acquired regarding the distribution and spread of red tides. In future studies, a variety of sensor evaluations and site inspections are necessary to improve the accuracy of the information obtained.

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PS_3_1

The complete mitochondrial genome comparisons of true jellyfishes Scyphozoans

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Scyphozoans are marine cnidarians which represented by approximately 200 species. They inhabit the deep sea to the coastal waters in all oceans, from polar to tropic. Although theoretically metazoan mitochondrial genome (mtDNA) has typical structure, nonbilaterian animal mtDNAs reveals multiple exceptions in structure. In the present study, we compare scyphozoans mtDNA structures with addition of an *Aurelia* species which were collected from Korea. Despite species richness, up to date there are only 10 mtDNA recorded from the class which belong to two different orders Semaeostomeae and Rhizostomeae. In comparison all Scyphozoa mtDNA were linear molecules which include 13 protein coding genes, 2 rRNAs and 2-6 tRNAs. The sizes of the mtDNAs were variable between 15,855 to 17,381 bp. The longest mtDNA belongs to *Cyanea nozakii* while the shortest belongs to *Rhopilema esculentum*. The protein coding gene orientations was identical for all 10 mtDNA. But the sizes of proteins were slightly different in Scyphozoa mtDNA. Mostly Rhizostomeae species protein coding genes were slightly shorter than the Semaeostomeae species. The location and orientation of rRNAs was also identical in comparison of the mtDNAs. The sizes of rRNA genes varieties showed similarity with protein coding gene size varieties. Same like protein coding genes mostly, Rhizostomeae species rRNA genes were slightly shorter than the Semaeostomeae species. Most scientists believe that the environmental factors are major triggering factor for blooming of jellyfish but genetic mechanism of blooming is still unclear because lack of genetic data of jelly fish. Our study provides additional data for further analysis of Scyphozoa molecular phylogeny.

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PS_3_2

Molecular approaches reveal biogeographic separation of the harmful jellies *Aurelia coerulea* and *A. limbata* along the eastern coasts of Korea

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The moon jelly *Aurelia coerulea* was widely distributed in Korean coastal waters, and its dense blooms caused harmful impacts to fisheries and environments. Recently, cold water moon jelly *Aurelia limbata* was described from the eastern coasts of Korea; however, distribution pattern of both species have not been investigated in Korea. In the present study, we determined nuclear rDNA and mitochondrial COI gene sequences of *A. coerulea* and morphologically-suspected *Aurelia limbata* collected from Yang Yang coasts (Eastern city, Korea). Upon comparisons of ITS sequences, *A. limbata*-suspected organisms were matched to that of *A. limbata* (98% similarity with *A. limbata*, but it was 89% to *Aurelia* sp.1 (Korean specimen, GenBank EU276014). Molecular surveys showed that *A. limbata* occurred separately to *A. coerulea*. This provided a molecular evidence to confirm *A. limbata* occurrence in Korea.

PS_3_3

Three species of family Diphyidae (Hydrozoa: Siphonophorae) in Korean Waters

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Siphonophorae is a unique gelatinous zooplankton, in which many individuals gather and live like a one superorganism. Individual's role in the colony differs greatly depending on their morphological difference, making them more unique in their own right. Despite its uniqueness, research of Siphonophorae still lacks in Korea. Especially, the family Diphyidae has a high diversity, but only few recorded in Korea. During the sampling trips in september 2018, various diphyids were collected from off the south coast of Korea and Jeju island. Some of these were identified to be *Eudoxoides mitra* and *Chelophyes appendiculata*, which are all new records in Korean waters. In addition, *Chelophyes contorta* has already been recorded in an ecological paper, but it lacked any morphological analysis. Therefore, this was also added. In this study, the morphological descriptions of these three species were provided. All have divided mouth-plate, and claw-shaped hydroecium. In the case of *Eudoxoides mitra*, it is not spirally twisted unlike in the *Eudoxoides spiralis*, and has also baso-dorsal ostial teeth. *Chelophyes contorta* and *Chelophyes appendiculata* have shorter hydroecium than *Eudoxoides mitra* and no ostial teeth. Main character in *Chelophyes contorta* is oblique club-shaped somatocyst. In the case of *Chelophyes appendiculata*, three ridges meet at the apex. Our findings have updated the confirmed Siphonophorae in Korea to be 3 suborders, 6 families, 3 subfamilies, 14 genera and 21 species.

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PS_3_4

Proteomic Investigation to Identify Anticancer Targets of *Nemopilema nomurai* Jellyfish Venom in Human Hepatocarcinoma HepG2 Cells

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Nemopilema nomurai is a giant jellyfish that blooms in East Asian seas. Recently, *N. nomurai* venom (NnV) was characterized from a toxicological and pharmacological point of view. A mild dose of NnV inhibits the growth of various kinds of cancer cells, mainly hepatic cancer cells. The present study aims to identify the potential therapeutic targets and mechanism of NnV in the growth inhibition of cancer cells. Human hepatocellular carcinoma (HepG2) cells were treated with NnV, and its proteome was analyzed using two-dimensional gel electrophoresis, followed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI/TOF/MS). The quantity of twenty four proteins in NnV-treated HepG2 cells varied compared to non-treated control cells. Among them, the amounts of fourteen proteins decreased and ten proteins showed elevated levels. We also found that the amounts of several cancer biomarkers and oncoproteins, which usually increase in various types of cancer cells, decreased after NnV treatment. The representative proteins included proliferating cell nuclear antigen (PCNA), glucose-regulated protein 78 (GRP78), glucose-6-phosphate dehydrogenase (G6PD), elongation factor 1 (EF1), nucleolar and spindle-associated protein (NuSAP), and activator of 90 kDa heat shock protein ATPase homolog 1 (AHSA1). Western blotting also confirmed altered levels of PCNA, GRP78, and G6PD in NnV-treated HepG2 cells. In summary, the proteomic approach explains the mode of action of NnV as an anticancer agent. Further characterization of NnV may help to unveil novel therapeutic agents in cancer treatment.

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PS_3_5

Feeding behavior of a box jellyfish, *Carybdea brevipedalia*

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Feeding of *Carybdea brevipedalia* Kishinouye, 1891 (Cubozoa: Carybdeidae) was observed and recorded in Dugok Beach and Namildae, a small fishing port adjoining a beach. Data were collected separately at night under artificial light and dark/dim light condition to consider the possible artefact of the light on their feeding behavior. Decapod larvae, mysids, swimming larvae of polychaetes and larval fish were the major prey items, while copepods, the most predominant zooplankton in the study area were not found in their gut. *Carybdea brevipedalia* was a strong vertical migrator, conspicuously ascending right before sunset in Dugok, while its distributional depth was not clearly different between day and night in Namildae. Individuals' gut contents were observed to be minimal during the day, while they started to prey on after sunset and finished 1 – 2 hour(s) before sunrise. Since the preying organisms were usually faster swimmers, they were captured passively by elongated tentacles of *C. brevipedalia.* More than 90 % and 80 % of individuals observed between 20:30 to 03:00 involved 1 – 4 preys in their guts in Dugok and Namildae, respectively. Digestion time varied from ca. 1.5 to 4.0 hours, depending on prey species. The results showed that *C. brevipedalia* is fishing for its prey rather than hunting.

PS_3_6

Molecular phylogeny of planthoppers according to mitochondrial protein coding genes

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The planthopper superfamily Fulgoroidea (Insecta: Hemiptera) is one of the most dominant groups of phytophagous insects with 20 families, containing a total of 12,500 species worldwide. All species in Fulgoroidea are plant-feeding, and many of them are economically significant pests of major agricultural crops such as *Metcalfa pruinosa*. *M. pruinosa* is an insect species in the superfamily Fulgoroidea which is also known as the citrus flatid plant hopper. This species was discovered in the eastern United States by Thomas Say, in 1830. This species is native to North America but has spread to most parts of Europe except southern Europe and has been reported in Korea first time in 2009. They prefers regions with high humidity, but they can survive in new habitats too which gives them chance to release into a nonnative area. It has been reported that a total of 74 species belonging to 41 families were confirmed as host plants in Korea. In South Korea, this pest attacked 145 plant species from 62 families. In the present study we analyzed the molecular phylogeny of Fulgoroidea species based on protein coding genes of mitochondrial genome and compare the phylogenetic relationships in the superfamily gene by gene. In total 19 species from six different families complete mitochondrial genome data with additional an invasive *M. pruinosa* species used for the analysis. This study contributes to the strengthening of the Fulgoroidea molecular genome library.

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PS_7_1

Fabrication of Novel Chitosan Composited Fibers from Paper Mill Sludge Biochar for Effective Removal of Phosphate

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Excess phosphorous levels in municipal and industrial effluents result in eutrophication of surface water. In this work, various biochar-based adsorbents were investigated as an adsorbent for the removal of phosphate ions (P) from aqueous solution using batch experiments. Paper mill sludge biochar produced under CO_2 and N_2 environments (BC-N and BC-C respectively) and chitosan/biochar composited fibers produced with BC-N and BC-C (FBC-N and FBC-C respectively) were tested for P sorption under uncontrolled pH conditions. BC-N, BC-C, FBC-N and FBC-C exhibited 1.9, 0.3, 4.0 and 6.2mg/g P adsorption capacity and 9.9, 1.7, 20.3 and 30.9% P adsorption percentages respectively. FTIR, EDS, and XPS studies suggested that the adsorption mechanism was possibly attributed to the ion exchange reaction and electrostatic attraction between the tested adsorbents and phosphate ions. In addition, precipitation with minerals and ligand exchange were also identified as the possible mechanisms of P sorption on the biochars and biochar modified fibers. The results of this study imply that chitosan-modified biochars have higher potential as a green and low-cost sorbent for remediating P contaminated waters.

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PS_7_2

Effect of Feedstock Type and Modification Method on Carbon Dioxide Adsorption Capacity of Biochar

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Biochar which is a porous carbonaceous material produced through thermochemical conversion of organic materials, might be a potential source for CO_2 capture. Modification of biochar with novel structures and surface properties may enhance CO_2 adsorption capacity of the pristine biochar. However, biochar properties which influence its CO_2 adsorption capacity may vary with the feedstock type and modification method. Therefore, this study was aimed to assess the effect of feedstock type and modification method (KOH and combination of KOH and CO_2 modification) on CO_2 adsorption capacity of biochar. Biochar was produced using 100% wood waste (W) and 70% wood waste + 30% chicken manure (WCM) through gasification. Biochar samples were activated using either 1 M KOH (WK, WCMK) or 1 M KOH and 500 mL CO_2 min^{-1} at 850 ° C (WKC, WCMKC). The modified and pristine biochar were assessed for physicochemical properties, CO_2 adsorption capacity and cyclic stability. WCMK showed the highest CO_2 adsorption capacity corresponding to the highest surface area, micro pore area and micro pore volume. Modification of biochar either with KOH or KOH and CO_2 enhanced the CO_2 adsorption capacity of pristine biochar due to increasing surface area, microporosity and micro pore volume irrespective of the feedstock type. Both WKC and WCMK showed rapid adsorption capacity and excellent regeneration ability irrespective of the feedstock type. However, as both KOH and KOH+CO_2 modification resulted in comparable CO_2 adsorption capacity, biochar modification with KOH will be a promising and cost effective option for capturing CO_2.

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PS_8_1

Screening aquatic insect predators for biological control of *Aedes aegypti* in Hanoi, Vietnam

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Dengue fever has rapidly spread throughout tropical Southeast Asia, including Vietnam, particularly in urban areas. Among the cities in Vietnam, Hanoi represents “hot spot” of dengue fever outbreak with a number of patients increased for recent years. The disease was transmitted mainly by the vector mosquito *Aedes aegypti.* The use of pesticides helped reducing mosquito populations in the early time, but many cases of pesticide resistance in *Ae. aegypti* have been reported in this region. Accordingly, biological control was suggested as an alternative environment-friendly method in controlling vector mosquito populations. An investigation of aquatic insect predators was conducted from 15 natural water bodies in Hanoi in 2018 to search for potential mosquito predators. Fifteen predator species belonging to Hemiptera, Coleoptera, and Odonata were sampled and six commonly found potential predator species (*Diplonychus rusticus*, *Eretes* sp., *Hydrobasileus* sp., *Anisop* sp., *Enithares* sp., and *Cercotmetus* sp.) were brought to the laboratory for predation efficiency experiments. Fourth instar larvae of *Ae. aegypti* were used as prey under laboratory conditions of photoperiod 16:8 (L:D) and water temperature 24-26°C. Three-hundred *Ae. aegypti* larvae were provided at each experiment and the consumption efficiency was evaluated by subtracting the number of live prey individuals after 24 hrs. Average 24-h predation rate was the highest in *Diplonychus rusticus* (68,9%) followed by *Hydrobasileus* sp. (66,3%). Predation rates were significantly different ($p<0.01$) among experimented predators. This result could provide basic knowledge for further research on the biological control of vector mosquitoes in tropical Southeast Asia.

PS_8_2

A new distributional record of the giant water bug *Lethocerus patruelis* (Hemiptera: Belostomatidae) in Thailand with notes on its conservation

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Giant water bugs in the genus *Lethocerus* (Hemiptera: Belostomatidae) are the world's largest aquatic insects (60-110 mm in body length), and have a global distribution. They are often top predators in shallow standing waters, such as wetlands and paddy fields. Their natural preys are amphibians, fishes, even snakes and turtles. Recently, Asian *Lethocerus* populations have declined dramatically and their conservational status was considered to be the threatened species. However, the distribution of Southeast Asian *Lethocerus* is still unclear. In this study, *Lethocerus* species were sampled from 13 sampling sites throughout Thailand, during May 2017 to June 2018. Based on our study, *L. indicus* was found in all sampling sites, whereas *L. patruelis* was found in only two sampling sites: Chiang Rai and Surat Thani Province, Northern and Southern, Thailand, respectively. This is the first discovery of *L. patruelis* in Thailand. An updated *L. patruelis* distribution was presented in this study: Southern Europe, Middle East, Mesopotamia, Persian Gulf, India, Pakistan, Myanmar, and Thailand as the easternmost distribution. The *Lethocerus* species have been facing threats in Thailand because these are commonly sold in local markets as foods, in addition to habitat loss. Therefore, the concern on the conservation of *Lethocerus* in Thailand should be raised, especially for *L. patruelis* which is rarely found in Thailand.

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PS_10_1

Temporal changes in the community structure of macrobenthos in the Bongam tidal flat of Masan Bay, Korea

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This study was conducted to detect annual changes in the community structure of macrozoobenthos in response to the fluctuating benthic habitat conditions in the Bongam tidal flat of Masan Bay, Korea. Faunal samples were collected by monthly from March, 2014 to April, 2016, and from October 2017 to October 2018. At each sampling time, we used box core samples (0.025 m^2) and collected four times per site during low tide period. As a results of sedimentation analysis and benthic community structures, the sedimentary type of the tidal flat was typical sandy bottoms consisted of over than 80% except May and June 2015. The total organic carbon (TOC) content increased up to 1.7% in May and June 2015, but the mean TOC was less than 1% during most of the study period. The number of species ranged from 6 to 16 during the study period. The density was lower in the summer season of 2014 compared to other study period. Polychaetes accounted for more than 80% of the total density. The maximum biomass ranged from 58.7 to 2,662.8 g wt/m^2 in 2018, for mass appearance of bivalve, *Laternula marilina*. The major dominant species were four deposit feeders such as *Heteromastus filiformis*, *Prionospio japonicus*, *Simplisetia erythraeensis*, *Hediste diadroma* and a filter feeder, *Laternula Marilina* in the Bongam tidal flat. There was little annual change in the composition of dominant species during the study period. The most dominant species was *H. filiformis* in the Bongam tidal flat. The density of *P. japonicus* showed the highest in April 2014, but its density rapidly decreased in winter 2015. Two deposit feeding nereidid polychaetes, *S. erthraeensis* and *H. diadroma* showed negatively correlated in their densities. *H. diadroma* has the largest density in 2015 and has continued to decline until 2018. On the other hand, *S. erthraeensis* showed a tendency to increase after 2015. In the Bongam tidal flat, the temporal change of sedimentation occurred in 2015, *H. diadroma* was temporally increased density while, *P. japonicas* was decreased since winter of 2015.

PS_10_2

Impact of environmental variables on the diversity and distribution of the megabenthos in the South Sea of Korea

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The South Sea of Korea is affected by three systems of currents: the high-temperature, high salinity Jeju Warm Current; the low-salinity Yangtze River discharge flow from China; and the cold-water bottom currents of the Yellow Sea. In addition, seasonal flow differences from various waterfalls drive environmental variability in these regions. As a result, the study area has high biodiversity, particularly the sea around Jeju Island, which is considered one of the world's most biodiverse areas; however, information on the diversity of the megabenthos is very limited. Therefore, in this study, we analyzed the diversity and distribution of the megabenthos in the South Sea based on environmental factors. Megabenthos samples were collected using 10-min trawls towed at 18 stations from 2015 to 2016. The dominant species (>5% of the total density) were *Anthopleura* spp. (Actiniaria), *Siphonalia spadicea fuscolineata* (gastropod mollusks), and two subtropical species, *Mactrinula dolabrata* and *Acila divaricate* (bivalve mollusks). There were differences in biodiversity among the three sea regions (southwest, southeast, and northwest of Jeju Island) and the frontal zone of the South Sea. The total numbers of individuals and major taxa were generally higher in the frontal zone of the South Sea and northwest of Jeju Island. Biomass was particularly high in the frontal zone of the South Sea. Environmental factor analysis showed that differences in biodiversity were related to sediment (grain size), salinity, and temperature. These results indicate that changes in marine environmental conditions in the South Sea of Korea affect megabenthos species composition and diversity.

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PS_10_3

Species composition and distribution of hull-fouling macrozoobenthos differs among research vessel navigation areas

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The purpose of this study was to identify and explore the distribution patterns of hull-fouling macrozoobenthos on Korea Institute of Ocean Science and Technology (KIOST) research vessels. In 2017 and 2018, five KIOST research vessels (R/Vs) were divided into three categories by navigation area: ocean (R/Vs Onnuri and Isabu), coastal (R/V Eardo), and local (R/Vs Jangmok 1 and Jangmok 2); the local class consisted of vessels operating in shallow coastal areas in eastern, western, and southern parts of the Sea of Korea. Hull-fouling species were collected from three hull areas at different depths (upper, middle, and bottoms) and from the thrusters and propeller areas, based on the hull waterline. A total of 38 species were collected, at a density of 8322 individuals/m^2 and biomass of 1620.2 g/WWt/m^2. We identified 19 crustacean species (50.0%), nine polychaete species (23.7%), four mollusk species (13.2%), and six species of other taxa (15.8%). The species numbers and mean densities were highest among crustaceans, among which *Balanus* spp. appeared in large quantities; mollusks comprised the greatest proportion of biomass. The coastal class R/V Eardo carried the largest number of macrozoobenthos species (21). Ocean classes R/Vs Isabu and Onnuri carried the fewest species (six and four, respectively). The densities and biomasses of hull-fouling macrozoobenthos were highest on the coastal class R/V Eardo and the local class R/V Jangmok 1, respectively. Hull-fouling species on ocean class R/Vs were found at high densities on the flat hull bottom, whereas those on coastal class R/Vs occurred at high densities in stern thruster area. The dominant species included *B. Amphitrite* (59.3%), *B. trigonus* (22.1%), *B.improvises* (7.1%) among crustaceans; *Hydroides ezoensis* (4.8%) among polychaetes; and *Crassostrea gigas* (4.1%) among mollusks. *B. Amphitrite* was dominant in the middle area and flat bottom parts of the hull in coastal and local class R/Vs, whereas other species such as *B. trigonus, H. ezoensis*, and *C. gigas* were dominant on the flat bottom of local class R/V Jangmok 2. Diversity indices of hull-fouling macrozoobenthos were highest for local class R/Vs Jangmok 1 and Jangmok 2, and lowest for ocean class R/V Isabu. The results of this study indicate that navigation areas are important determinants of the species composition and the diversity of hull-fouling macrozoobenthos on R/Vs.

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PS_10_4

Species composition and community structure of the soft-bottom macrobenthos at the coastal and its adjacent areas of Dokdo, the East Sea of Korea

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This study investigated the species composition and community structure of the soft-bottom macrobenthos around coastal and its adjacent areas of Dokdo. Animals were collected using a Smith-McIntyre grab ($0.1m^2$) at 13 sites in May and August 2017. The mean depth of the shallower sites was 56m and the mean depth of its adjacent sites was 1,490m. There was no variation of the bottom salinity between at the shallow and deep areas. The bottom temperature increased from spring to summer season, but the bottom dissolved oxygen decreased. A total of 158 species/$4.1m^2$ were collected from 111 species/$2.1m^2$ in May to 107 species/$2.0m^2$ in August. These number of species was higher than that of the coastal of East Sea. The mean density of the macrobenthos was 542 individuals/m^2 from 267 individuals/m^2 at deeper area to 1,120 individuals/m^2 at shallow area. The dominant species (>2% of the total density) were *Melita denticulata* (amphipod), three mollusks *Tucetonella munda*, *Limatula japonica*, and *Pleuromeris pygmaea*, and three polychaetes *Syllis amica*, *Amphinome* sp1., and *Terebellides horikoshii*. The most of dominant species appeared at the coastal area of Dokdo, but polychaete *T. horikoshii* appeared only at deeper area of Dokdo. The community structure of the macrobenthos divided into four groups by the environmental conditions. These result indicate that variations in marine environmental conditions from shallow to deep area of Dokdo influence the species composition and community structure of macrobenthos.

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PS_10_5

Fluorocolorimetric Detection of Endocrine Disruptors Using Aptamer-Facilitated Gold Nanoparticles

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Endocrine disruptors (EDCs), as xenoestrogens, have been suspected to be associated with reproductive dysfunction and physiological abnormality in human. Among EDCs, bisphenol A (BPA), phthalate, and nonylphenol (NP) are of major concern, due to their environmental or human exposure from plastics and detergents. For vulnerable people, a rapid and simple detection of EDCs is highly demanded. Here we report a simple EDC assay using aptamer-facilitated gold nanoparticles (AuNPs). SELEX-derived anti-EDC aptamers triggered self-assembly of unmodified AuNPs (citrate-stabilized AuNPs) in the presence of EDCs, leading to a color change in the AuNP solution from reddish to purple upon the addition of high salt. We combined fluorescence measurement by SYBR Green with the AuNP colorimetry to enhance detection sensitivity. In BPA, the detection sensitivity was achieved as low as 1 ppb, which was greater than those of other reported methods. This method also enabled a selective and sensitive detection of BPA from real samples including thermal papers or food cans. Furthermore, multiple AuNP-based colorimetry using three EDC aptamers resulted in a rapid determination of BPA, phthalate, and NP with high selectivity. We suggest that this aptamer-facilitated AuNPs will offer many applications in the field of environmental science.

PS_10_6

Impacts of a massive aquaculture of Manila Clam (*Ruditapes philippinarum*) on the macrobenthic communities in a tidal ecosystem in Korea

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We investigated the biological impacts of the massive aquaculture of Manila Clam (*Ruditapes philippinarum*) on the macrobenthic communities in a tidal ecosystem in Korea. We collected macrobenthos (>1 mm long) seasonally using a can-core (0.1 m^2) in intertidal zone of Geunsoman, Taean from April 2011 to December 2014. At Geunsoman, we found 146 macrobenthos species, including 60 polychaetes, 53 crustaceans, and 16 mollusks. The dominant species was *R. philippinarum* (20,020 ind./m^2), followed by *Heteromastus filiformis*, *Ceratonereis erythraeensis*, and *Ampharete arctica. The mean grain size of sediment were 3.01 ± 0.84 Φ, and TOC of sediment were 0.60 ± 0.44. The correlation analysis showed that the R. philippinarum* density correlated with the evenness and diversity. *R. philippinarum* did not have any associations with any dominate species more than 1% totally density. Surveys showed that *R. philippinarum* share space with other macrobenthos, but do not affect each other. This is because there is little competition among macrobenthos species in aquaculture. In conclusion, the factors affecting *R. philippinarum* are intraspecies competition, and the more clams, the more competition due to space constraints.

PS_10_7

Effects of booster biocides and by-products from vessels on embryo test of a sea urchin, *Mesocentrotus nudus*

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In this study, we aimed to assess the toxicity of biocide including of antifouling paint and by-products from vessels on embryos of a sea urchin, *Mesocentrotus nudus*. In this study evaluated toxicity on the 5 kinds of biocide (Sea-nine 211, Diuron, Irgarol 1051, CuPT, ZnPT), water jet from R/V EARDO and ISABU in KIOST, and water jet extracted with MeOH. As a result of the fertilization rate of sea urchin for 5 kinds of biocide, the value of EC_{50} of Sea-nine was 8.134 μg/L, but those of Diuron and Irgarol were 10,777 μg/L and 4,476 μg/L, respectively. The value of EC_{50} of CuPT and ZnPT were 3.423 μg/L and 6.488 μg/L, respectively. Among 5 AFS active substances, the highest toxicity was found in CuPT. To assess the adverse effects of the wastes on marine biota from ship's surface during in-water cleaning activities, we conducted the toxicity test for by-products using sea urchin embryos. The fertilization rate of sea urchin embryos exposed on the water samples from the water jet operation on the R/V EARDO was 79±5.8% at 1000-fold diluted solution, and the fertilization rates exposed in 10-fold and 100-fold diluted solutions were 0.2±0.5% and 2.3±1.4%, respectively. The fertilization rate in the water jet samples from the R/V ISABU was 0.2% in 10-fold diluted solutions, but normal fertilization was found (>90%) in 100-fold diluted solution. The fertilization rate on the MeOH extracted solution of wastes from the R/V EARDO was 0% in both 30 and 300-fold diluted solutions. The fertilization rate was more than 90% in 3,000-fold diluted solutions. The fertilization rate on the MeOH extracted solution from the R/V ISABU was 0% in both 2.5 and 250-fold diluted solutions. The normal fertilization was found (>90%) in 2,500-fold diluted solutions. The highest toxicity on sea urchin embryos was found in the wastes from the water jet operation on the R/V EARDO, and the toxicity of MeOH extract was higher than wastes from the R/V ISABU.

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PS_10_8

Seasonal phytoplankton community using microscopic and Chemotax pigment analysis in Seomjin River Estuary, Korea

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Biotic and abiotic factors in estuaries have dramatic gradients due to the land-derived input and tide-induced exchanges with open seawater. To assess how environmental condition influences the spatio-temporal distribution of phytoplankton, we investigated the phytoplankton communities using microscopic and HPLC pigment analysis along a salinity gradient at 7 stations in the Seomjin River estuary (SRE), Korea. As a result of the both analysis, although marine planktonic diatoms generally dominated downstream in the high or middle salinity area, the differences in dominant species were associated with salinity gradient, which changed rapidly more than 10. In particular, pigments fucoxanthin and alloxanthin in late spring was high in upstream of SRE. In summer, peridinin pigment in downstream and diatoms in upstream was relatively high. In autumn, although cryptomonas species were kept to high levels in microscopic analysis, fucoxanthin pigment originated diatoms in the CHEMTAX analysis have contributed, implying that there was coexistent with non-identified small sized phytoplankton. In winter, diatoms groups have greatly occupied in both microscopic and pigment analysis in most stations. Therefore, the spatial distribution of phytoplankton has markedly changed along salinity gradients even though there were differences of seasonal total biomass and community composition of phytoplankton in the SRE. In particular, the PPCs (photoprotective carotenoid pigment): PSCs (photosynthetic caroteniod pigment) ratio was relatively low during four seasons, implying that there was suitable habitat for diatom owing to the high turbulence area of rapid water movement in the SRE. In addition, we have a good agreement between microscopy and chemotaxonomy data that pigment analysis may have contributed to assess the complex estuarine phytoplankton community even lead to cell death and ultimately changes the species composition.

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PS_10_9

Environmental factors affecting dynamics of phytoplankton community in port baseline surveys in Korea

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To understand the environmental factors affecting dynamics of phytoplankton communities at the busiest ports (Busan, Ulsan, Incheon and Gwangyang) of Korea, we seasonally investigated the physico-chemical factors and phytoplankton assemblages from February 2007 to November 2008. The majority of the phytoplankton communities were diatoms (78%). The highest abundance of diatoms were observed at Busan in summer 2007, and at Ulsan in spring 2007. *Cheatoceros debilis* and *Ch. pseudocrinitus* occupied over 60% diatoms at Busan, and *Detonula pumilia* dominated at Ulsan port. The port of Incheon and Gwangyang is characterized as eutrophic and semi-enclosed environment. The abundance of diatoms peaked in winter when *Skeletonema costatum* dominated with lower salinity, higher concentrations of chemical oxygen demands and total suspended solid at Incheon and Gwangyang ports compared to ports of Busan and Ulsan. When diatoms bloome, abundance of diatoms were observed with relatively low concentrations of silicate and nitrate ($p<0.001$), indicating prosperous uptake of dominated diatoms. The next dominant group dinoflagellates distributed frequently at Busan, Ulsan and Gwangyang ports in summers, when their abundance was significantly correlated with increasing temperature and decreasing salinity ($p<0.05$). Also, concentrations of phosphate was high (>1 μM) at the four ports in summers. Exceptionally, abundances of dinoflagellates occurred at low density during the study period at Incheon port. At the ports surveyed, the predominant diatoms were characterized by low concentrations of nutrients such as silicate and nitrate, while dinoflagellates mainly occurred in summers with increasing temperature, low salinity and high phosphate concentrations.

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PS_10_10

Distribution of mesozooplankton in the deep-sea hydrothermal vent in the Indian Ridge

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Mesozooplankton from the Indian Ridge hydrothermal vent fields were collected with a 1 m^2 multiple opening-closing net and environmental sensing system (MOCNESS) to examine the distribution, taxonomic and species composition. The hydrothermal vents Solitaire(INVENT A), Onnuri Vent Field (OVF), and reference site (ref-site) sampling were conducted with oblique tows from ~100 m above the bottom of the basin (~2,500 m) to the surface. The total abundance of mesozooplankton were 26,376 inds. 100 m^{-3}, 82,344 inds. 100 m^{-3}, 97,663 inds. 100 m^{-3}, in INVENT A, OVF and ref-site, respectively. The abundance were higher at the surface mixed layer (0-200 m) (INVENT A: 19,478 inds. 100 m^{-3}; OVF: 72,954 inds. 100 m^{-3}; ref-site: 77,382 inds. 100 m^{-3}). The taxonomic groups foraminiferans, copepods, chaetognaths, radiolarians, ostracods, appendicularians, crustacean larvae, amphipod larvae, polychaete larvae, and mollusc larvae appeared at all survey stations. Copepods (immature and adults) were dominantly distributed (average = 72.7%) in all the stations. The dominant adult copepods were poecilostomatoida *Oncaea media* (INVENT A: average = 3.5%; ref-site: average = 2.4%), and calanoida *Paracalanus aculeatus* (OVF: average = 2.9%). Gastrodpod larvae, bivalve larvae and amphipod larvae appeared at INVENT A and OVF, and decapod larvae, polychaete larvae and gastropod larvae appeared at ref-site. The bivalve larvae that appeared at OVF was morphologically similar to *Bathymodiolus* spp. that inhabits in the hydrothermal vents. The gastropod larvae that appeared at OVF was morphologically similar to benthic species *Phymorphynchus* spp. The macrobenthic larvae of gastropods and bivalve associated with the hydrothermal vents were collected at surface mixed layers, indicating that larval forms may be dispersed ~2,000 m above the vents.

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PS_10_11

Population genetic structure of chum salmon, *Oncorhynchus keta* from South Korea: identification of management units for its conservation

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The chum salmon (*Oncorhynchus keta*), known as a Pacific salmon, is widely distributed from the Far East to North America along the Pacific Rim. This species is an important fisheries resource with a high economic and commercial value. They have an anadromous life style where they hatch in freshwater and migrate to the sea for growth, then return to their natal rivers to reproduce. Their homing behavior sometimes lead to decrease within-population genetic diversity resulting from limited gene flow occurring among geographically disconnected populations, elevating the risk of local extinction. As an effective application of genetic data to the fisheries management, elucidating the population genetic structure of the chum salmon using molecular markers will assist in determining its management units. Using mtDNA control region sequences and eight nuclear microsatellite loci, we assessed the current population status of *O. keta* in South Korea by estimating the level of genetic diversity and genetic structure for 16 populations (including ten wild and six hatcheries) from 11 tributaries within major returning river basins. The analyses showed the similar level of genetic diversity between wild and hatchery populations with a total of seven mtDNA haplotypes and 25.4 alleles per microsatellite. Both markers revealed that genetic differentiation (F_{ST}) between populations tend to be low, suggesting a moderate level of gene flow taking place among those populations. For future conservation, we suggest that the Korean salmon population can be considered as a single stock for its management unit. Nonetheless, we should make an effort to preserve the unique haplotypes only detected in particular populations.

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PS_10_12

Abalone mortality associated with harmful algae *Karenia mikimotoi* and *Cochlodinium polykrikoides*

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In summer 2016, *Karenia mikimotoi* at about 1,200 cells ml^{-1} hit local abalones *Haliotis discus hannai* cage farms. The blooms were accompanied by the abalone mortality and were blamed for the mortality as field and laboratory studies had witnessed the abalone vulnerabilities to *K. mikimotoi*. However, ambiguities are still existing as most of the information are from sensitive early stages. To gain more realistic data we exposed adult abalones to *K. mikimotoi* (KM02 KSS) at up to 20,000 cells mL^{-1} for up to 48 h at 6 temperature regimes in 30L chamber equipped with full circulation system. Each temperature regime was achieved by doing the test when farm temperature reached each target to eliminate study stress of temperature acclimation. The 6 target temperatures were 23, 26, or 28℃ in temperature increasing season and 28, 26, or 23℃ in decreasing season. *K. mikimotoi* damage potential was compared with *Cochlodinium polykrikoides* and *Tetraselmis suecica* at corresponding biomass on the basis of total carbon. *K. mikimotoi* employed in our study was harmless to the abalone at concentration up to 20,000 cells mL^{-1} for up to 48 h in all test temperatures except for one regime, 28℃ in temperature increasing season ($P<0.05$). Interestingly, no algal intact and harmless *T. suecica* at the damaged temperature regime induced about 15% mortality at the end of the test, suggesting that the damage might be due to temperature-increasing stress other than the alga-borne harmful effect. In the comparison of damage potential by species, *C. polykrikoides* was most harmful, suggesting that *K. mikimotoi* might not be the main culprit of 2016 abalone mortalities. However, our conclusion has something uncertain and thus verified. One of them is if the tested culture strain is as harmful as wild one. This together with other considerations remains as a subject of further study.

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PS_10_13

Risk assessment of in situ application of microbubble ozonation to cyanobacteria control

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Harmful cyanobacteria can produce toxins and odor compounds that may bring out adverse effects on humans as well as wildlife. Ozonation has been used to treat harmful cyanobacteria in situ. However, there is a possibility to cause adverse effects to other aquatic organisms because of ozone toxicity. Recently, microbubble technology has been proposed to enhance the dissolved concentration of ozone, which may aggravate the adverse effect of ozone. Nevertheless, there is no study about risk assessment of microbubble ozonation of cyanobacteria on aquatic organisms. In this study, *Daphnia magna* which is a representative species of toxicity assessment was used to assess the adverse effect of microbubble ozonation. The removal of *Microcystis aeruginosa* (1.74 x 10^6 cell/ml) was 82.9% by microbubble ozonation (initial O_3 = 1.55 mg/L) for 30 min, and further completely removed by *Daphnia magna* for 48 h. Moreover, ever, no mortality was observed in *D. magna* in this experimental condition. This study suggests that microbubble ozonation is a safe and useful tool to remove harmful cyanobacteria without critical hazard on *D. magna*.

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PS_10_14

A simple and efficient method for removing of ricin B chain from unknown ricin sample

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Ricin is the one of the most dangerous protein found in caster bean (*Ricinus communis*). This protein is biohazardous substance designated as bioterrorism agent and chemical warfare agent by US Centers for Disease Control and Prevention. Ricin is composed of two subunits; toxic A chain (acting as ribosome-inactivation enzyme) and carbohydrate-binding B chain (acting as lectin protein that has various binding sites of glycoproteins or glycolipids). Ricin binds to the cell surface to recognize glycoprotein or glycolipids by the B chain activity. It enters the cell by endocytosis in membrane vesicle. And it is transported to endosomes and is dissociation in ER; A chain and B chain. In the cytosol, the separated ricin A chain inactivates ribosomes by cleaving an adenine Structural changed rRNA is unable to bind elongation factors. As a result, rRNA loses protein synthesis function.

In this study, we present a simple and efficient method for removing of ricin B chain from unknown ricin sample. To determine sugar binding affinity of ricin B chain, the activity of the ricin B chain is examined by comparing two different carbohydrate (galactose and mannose)-modified agarose bead. The ricin B chain in crude extract are purified with galactose-coated and mannose-coated bead packing column. Existence of ricin B chain confirmed by SDS-PAGE and immunoblot analysis indicates that galactose-agarose bead has better capture efficiency than mannose-immobilized bead (73% and 32%, respectively). These result demonstrates that purification of ricin B chain is more efficient using galactose agarose because of specifically strong galactose binding site in Try248 of the ricin B chain. The established method can be used to purify the active ricin B chain and to analyze a toxic ricin sample.

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PS_10_15

A rapid immunochromatographic testing strip using catalytic nanomaterials for highly sensitive point of care test

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Nanomaterials have been attracting a great attention in many fields because of their unique properties, which possess different properties from the bulk state of the materials. Among them, metal nanoparticles have been applied to various fields such as electronics, information storage and catalyst due to theirs optical/physical/chemical/electrical/catalytic properties. Recently, they have been expanding their fields of application to optoelectronics, sensors, biological imaging and medical diagnosis fields.

Lateral Flow Assay (LFA), known as lateral flow immunochromatographic assay, is one of the most successful diagnostic tools commercially available for point-of-care testing due to theirs simplicity, low cost, user-friendly operation, and portability. With the advantages over conventional equipment-based analytical methods, LFA technique is widely used as well-established platform for rapid bio/chemical analysis in low-resource settings. However, common LFA method suffers from the lack of sensitivity and the limited quantitative dynamic range leading to misdiagnosis in the early stage of disease.

In this study, we synthesize several types of nanomaterials, which are successfully integrated into an immunochromatographic assay. The use of metal nanoparticles with high catalytic activity has been shown to improve the sensitivity of LFAs superior to conventional gold nanoparticle lateral flow assays, and test results could readily be evaluated without expensive instruments. For the future, we are planning to apply LFA combined with nanocatalysts to practical applications for bio-disaster analysis.

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PS_10_16

Green Light as Supplementary Light for Enhancing Biomass Production of *Ettlia* sp. and Preventing Population Invasion from Other Microalgae

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The biomass and carotenoid productivities of a freshwater microalga, *Ettlia* sp. YC001 (Chlorophyta, Chlamydomonadales), were investigated in continuous culture systems irradiated with various LEDs. Green light was effectively used by *Ettlia* sp. for increasing its biomass compared to blue and red LED light. This effective use of green light was assumed to be beneficial for *Ettlia* sp., especially in competition with other microalgae. Thus, when green and white LEDs were used simultaneously, *Ettlia* sp. outcompeted *Chlorella vulgaris* without losing any overall biomass productivity. Although, *Ettlia* sp. also showed relatively low oxygen production under green light, high carotenoid content which act as light-harvesting pigments and pass energy on to chlorophylls, contributed to enhancing biomass productivity. Notwithstanding, LEDs are potentially useful for identifying strain specific photosynthetic characteristics of microalgae, thereby increasing their biomass productivity and controlling contamination from other microalgae in open culture systems.

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PS_10_17

Algicidal effects of *Pseudoruegeria* sp. M32A2M against toxic dinoflagellate *Alexandrium tamarense*

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Harmful algal blooms (HABs) have frequently occurred in freshwater and seawater. These HABs causes serious problems to the public health and the aquatic environment globally. Blooms of toxic *Alexandrium* species are often reported in Korea. Especially, *Alexandrium tamarense* is one of the most well-known toxic HAB-causing species; it causes paralytic shellfish poisoning (PSP) in both shellfish and fish. In this study, a bacterial strain with algicidal effects in *A. tamarense* was isolated from the South Sea of Korea. The algicidal bacterium was identified, and the algicidal activity of the strain was investigated. After 24 h inoculation with 10% bacterial culture medium, the release of cellular subsances from *A. tamarense* was confirmed by microscopic analysis. The supernatant and heat treatment were maintained high algicidal activity. This showed that the algicidal extracts were not a protein. We evaluated the algicidal activities of strain M32A2M against other species that cause harmful algal blooms. The algicidal bacterium could be applied to control HABs for field application.

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PS_10_18

Specific oceanographic characteristics and phytoplankton responses influencing the primary production around the Ulleung Basin area in spring

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The Japan/East Sea (JES) is a marginal, semi-closed sea in the northwestern Pacific. The Ulleung Basin area, which is located near the subpolar front of JES, is known to have high primary production and good fisheries in spring season. After episodic wind-driven events during the spring of 2017, horizontal and vertical profiles of physical chemical biological factors were investigated at 29 stations located in the Ulleung Basin area. In addition, growth responses of phytoplankton communities to nutrient additions were evaluated by bioassay experiments to understand the fluctuation of phytoplankton biomass. Because of strong northwestern wind, phytoplankton biomass was scattered and upwelling phenomenon might be suppressed in this season. The phytoplankton abundances in the coastal stations were significantly higher than offshore and island stations. In contrast, the nutrient and chlorophyll-*a* concentrations and the phytoplankton biomass were quite low in all locations. Bacillariophyceae was dominated group (> 75.1% for coastal, 40.0% for offshore and 43.6% for island stations). In the algal bioassays, the phytoplankton production was stimulated by N availability. The in vivo Chl. a values in the +N and +NP treatments were significantly higher than the values in the control and the +P treatments. Based on the field survey, the higher nutrients in coastal waters affected the growth of diatom assemblages, however, little prosperity of phytoplankton was observed in the offshore waters despite the injection of sufficient nutrients in bioassay experiments. The growth of phytoplankton depended on the initial cell density. All of results indicated that a dominant northwestern wind led to a limited nutrients condition at euphotic layers, and the low level of biomass supply from the coasts resulted in low primary production. Both supplying nutrients and introducing phytoplankton through the currents are critical to maintain the high productivity in the Ulleung Basin area of JES.

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PS_10_19

Morphological changes of a psychrotrophic Pseudoalteromonas species after exposure to sublethal concentrations of vancomycin

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Pseudoalteromonas aliena strain EH1 was isolated from the Chukchi Sea, one of the Arctic oceans located between Siberia and Alaska. The temperature, pH and NaCl ranges for *P. aliena* bacterial growth were determined to be 10-30℃, pH 6-8 and 0.5-3% of NaCl with an optimal range of 20℃, pH 7, and 2% of NaCl. The cell morphology of *P. aliena* strain EH1 was observed through Scanning Electron Microscopy (SEM). SEM has been utilized to analyze the surface and the morphological changes. The micrographs of surface showed that EH1 is a rod shaped bacteria with a bumpy and rough surface. Its size is about 1.3 μm. Through cell division, some of EH1 that is the size of 2.5 μm being roughly twice the number. When EH1 was treated with 20 μg/ml of vancomycin, EH1's width has almost doubled in size, and its length also increased up to 1.8 μm. Furthermore, when EH1 was treated with 50 μg/ml of vancomycin, its length was about 1.8 μm, similar to EH1 treated with 20 μg/ml of vancomycin. However, observation of the micrograph taken at the same scale, the difference in thickness was significant when comparing between EH1 treated with 20 μg/ml and 50 μg/ml. In extreme cases such as treating antibiotics, EH1 was seen to have an increased length up to 4.2 μm when treated with vancomycin and its thickness was similar to the length of cells without antibiotic treatment at 1.2 μm.

PS_10_20

Accumulation of micoplastics in sheepshead minnow (*Cyprinodon variegatus*)

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Microplastics problem has been issued in worldwide, as they are dispersed globally in environment and may cause adverse effect in ecosystem. Microplastics have small size (less than 5 mm) so they can be easily ingested in fishes, copepods, bivalves and other living organisms when they are exposed in marine environment.

In this study, we exposed sphere shaped polyethylene microplastics (150- 180 um) in sheepshead minnow (*Cyprinodon variegatus*), marine teleost, and evaluated the microplasitcs uptake and depuration kinetics. Exposure was performed for 10 days at 10 mg Microplastics/L concentration, and depuration was preceded for 4 days by transferring to clean (absence of microplastics) water. For the chemicals bioaccumulation test, in general, food is prohibited during the exposure period. We wondered how the food supply affects the uptake and depuration of microplastics, as the fishes can continuously have food in the environment. Thus, we exposed fishes by dividing two groups, with food or without food.

Exposed fishes organs were dissected and analyzed the amount of accumulated microplastics. Measurement was performed according to the exposure time. There was no specific trend of accumulated amount of microplastics in gills, but there still existed microplastic particles even after the 4 days of depuration time. In case of digestive system, accumulated microplastics were dramatically increased during exposure, and there still existed some particles after the depuration time.

From this research, we evaluated microplastics uptake and depuration kinetics in fish, and found that prolonged exposure of microplastics can affect to organisms by existing in the body.

PS_10_21

Developmental toxicity of bisphenol A and their structural analogues in *Xenopus laevis* embryos

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Bisphenol A (BPA) is often used in combination with other chemicals to manufacture plastics and resins. For example, BPA is used in polycarbonate, which is a high performance transparent, rigid plastic. Polycarbonate is often used for the production of food containers, such as returnable beverage bottles, infant feeding bottles, tableware and storage containers. Residues of BPA are also present in the epoxy resins which used to make protective coatings and linings for food and beverage cans and vats. BPA can migrate in small amounts into food and beverages stored in materials containing the substance. BPA subsequently was found to leach from not only plastics but also resins in tin cans. Various conditions were found to facilitate the leaching process, including photochemical breakdown, exposure to high temperatures, the presence of ethanol, and the age of the plastic or resin. A lot of research suggested that BPA produced estrogenic effects in cells at levels 5 to 10 times lower than those used for safety assessments by companies that manufactured polycarbonate plastics. BPA is association with reproductive and developmental toxicity in animals. At present, BPA was banned from infant and children's products, including, variously, cans of infant formula, baby bottles, and sippy cups in Canada, Europe, Sweden, and the United States. However, several structural analogues of BPA, such like bisphenol F (BPF), and bisphenol S (BPS), have been used as its substitutes in many applications and consequently detected in the environment, and human specimen such as urine and serum. While BPA has been frequently reported for thyroid hormone disruption and estrogenic effects in both experimental and epidemiological studies, less is known for the BPA analogues. In the present study, developmental toxicity of BPF and BPS were investigated, and compared with those of BPA, using frog embryo teratogenesis assay-*Xenopus* (FETAX). The LC_{50} values of BPA and BPF were calculated to be 22.3 and 50.2 μM, respectively. For BPS, there was no significant increase in mortality even in the 500 μM concentration. In surviving tadpoles, head malformation, abnormal gut coiling and ventral bilster significantly increased by BPA at 22 μM. For BPF, head malformation significantly increased at 10 μM. BPS did not significant increased abnormalities in surviving tadpoles. The lowest observed effect concentrations (LOEC) of BPA and BPF for developmental abnormalities were 22 and 10 μM, respectively. The EC_{50} values of BPA and BPF for malformation were 20.5 and 4.1 μM, respectively. The teratogenic indices (LC_{50}/EC_{50}) of BPA and BPF were calculated to be 1.09 and 12.24, respectively. Suggest the teratogenic potential of BPF. Together, the developmental toxicity of BPA and their structural analogues was in the following order: BPA, BPF and BPS.

PS_10_22

Development and Application of synthetic polymer based bio-sorbents to Control Harmful Alga, *Microcystis aeruginosa*

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Harmful algal bloom (HAB) has become a serious water pollution, since predominant microalgal species responsible for HAB secrete several toxic compounds such as microcystin-LR from *Microcystis* species, anatoxin-a from *Anabaena* species and so on. Therefore, it is urgently necessary to find a way suppressing HAB. So far, there have been many different approaches to suppress HAB including sedimentation, filtration, oxidizing agent/algicide treatment and UV sterilization and so on. However, these previous approaches have been implicated with associated problems impacting our ecosystems, thus it is urgently required to develop alternative strategy with eco-friendly features to control HABs.

In this study, we propose a novel way based on adsorption strategy to deal with HAB, which would be feasible to eliminate biomass responsible HAB without serious environmental impacts. Furthermore, the adsorption strategy possesses unique advantages over traditional adsorption techniques. First, ‘sorbents’, the agent of the adsorption, were mainly generated based on waste biomass, *E. coli.* In addition, the sorbents are suitable for further chemical modifications such as PEI (polyethyleneimine) deposition toward increasing functional groups on the surface, which led to significant enhancement of the sorbent capability. Consequently, newly designed and generated ‘sorbents’ were applied to control *Microcystis aeruginosa* bloom, demonstrating the possibility of our strategy against HAB.

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PS_10_23

Control of harmful alga, *Microcystis aeruginosa*, using adsorptive technique by chitosan sorbents

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Harmful algal bloom (HAB) has become a serious water pollution, since some microalgae secrete toxic compounds such as microcystin-LR from Microcystis species, anatoxin-a from Anabaena species and so on. So, it is urgently necessary to find a way suppressing HAB. There have been many different methods to suppress HAB including sedimentation, filtration, oxidizing agent/algicide treatment and UV sterilization and so on. However, these methods have only temporary effects causing additional secondary problems in water ecosystem. So, in this study, we attempted to develop ‘adsorption’ technique, directly suppressing HAB in freshwater.

Microcystis aeruginosa, a dominant species of causing cyanobacterial harmful algal blooms (CyanoHABs) is known to be made problems such as the landscape issue occurred from CyanoHABs and secure safe tap water causing of their neurotoxins, microcystin, when the CyanoHABs was occurred. Currently, the technologies to correspond CyanoHABs are focusing on the reduction of the cell density. In this study, we attempted to use the fiber type sorbents made by chitosan, which has been reported to be non-toxicity, has antimicrobial properties and extracted natural waste, for the development of an eco-friendly control against CyanoHABs. From this study, we examined the relationship between surface area of the sorbents and its adsorption capacity, and its ability to reduce cell density at different stage. (Korea Standard) Additionally, The chitosan sorbents had tested ecological toxicity on Daphnia magna. The results of this study suggest the possibility of controlling CyanoHABs using the adsorptive tecniques.

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PS_10_24

The identification of IgE binding proteins in non-biting midges (*Cricotopus bicinctus*), potentially potent producers of allergens around the river

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Introduction

Chironomids are widely and abundantly distributed in the vicinity of ponds and rivers as well as artificial dammed pool for irrigations. Chironomid larvae are known to contain hemoglobin, which have been described as a major allergen, and the adults that have no hemoglobin also have been reported to contain allergens.

Objective

The aim of this study was to identify and characterize possible IgE binding proteins in adults of *Cricotopus bicinctus*, a popular species in Korea.

Methods

Sera from individuals living near the river, having positive IgE to *C. bicinctus* extract, were used for immunoblotting. *C. bicinctus* extracts were separated by 1-dimensional electrophoresis, and IgE-reactive proteins were analyzed by nano-LC-MS analysis.

Results

The IgE-positive rate and IgE level of *C. bicinctus* antigen were higher in residents near the river than those who live far the river. Serum samples with high IgE level to *C. bicinctus* extract by ELISA were collected from residents in living around the river. The presence of about 42 kDa and 60 kDa protein homologues to the actin protein isoform and putative ATP synthase subunit alpha were identified in an extract from *C. bicinctus*, respectively, and sequence coverage was determined using inclusion lists for tandem mass spectrometry based on homologous sequences.

Conclusion

Two IgE binding proteins were identified in *C. bicinctus* extract showing sequence similarity with actin and putative ATP synthase subunit alpha, respectively. These IgE-binding proteins will be useful for further studies or clinical applications.

PS_10_25

Spatial characteristics of microplastics and mesozooplankton in the surface mixed layer of South Sea of Korea and Northern East China Sea

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The spatial characteristics of microplastics and mesozooplankton was surveyed to understand the possible impact of microplastic-to-zooplankton at 27 stations in the surface mixed layer of South Sea of Korea(SSK) and Northern East China Sea(NECS) during August 2016. The samples were collected using bongo net (mesh size: 200 μm) and physico-chemical properties were obtained by conductivity-temperature-depth sensors. The offshore waters were relatively warmer and low-saline (Avg. 30.7°C, 27.4 psu) compared to coastal waters (Avg. 28.6°C, 28.8 psu). The total microplastic abundance ranged from 1.16~22.05 particles/m^3, in which the abundance peaked at eastern most station of the study area. Types of microplastics observed were fragment, fiber, paint particles, and film, of which polymer types were polyester, acrylic, epoxy resin, alkyd-resin and polyester-alkyd. Fiber (Avg. 57.7%) and paint particles (Avg. 39.6%) were ubiquitously dominant. The total mesozooplankton abundance ranged from 778~13,728 inds./m^3, of which peaked at western most station of the study area. The average dominant taxa groups for all stations were immature copepods (31.9%), adult copepods (31.9%) and cladocerans (7.5%). Cluster analysis of microplastics divided stations into 4 major groups. The dominant microplastics in group-1 were paint particles (66.7%), and dominant mesozooplankton taxonomic groups were copepods (immature and adults; 60.0%) followed by appendicularians (20.0%). Group-2, group-3 and group-4 were all dominant in fiber (group-2: 87.7%, group-3: 45.6%, group-4: 50.7%), and copepods (group-2: 70.2%, group-3: 69.1%, group-4: 54.2%), however next dominant mesozooplankton groups differed, in which group-2 and -3 were cladocerans (group-2: 12.5% group-3: 11.0%), and group-4 were thaliaceans (9.8%). The ratio of microplastic-to-zooplankton ranged from 0.0001~0.0205 (Avg. 0.0028), in which ratio peaked at two stations of group-4. Above results suggest that numerically dominant fibers and paint particles, which is widely distributed, are likely to be encountered frequently with mesozooplankton and zooplanktivores in the SSK and NECS.

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PS_10_26

Metabarcoding Analysis of Red-Tide Waters in Goeje (South Korea)

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Red tide is a common name for an algal bloom of a few species of dinoflagellates in coastal waters which takes on a red or brown color depending on the type of algae. It is also referred to as harmful algal blooms (HABs), which emphasize harmfulness. Harmfulness of HABs is not limited to the health of people and marine ecosystems in the affected region and regional economies. In Korea, total direct losses due to HAB from 2001 to 2012 were about 52 million US dollar. Recently, molecular techniques are now being applied as an alternative method for its fast and reliable species identification. The next generation sequencing (NGS) technique are now being paid attention for its capacity to analyze the whole community structure of the collected samples with relatively low cost and time. Metagenome data generated by two different universal primer sets (16S & 23S universal primers) were compared to understand the precise changes of both heterotrophic bacterial species and photosynthetic phytoplankton species during the bloom. Waters collected from the region (Geoje, Gyengsangnamdo) with the algal blooming were also analyzed by the 23S primer set. First, we identified that biomass of heterotrophic bacteria was much higher than the harmful algal species. Second, we identified that community structure between the center of blooming region and water near the blooming region were extremely similar each other compared with those of distantly located region from the blooming. As the result, we were able to know that community structure changes before we detect the change in color in waters. In addition, several bacterial species change in correlation with the harmful algal blooming. This result would provide the useful information about the process of the algal blooming and its early forecasting to prepare the harmful algal invasion in ocean.

PS_10_27

Predicting the potential habitat and risk assessment of *Aster subulatus* var. *sandwicensis* using MaxEnt

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This study was conducted to predict the potential distribution and risk of invasive alien plant, *Aster subulatus* var. *sandwicensis*, in agricultural area of South Korea. We collected 146 presence localities of *A. subulatus* var. *sandwicensis* using field survey and literature search and estimated the potential distribution area of *A. subulatus* var. *sandwicensis* using maximum entropy modeling (MaxEnt) with six bioclimatic variables. Two different kinds of agricultural risk index, raster risk index and regional risk index, were estimated. The 'raster risk index' was calculated by multiplying the potential distribution by the field area in 1´1 km and 'regional risk index' was calculated by multiplying the potential distribution by field area proportion in the total field of South Korea. The predicted potential distribution of *A. subulatus* var. *sandwicensis* was almost matched with actual presence data. The annual mean temperature had the highest contribution for distribution modeling of *A. subulatus* var. *sandwicensis*. Area under curve values of the model was 0.744. Currently, the highest regions were Jeju for agricultural risk index. However, in 2050 and 2080, the agriculture risk index is expected to have the greatest impact on Daegu and Chungcheongnam-do. This research was supported by Ministry of Environment(201807042002).

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PS_10_28

The Evaluation of invasive species in Soyang Lake, using AS-ISK (Aquatic Species Invasiveness Screening Kit)

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Soyang Lake, located in Chuncheon-si Gangwon-do is a multipurpose dam built for the purpose of water supply, foold control and power generation. Indiscriminate fishing is an issus every year with the aim of increasing fishermen's fishresources. Based on literature review of fish species record from 1997 to 2016, a total of 19 fish species were known from Soyang Lake. Invasive species was evaluated using AS-ISK(Aquatic Species Invasiveness Screening Kit). Anlyses resulted into the evaluation of five species: Carassius cuveri, Carassius auratus, Silurus asotus, Lepomis Macrochirus and Micropterus salmiodes as 'high risk', and these 'high risk' species group are determined to cause a decrease in native species habitats, food resource, and breeding (Threshold=19, UK). Therefore, this study was conducted to provide basic data to assess the invasive species and to suggest conservation measures for native species.

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PS_10_29

Pyrosequencing and morphological analyses reveal high diversity of freshwater phytoplankton in Paldang reservoir (Korea)

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Environmental monitoring of the succession of phytoplankton communities in freshwater ecosystems is critical in efficient water quality management. In this study, we analysed the monthly dynamics of eukaryotic phytoplankton diversity and community structure in a freshwater reservoir (Paldang reservoir, Korea) using small subunit ribosomal RNA (SSU) pyrosequencing. We analysed physicochemical and biological parameters of water samples collected at monthly intervals from March 2012 to February 2013. The occurrence of phytoplankton exhibited a monthly variation: low in September (13.2%) and February (9.7%) and high in May (75.5%), July (76.5%), August (86.3%), and November (70.6%). We observed greater phytoplankton diversity predominantly represented by diatoms (37.4%), dinoflagellates (29%), cryptophytes (16%), and chlorophytes (10.4%). In early and mid-spring, diatoms, particularly *Stephanodiscus* spp., were dominant; however, in late spring and early summer the cryptophyte, *Cryptomonas* spp. was dominant, and the dinoflagellate *Peridionopsis* sp. was dominant in late summer and late autumn. Overall, our molecular results represented a typical pattern of seasonal phytoplankton succession in temperate regions. Pyrosequencing detected more phytoplankton taxa that were unresolved under microscopy, suggesting the usefulness this method in continuous monitoring of phytoplankton communities in freshwater ecosystems.

PS_10_30

Diversity and seasonal changes of cyanobacteria in Paldang reservoir (Korea) explored by 16S rDNA metagenomcis

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Cyanobacteria are the major component of the bloom forming community that has to be monitored frequently. Hence, we have analyzed molecular diversity and seasonal changes of cyanobacteria in Paldang reservoir using morphological and 16S rRNA pyrosequencing. The samples were collected from four stations during Mar.? Dec. 2012. Totally, 40 phylotypes of cyanobacteria were identified after comparing 49,131 pyrosequence reads. The cyanobacterial genera such as Anabaena, Aphanizomenon, Microcystis, Synechocystis were predominantly present in the samples. However, majority of cyanobacterial sequences (65.9%) identified here were of uncultured origin. In contrary, morphological identity of cyanobacteria revealed different pattern which resolved eight cyanobacterial genera. Seasonal pattern of cyanobacterial community was also observed, with no occurrence in Mar. and Dec. The relative abundance of cyanobacterial sequences was observed as high in Aug. These suggested that pyrosequencing approach can reveal cyanobacterial diversity that undetected morphologically, and can be used as a reference for studying and monitoring of cyanobacterial communities in Paldang Reservoir.

PS_10_31

A Case Report on the Introduced Species, *Chelydra serpentina*, found in the wild of South Korea

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The influx of invasive organisms around the world is directly or indirectly affecting not only ecosystems but also human being. The social and economic costs for investigating and eliminating the damage by invasive organisms are also rapidly increasing. In this study, we report the characteristics of the environment which found the snapping turtle, *Chelydra serpentina,* on March 20, 2019 (N36° 16’ 50.78’’, E127° 07’ 01.46’’, elevation 48m above sea level) in Nonsan-si, Chungnam, South Korea. A male turtle, about 30 cm in carapace length, was caught in a tractor preparing for farming. The location where the turtle found was in the middle of a damp argument, and the turtle was resting at a depth of about 20 cm. The beak to the front of the eye was cut off by the influence of the tractor, and the back shell was partially broken. We estimated that the turtle came from one of two reservoirs about 430m north or about 350m southeast from the discovery site. In Korea, March is the time when turtles hibernate. On the other hand, there is a possibility that *C. serpentina,* known as aquatic habitats, was hibernating in paddy fields because the location was considerably far from the reservoirs. The introduced turtles including wolf turtles have been reported consistently throughout the country in recent years. In particular, wolf turtles have caused direct damage not only to ecosystems but also to humans. In this study showed that the management strategies for invasive organism, *C. serpentina,* are urgent.

This study was carried out with support from the Project on the Development of Risk Assessment and Species Distribution Modeling for Alien Amphibians and Reptiles (RE201807039). We thank to Lee Joon-seok for the Chungnam Wildlife Rescue Center and Jeong Yu-jung for the Seoul National University Park who provided the details of the turtles.

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PS_10_32

Survey on Invasive Amphibians and Reptiles Traded Online in South Korea

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Invasive species cause global problems that compete with native species or damage ecosystems by carrying pathogens. In South Korea, the introduction of alien species for ornaments and pets is constantly increasing, and there have been reports of discovery in the wild. Although amphibians and reptiles account for the second-highest proportion of the animal taxa imported into the country, the exact species and quantity of transaction have not been known until now. In this study, 25 online pet shops have been selected to survey foreign amphibian and reptile listings and prices that are actually traded. We examined whether species of ecosystem- disturbing-organisms or endangered wild species are traded and compared with the official list of introduced species. The survey confirmed that a total of 76 families, 677 species were traded in five orders (Anura, Cadata, Crocodyria, Squamata and Testudines). Our list included American bullfrog (*Lithobates catesbeianus*), an ecosystem disturbance organism, and Reeves' turtle (*Mauremys reevesii*) designated as a Class II endangered wildlife species of Korea and natural monument No. 453. Among the listed species, 10 invasive species, including River cooter (*Pseudemys concinna*) were found in wild.

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PS_10_33

Distribution of Exotic Turtles and Comparison with Red-Eared Turtles in Korea

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The Red-eared turtle designated as ‘ecosystem disturbance organism’ by the Ministry of Environment was imported to South Korea in 1970 and spread nationwide due to extension of pet market and trade. However, there has been few studies on the distribution and habitat characteristics of the Red-eared turtles and exotic turtles. In this study, we found the coordinates of the exotic turtles by compiling the nationwide distribution survey results. We used data from the third National Survey of Natural Resources from 2006 to 2012 and Nationwide Survey of Non-native Species in Korea from 2015 to 2018. We analyzed the distribution and habitat characteristics with four variables; land cover, temperature, altitude, and water use. The Chinese striped wooden turtles were distributed in the highest habitat temperature of 13.50℃ than other species ($p<0.05$). Altitude did not differ significantly among the exotic turtle species. More than half of exotic turtles (60%) was distributed in inland waters. While most of 151 exotic turtles were found in artificial water environment, 239 red-eared turtles in their natural environment. From this study, we found that temperature zone of these exotic turtles depended on species and that Chinese striped wooden turtle were likely to be distributed in warm southern regions compared to other species. In addition, many red-eared turtles in the natural environment indicates that they have already been spread to field. While many other exotic turtles in artificial water environment, indicates that they have not done yet to spread in nature.

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PS_10_34

A study on planting combination methods for considering plant invasiveness to urban vegetation communities

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Urban environment plantings composed primarily of exotic species and cultivars, organised in culturally informed arrangements, rather than as ecologically-based plant communities. Moreover that is also managed relatively intensively to reduce competition between planted stock and spontaneously invading weeds. The vegetation technique of urban gardens such as green roof and rain garden has limited only to drainage area and vegetation soil, and there is insufficient information on planting composition. This study was carried out to develop a planting combination method suitable for urban environmental conditions.

The method derivation step is as follows. First, plant type was classified into 3 types according to plant growth characteristics. Second, three plant species were selected for each plant types and the plant combination was derived from the factorial design analysis. Third, from May to October, the image data of the changes of the monthly growth were digitized by CAD program. Finally, the planting combination models descrided to factorial experiments with interactions. The results showed that *Phalaris arundinacea* var. picta, *Mentha piperascens*, and *Pennisetum alopecuroides* were highly correlated with all watershed plants and were highly affected by the surrounding plants *Houttuynia cordata* and *Heuchera sanguinea*. This study has an opportunity to increase the use of native ‘habitat’ plantings in urban landscapes in Korea.

PS_10_35

Bisphenol A and their structural analogues induces neural tube deformities during *Xenopus laevis* embryos development

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The bisphenols are a group of chemicals which often used in combination with other chemicals to manufacture plastics and resins. Bisphenol A (BPA) and S (BPS) have been shown to be endocrine disruptors. Due to its high production volumes, leading to its spreading and potential accumulation in a variety of environmental matrices, even though it has a fairly short half-life. In the present study, developmental toxicity of bisphenol F (BPF) and BPS were investigated, and compared with those of BPA, using frog embryo teratogenesis assay-*Xenopus* (FETAX). The LC_{50} values of BPA, BPF and BPS were calculated to be 22.3, 50.2 and 1640.5 μM, respectively. In surviving tadpoles, head malformation, abnormal gut coiling and ventral bilster significantly increased by BPA at 22 μM. For BPF, head malformation significantly increased at 10 μM. The EC_{50} values of BPA and BPF for malformation were 20.5 and 4.1 μM, respectively. The teratogenic indices (LC50/EC50) of BPA and BPF were calculated to be 1.09 and 12.24, respectively. Suggest the teratogenic potential of BPF. Considering the high proportion of head malformation in surviving tadpoles, we examined the effects of bisphenols on *X. laevis* embryo development. *X. laevis* embryos at blastula stage were treated with bisphenols until neurula stage (Nieuwkoop and Faber stage 22). In bisphenols treated neurula, abnormalities such as neural tube deformity, abnormal notochord and abnormal somite were observed. The neural tube deformity was significantly increased by 22 μM BPA. In histological analysis, the neural tube area was significantly increased by 10 mg/L BPF. The lumen area of neural tube was significantly decreased by 22 μM BPA. The notochord area was significantly increased by 22 μM BPA and 1 μM BPF. The neural tube epithelia area was significantly increased by 50 μM BPF and 1 mM BPS. In order to find out the reason of neural tube deformity, we determined a series of genes that regulate embryonic differentiation such as N-cadherin, E-cadherin. Cadherin, a calcium-dependent cell-cell adhesion molecule with pivotal roles in embryonic development. As the key molecule of the cadherin-catenin-cytoskeleton complex, it is important for neurulation. We tested the mRNA expression of E-cadherin and N-cadherin using RT-qPCR. As the results, the E-cadherin mRNA expression was significantly increased by 22 μM BPA and decreased by 1 μM BPF. In BPS treated embryo, the expression of E-cadherin mRNA was not significantly changed. The N-cadherin mRNA expression was significantly increased by 1 μM BPA and BPS. In BPF treated embryo, the N-cadherin mRNA was significantly decreased by 50 μM BPF. This will lead to a series of abnormalities such as head cartilage abnormalities. Together, BPA induced head dysgenesis t driven by disruption of molecular regulation mechanism in *X. laevis* embryos. The developmental toxicity of bisphenols in *X. laevis* is in the following order: BPA, BPF, and BPS.

PS_10_36

Effect of the microplastic on meiofauna and nematodes

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Over the last 50 years, the use of plastics has increased rapidly, and a large amount of plastics has entered the marine environment. Plastics introduced into the oceans become smaller in size and become microplastic, affecting small organisms in the marine ecosystem. However, few studies have examined the impact of microplastics on marine ecosystems. The purpose of this study was to find out that the nematodes (*Enoplolaimus* sp.) ingests a microplastic and differences in ingestion rates of nematodes. The samples for the study were collected from mallipo intertidal sandy sediments. The experiment used a Petri-dish with a 4 block, each block was placed *Enoplolaimus* sp. (20 individuals). The microplastic for the experiment was used for four different sizes (10 ㎛, 5 ㎛, 1 ㎛, 0.5 ㎛). In experiment 10 ㎛ microplastic ingestion rate of the nematode was found to average 27.5%. In experiment 5 ㎛ microplastic ingestion rate of the nematode was found to average 60.9%. In experiment 1 ㎛ microplastic ingestion rate of the nematode was found to average 67.9%. In experiment 0.5 ㎛ microplastic ingestion rate of the nematode was found to average 73.0%. As the size of the microplastic decreased, ingestion rate of nematode was increased. One-way ANOVA analysis to determine the difference between the ingestion rate according to the microplastic sizes shows that there was significant difference between ingestion rates of nematodes in 10 ㎛ and 5 ㎛, 1 ㎛, 0.5 ㎛ ($p < 0.05$).

PS_10_37

Development of diagnosis model of six invasive Convolvulaceae plant seeds by lipid analysis using Matrix assisted Laser Desorption Ionization Time-of-flight Mass spectrometry (MALDI TOF MS)

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Lipid analysis using MALDI TOF MS is easy, rapid and high-throughput technology. The purpose of this study is to establish a diagnosis model by lipid profiling of invasive Convolvulaceae plant seeds in Korea using MALDI TOF MS. Lipid extracts from seeds of six Convolvulaceae species(*Ipomoea purpurea, I. hederacea, I. hederacea var. integriuscula, I. lacunose, I. triloba, Quamoclit coccinea*) were analyzed by MALDI TOF MS with 9-aminoacridine matrix and reflector mode. As a result, various sulfoquinovosyl diacylglycerol(SQDG), phosphatidylinositol(PI) and sterol lipid(ST) were detected in Convolvulaceae seeds. MALDI TOF MS spectra were showed significant qualitative and quantitative differences among species. Twenty three peaks were determined for potential diagnosis biomarkers which showed significant difference using Kruskal-Wallis test. Diagnosis model estimations were carried out on Genetic Algorithm, Support Vector Machine(SVM), Supervised Neural Network and Quick Classifier. Inter alia, SVM model which had 83.42% prediction accuracy was the best diagnosis algorithm.

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PS_10_38

A Large-scale production and microwave-assisted extraction of shikimic acid from the aerial parts of *Sicyos angulatus* (Cucurbitaceae) in Korea

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This experiment was conducted to determine the optimal conditions for large-scale production of shikimic acid from *Sicyos angulatus* (Cucurbitaceae). Glyphosate (N-phosphonomethyl glycine) was treated to whole plants of S. angulatus with recommended lethal dosage 0.39, 0.77 and 1.54 gai/L in Anseong, Gyeonggi-do, Korea and plants were collected in parts (stems, leaves, and fruits) for 6 days after treatment (DAT). Extraction of shikimic acid was conducted by microwave-assisted extraction (MWAE), which is a rapid and effective method for recovering shikimic acid. Each sample 2 g was mixed with 20 mL of double distilled water adjusted at pH 2.0 and equilibrated by shaking for 30 minutes at 180 rpm. Afterwards, shikimic acid of samples was extracted by microwave at 60 °C for 10 sec and separated by HPLC with μ Bondapak NH2 column (I.D. 300 mm × 3.9 mm, Waters Technology), at a flow rate: 1 ml min^{-1}, detection: 215 nm, and eluent: $H_3CN/H_2O/H_3PO_4$ (9:1:0.1). Shikimic acid contents of all plants tissues highly increased over 4 times after treatment and of stems dramatically increased about 90 times from 7.02 to 643.91 μg/g of fresh weight at 5 DAT and 1.54 gai/L. Shikimic acid contents of leaves were not significantly different by glyphosate dosage but of stems and fruits were the highest at 1.54 gai/L. At the each dosage, shikimic acid contents of leaves and fruits were the highest at 6 DAT but stems didn't show significant differences except 0.77 gai/L. In conclusion, the optimal conditions were 1.54 gai/L of glyphosate dosage and 6 DAT for large-scale production of shikimic acid.

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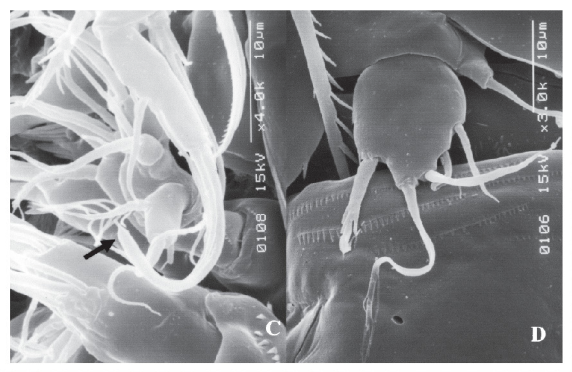
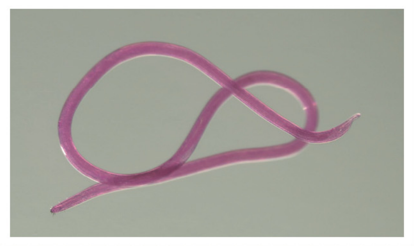
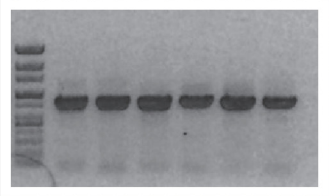
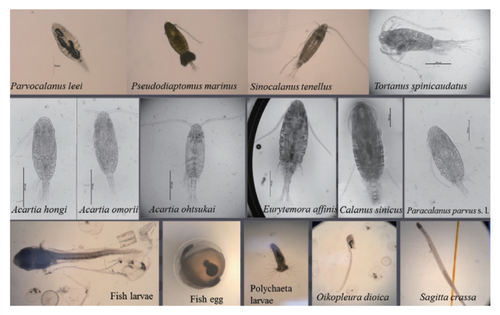
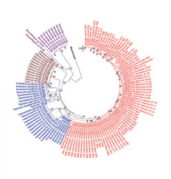

0108 15kV x4.0K 10μm
C
0106 15kV x3.0K 10μm
D






Parvocalanus leei
Pseudodiaptomus marinus
Sinocalanus tenellus
Tortanus spinicaudatus
Acartia hongi
Acartia omorii
Acartia ohtsukai
Eurytemora affinis
Calanus sinicus
Paracalanus parvus s. l.
Fish larvae
Fish egg
Polychaeta larvae
Oikopleura dioica
Sagitta crassa

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15th International Meiofauna Conference in Korea - "The Future of Meiofauna Study"
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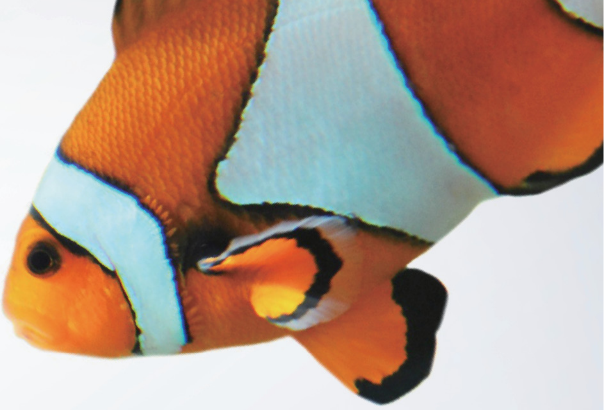


해양생명연구소재는 해양생명자원 기탁등록보존기관에서 분양 받으세요

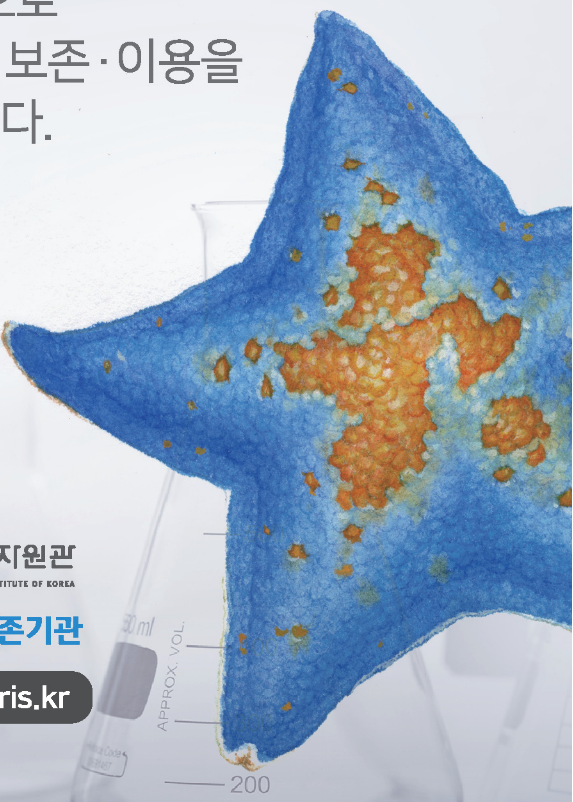
표본

유전자원

추출물

배양체

해양생명자원 기탁등록보존기관 사업은
해양수산부 전략사업으로
해양생명자원의 체계적인 확보·보존·이용을
목적으로 하고 있습니다.



해양수산부

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1 기초연구 인프라를
연결하다

2 기초연구 인프라를
혁신하다

3 과학기술 강국의
미래가 시작되다

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세계일류의 기초연구 인프라 기관입니다.

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세계적 대형 연구장비 운영, 차세대 분석 장비 및 분석기술 개발,
기초원천 및 융합연구 등 개방형 연구협력을 통해 세계 최고 수준의
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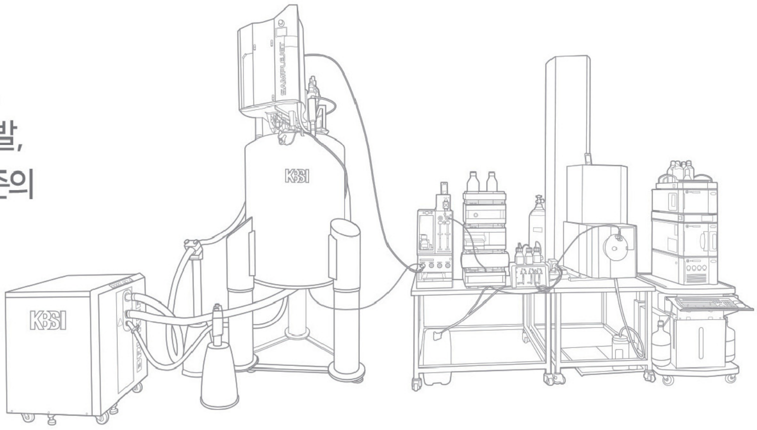

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'이 학술지는 정부재원(과학기술진흥기금 및 복권기금)으로 한국과학기술단체총연합회의 지원을 받아 발간되었음'