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2022 Annual Meeting and International Conference of the Korean Society of Environmental Biology

Climate Change, Biodiversity, and ESG

Oct. 19(Wed) ~ 21(Fri), 2022
Paradise Hotel, Busan, Korea

Organized by

Korean Society of Environmental Biology

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주최: 한국환경생물학회

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Opening remarks

Ladies, gentlemen, and honored guests,

On this beautiful afternoon and at this nice place, we meet here to have the Annual Meeting and International Conference of the Korean Society of Environmental Biology in 2022. On behalf of the members of our society, I would like to extend my gratitude and a warm welcome to our plenary and featured speakers and presenters, especially those coming from overseas.

As the world is getting to overcome the pandemic, many of us are embracing the opportunity to reconnect – with each other, and with efforts to restore connections within nature.

The theme of this conference is "Climate change, Biodiversity and ESG". While ESG concept is relatively new to our society members, it is the key factors when measuring the sustainability and ethical impact of an investment in a business society. Biodiversity and climate change are drawing considerable attention in ESG, but understanding and implementation of these are less mature than the Society and Governance factors. Since our society members have been conducting outstanding research in the field of biodiversity, climate change and pollution issue, I am confident that we will be able to fill the missing piece in ESG.

The prime goal of this conference is to further strengthen the ESG strategy to the challenges we all face in a world where biodiversity and climate security have become defining issues. To achieve this goal, environmental biology research requires active collaboration with other fields, and I am confident that this conference will be a good start to collaborate and contribute our research for sustainable and resilience society.

In this conference, we prepare two plenary lectures and more than 10 special sessions to share our work, knowledge and experiences, and look to the future in environmental biology and ESG.

Again, I welcome you all to the Annual Meeting and International Conference of the Korean Society of Environmental Biology in 2022. Special thanks to Dr. Rhee, Jay Hyuk and Dr. Park, Won Seog, the keynote speakers, and also to the sponsors who helped make this conference possible. For those of you coming from other countries I hope you have a wonderful time in this beautiful city of Busan.

I wish you a fruitful and worthwhile conference.

Thank you and enjoy your stay.

October, 2022
President of Korean Society of Environmental Biology, **Kijong Cho**

Program at a Glance

Date/Time		Day 1			Day 2				Day 3		
		Oct. 19 (WED)			Oct. 20 (THU)				Oct. 21 (FRI)		
		Grand1+2+3	Grand 4	P	Grand1+2+3	Grand 4	Sydney	P	Grand1+2+3	Grand 4	P
8	00-10				Registration			Poster A (Miami + Venice)			Poster B (Miami + Venice)
	10-20										
	20-30										
	30-40				Student Oral Presentation 1	Student Oral Presentation 2	Special Symposium				
	40-50										
	50-60										
9	00-10								Registration		
	10-20										
	20-30										
	30-40								Session 10	Session 11	
	40-50				Coffee Break						
	50-60										
10	00-10				Award & Special Lecture 1 (구양환경생물학상 시상식 및 수상자 특별강연)						
	10-20										
	20-30										
	30-40										
	40-50										
	50-60										
11	00-10				Group Photo						
	10-20				Coffee Break / Poster Presentation A				Coffee Break		
	20-30										
	30-40				Session 3	Session 4	Session 5		Special Lecture 2		
	40-50										
	50-60										
12	00-10	Registration		Poster A (Miami + Venice)					Closing Ceremony & Awards		
	10-20										
	20-30										
	30-40										
	40-50										
	50-60										
13	00-10	Opening Ceremony & Celebratory Photo									
	10-20				Lunch						
	20-30	Plenary Lecture 1									
	30-40										
	40-50										
	50-60	Coffee Break									
14	00-10	Keynote Session									
	10-20				Session 6	Ⓔ Session 7	General Oral Presentation	Poster B (Miami + Venice)			
	20-30										
	30-40										
	40-50										
	50-60										
15	00-10										
	10-20	Coffee Break									
	20-30										
	30-40	Plenary Lecture 2									
	40-50										
	50-60				Coffee Break						
16	00-10	Coffee Break									
	10-20	Session 1	Session 2		Young Scientist & Student Oral Presentation 3	Ⓔ Session 8	Session 9				
	20-30										
	30-40										
	40-50										
	50-60										
17	00-10										
	10-20										
	20-30										
	30-40										
	40-50										
	50-60	Coffee Break			Coffee Break / Poster Presentation B						
18	00-10						General Assembly Member Meeting				
	10-20										
	20-30										
	30-40										
					Banquet						

Ⓔ English session

Program Timetable

Title	2022 Annual Meeting and International Conference of the Korean Society of Environmental Biology
Theme	Climate Change, Biodiversity, and ESG
Date	Oct. 19(Wed) ~ 21(Fri), 2022
Venue	Paradise Hotel, Busan, South Korea

Oct. 19 (WED)

Time	Program		
12:00~	Registration		
13:00~13:15	**Opening Ceremony** (Grand Ballroom 1+2+3) Opening address: Kijong Cho (President of KOSEB) Congratulatory message : Min Hwan Suh (President of NIBR)		Poster A
13:15~13:20	Celebratory Photo		
13:20~13:50	**Plenary Lecture 1** (Grand Ballroom 1+2+3) "Pursuing the ESG in post-2020 global diversity framework under convention on biological diversity" Won Seog Park (Chung-Ang Univ.)		
13:50~14:00	Coffee Break / E-부스 상영		
14:00~15:10	**Keynote Session** (Grand Ballroom 1+2+3) "How corporate are responding to twin challenges : climate change and biodiversity loss"		
15:10~15:30	Coffee Break / E-부스 상영		
15:30~16:00	**Plenary Lecture 2** (Grand Ballroom 1+2+3) "Sustainability and ESG management" Jay Hyuk Rhee (Korea Univ.)		
16:00~16:10	Coffee Break / E-부스 상영		
16:10~17:50	**Special Session 1** (Grand Ballroom 1+2+3) "ESG special session on climate risk and biodiversity (TCFD VS TNFD)"	**Special Session 2** (Grand Ballroom 4) "Development of integrated models for climate change adaptation"	
17:50~18:00	Coffee Break / E-부스 상영		

Oct. 20 (THU)

Time	Program			
08:00~	Registration			
08:30~09:40	**Student Oral Presentation 1** (Grand Ballroom 1+2+3)	**Student Oral Presentation 2** (Grand Ballroom 4)	**Special Symposium** (Sydney) "Endocrine disruptors and alternative chemicals"	Poster A
09:40~10:00	Coffee Break / E-부스 상영			

10:00~11:00	**Award & Special Lecture 1** (Grand Ballroom 1+2+3) 제1회 구양환경생물학상 시상식 및 수상자 특별강연 "Microplastic and endocrine disruptor: Role of environmental biology in ESG era"			Poster A
11:00~11:10	Group Photo			
11:10~11:30	Coffee Break / Poster Presentation A (Miami + Venice)			
11:30~13:10	**Special Session 3** (Grand Ballroom 1+2+3) "The role of small and medium-sized enterprises (SMEs) in Korea's advanced environment"	**Special Session 4** (Grand Ballroom 4) "Environmental protection and remediation"	**Special Session 5** (Sydney) "The role of liberal education in the age of environmental crisis"	
13:10~14:10	Lunch			
14:10~15:50	**Special Session 6** (Grand Ballroom 1+2+3) "Paradigm shift and challenge for cooperation for effective public communication of science and technology"	**Special Session 7** (Grand Ballroom 4) "Diverse aspects of omics in ecological studies"	**General Oral Presentation** (Sydney)	Poster B
15:50~16:10	Coffee Break / E-부스 상영			
16:10~17:50	**Young Scientist & Student Oral Presentation 3** (Grand Ballroom 1+2+3)	**Special Session 8** (Grand Ballroom 4) "Linking international perspectives for advances in environmental research"	**Special Session 9** (Sydney) "Exploration of organic substances in various environmental systems by analytical science and technology"	
17:50~18:10	Coffee Break / Poster Presentation B (Miami + Venice)			
18:10~18:40	**General Assembly Member Meeting** (Sydney)			
18:40~	Banquet			

Oct. 21 (FRI)

Time	Program		
09:00~	Registration		
09:30~11:10	**Special Session 10** (Grand Ballroom 1+2+3) "Diversity of the undiscovered taxa in Korea"	**Special Session 11** (Grand Ballroom 4) "Post 2020, the conservation strategy of wild plants seed in Baekdudaegan National Arboretum"	Poster B
11:10~11:30	Coffee Break / E-부스 상영		
11:30~12:00	**Special Lecture 2** (Grand Ballroom 1+2+3) "Effects of persistent herbicides on physiology and biochemical responses to the marine phototrophic dinoflagellates" Jang-Seu Ki (Sangmyung Univ.)		
12:00~12:20	**Closing Ceremony & Awards**		

Plenary Lecture 1

Date & Time : Oct. 19 (Wed) 13:20 - 13:50
Room : Grand Ballroom 1+2+3

Chair: Prof. Chan woo Kim
Gyeongsang National University, Korea

13:20 - 13:50	PL-1	**Pursuing the ESG in post-2020 global diversity framework under convention on biological diversity** Won Seog Park (Chung-Ang University, Korea)

Plenary Lecture 2

Date & Time : Oct. 19 (Wed) 15:30 - 16:00
Room : Grand Ballroom 1+2+3

Chair: Prof. Chan woo Kim
Gyeongsang National University, Korea

15:30 - 16:00	PL-2	**Sustainability and ESG management** Jay Hyuk Rhee (Korea University, Korea)

PL-1

Pursuing the ESG in post-2020 global diversity framework under convention on biological diversity

Won Seog Park[pc]

School of Law, Chung-Ang University, Seoul 06974, Korea

The ongoing negotiation for the development of Post-2020 Global Biodiversity Framework(GBF) under the Convention on Biological Diversity aims to catalyze, enable and galvanize urgent and transformative action by all governments and all of society to halt [and reverse] global biodiversity loss. Toward this end, the GBF envisages 2050 Vision, 2030 Mission, 4 Goals and 22 2030 Action Targets in its basic structure. Inevitably, this GBF contains many ESG elements in its components. Especially, 22 action-oriented targets for urgent action over the decade to 2030 reveal many ESG elements such as climate change, ocean acidification, sustainable management and use of wild species, discharge of plastic or electronic wastes, pesticides and other toxic chemical, etc.

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PL-2

Sustainability and ESG management

Jay Hyuk Rhee[PC]

Korea University Business School, Seoul, Korea

With the emergence of so-called ESG era, many corporations are under increasing pressures to incorporate ESG practices into their daily business operations. As a result, more attention has been given to the meaning of stakeholder capitalism as well as the mechanisms through which ESG performance can be measured. To better deal with the future of ESG, corporations should also prepare for emerging requirements that are discussed at diverse levels of ecosystem.

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Special Lecture 1
(제1회 구양환경생물학상 수상자)

Date & Time : Oct. 20 (Thu) 10:30 - 11:00
Room : Grand Ballroom 1+2+3

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

10:30 - 11:00	SL-1	**Microplastic and endocrine disruptor: Role of environmental biology in ESG era** Myung Chan Gye (Hanyang University, Korea)

Special Lecture 2
(2022 과총 우수논문상 수상자)

Date & Time : Oct. 21 (Fri) 11:30 - 12:00
Room : Grand Ballroom 1+2+3

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

11:30 - 12:00	SL-2	**Effects of persistent herbicides on physiology and biochemical responses to the marine phototrophic dinoflagellates** Jang-Seu Ki (Sangmyung University, Korea)

SL-1

Microplastic and endocrine disruptor: Role of environmental biology in ESG era

Myung Chan Gye[PC]
Department Life Science, Hanyang University, Seoul 04763, Korea

Environmental contamination of microplastic (MP) and endocrine disruptor (ED) are the emerging interrelated environmental subject and should be treated as an important mater of environmental, social and governance (ESG). Microplastic is a small sized (< 5 um) plastic made of complex chemicals including industrial resin components and plasticizers. Until recently, 8.3 billion tons of plastic was produced and.3 billion tons of plastic waste are generated. Inevitably, a lot of plastic waste has been dumped into the environmental media. By the way, in the freshwater and seawater system MP can be produced via physical stress cracking of plastic. Once generated, MPs meet to toxic chemicals such as persistent organic pollutants (POPs) and EDs due to their lipophilic nature and increased surface volume ratio. Beside of the cellular toxicity of MPs as particulate matter, the chemical transfer of environmental toxicants including EDs to MPs though food web became hazardous to human as well as wild lives. Recently, large efforts to develop the less toxic plastics made of alternative resin and plasticizers have been conducted in the plastic engineering and toxicological science. Nonetheless, manufacturing the conventional plastic wares is still a growing economy and MP contamination of is threatening the wild lives as well as human. In accordance to ESG, surveillance of the environment contamination by plastic and MPs, their impact on ecosystem, and toxicological information of newly developed plastic components became the important subject in environmental biology, sustaining our life.

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SL-2

Effects of persistent herbicides on physiology and biochemical responses to the marine phototrophic dinoflagellates

Jang-Seu Ki^{PC} and Han-Sol Kim

Department of Biotechnology, Sangmyung University, Seoul 03016, South Korea

The chloroacetanilides are the most used herbicides worldwide and contaminate aquatic environments, affecting marine phototrophs. Their sub-lethal toxicity has been evaluated using freshwater algae; however, the modes of cellular toxicity and levels of toxicity to marine organisms are not fully understood. Herein, we assessed the cellular and molecular effects of chloroacetanilides on marine phototrophs using the dinoflagellate *Prorocentrum minimum* and three herbicides, including alachlor, metazachlor (MZC), and pretilachlor (PRE). Cell density, pigment contents and photosynthetic parameters (*Fv/Fm* and PI_{ABS}) were considerably decreased with increase of the herbicides exposed time and doses. EC_{50} was calculated to be 0.373 mg/L of alachlor, 0.647 mg/L of MZC, and 5.302 mg L^{-1} of PRE. In addition, they significantly induced photosynthesis genes, including *PmpsbA*, *PmpsaA*, and *PmatpB*, and the antioxidant *PmGST*, but not *PmKatG*. These findings were well matched to reactive oxygen species (ROS) production in the herbicide-treated cells. Interestingly, we observed inflated vacuoles, undivided chloroplasts, and breakdown of thylakoid membranes in the herbicide-treated cells. These support the hypothesis that chloroacetanilide herbicides severely damage chloroplasts, resulting in dysfunction of the dinoflagellate photosynthesis and possibly marine phototrophs in aquatic environments.

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Keynote Session

How corporate are responding to twin challenges : climate change and biodiversity loss

Date & Time : Oct. 19 (Wed) 14:00 - 15:10
Room : Grand Ballroom 1+2+3

14:00 - 15:00	KS-1	**How corporate are responding to twin challenges : climate change and biodiversity loss** Ah Ryung Lee (KPMG Korea, Korea)

KS-1

How corporate are responding to twin challenges: climate change and biodiversity loss

Ah Ryung Lee[PC]

Strategy Consulting Group, KPMG Samjong Accounting Corp., Seoul 06236, Korea

As the financial society requires not only robust financial growth, but also sustainable management strategies, corporations encounter various type of business risks in respect of ESG (Environmental, Social, Governance) issues. During the COVID-19 pandemic, the climate crisis and biodiversity loss were identified one of the most severe risks towards the world and global society. Corporates are urged to respond to inevitable challenges (climate change and biodiversity) since these twin risks are closely connected to business performance and corporates' long-term value. Most valuable stakeholders believe that mid-to-long term strategies and detailed action plans for tackling ESG risks demonstrate corporates' competitiveness within the industries and would bring substantial financial and non-financial outcomes.

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Special Symposium

Endocrine disruptors and alternative chemicals

Date & Time : Oct. 20 (Thu) 08:30 - 09:40
Room : Sydney

Chair: Prof. Myung Chan Gye
Hanyang University, Korea

08:30 - 08:50	SS-1	**Utility of an embryonic zebrafish assay for evaluating endocrine disrupting potentials of chemicals and newly developed their alternatives** Kitae Kim (Seoul National University of Science and Technology, Korea)
08:50 - 09:10	SS-2	**Endocrine disruption potential of bisphenol A and its analogues** Myung Chan Gye (Hanyang University, Korea)
09:10 - 09:25	SS-3	**Development of low-cost alternatives with lower endocrine disrupting activity (Substitutes for nonylphenol surfactants)** Sung Hun Jung (SFC. Co., Ltd, Korea)
09:25 - 09:40	SS-4	**Physical and biological property of 1,4-bis(2-ethylhexyl) cyclohexane-1,4-dicarboxylate** Myungik Yoo (Hanwha Solutions, Korea)

SS-1

Utility of an embryonic zebrafish assay for evaluating endocrine disrupting potentials of chemicals and newly developed their alternatives

Kitae Kim[PC]

Department Environmental Engineering, Seoul National University of Science and Technology, Seoul 01811, Korea

Endocrine disruption effects of chemicals have been widely recognized, but relatively little is known about relative potency of legacy chemicals and newly developed alternatives. This difficulty stems from the varying definition of endocrine disruption and the complexity of bioassays used for evaluating endocrine disrupting effects. Here, the reliable definition of endocrine disruption and what kind of bioassays are available for each defined endocrine disruption will be introduced. More importantly, the utility of an embryonic zebrafish model as promising in vivo model will be introduced with the state-of-the-art techniques employed for evaluating diverse endocrine disruption effects. Lastly, the case study on the disruption of thyroid hormone and its related toxicity mechanism that underlies in conventional- and their alternative of chemicals such as phthalates, flame retardants, and UV-filters will be presented.

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SS-2

Endocrine disruption potential of bisphenol A and its analogues

Myung Chan Gye^{PC}

Department Life Science, Hanyang University, Seoul 04763, Korea

Environmental contamination of endocrine disruptor (ED) is the emerging environmental subject and should be treated as an important mater of environmental, social and governance (ESG). In accordance to ESG, surveillance of the environment contamination by EDs, their impact on ecosystem, and toxicological information of alternative plastic components became the important subject in environmental biology, sustaining our life. Bisphenol A (BPA), well known estrogenic ED has been used to manufacture polycarbonate and epoxy resin. Polycarbonate is 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. BPA is associated 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. Recently, several structural analogues of BPA, such like bisphenol F (BPF), and bisphenol S (BPS), have been used 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 BPA, BPF and BPS were investigated 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, suggesting the teratogenic potential of BPF. In the stage 45 tadpoles, 10nM BPA, 100nM BPF, and 100nM BPS significantly increased *vtg* mRNA in liver. This suggests that BPF and BPS have estrogenic potential, and which is one tenth of BPA. Taking into account the fact that BPA (0.004~22.04nM), BPF (0.55nM~5.92nM) and BPS (~0.168nM) contaminated the freshwater system in Korea, current contamination levels of BPA and its analogues exceed the safety lavel for amphibian development in the certain area of freshwater system in Korea.

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SS-3

Development of low-cost alternatives with lower endocrine disrupting activity (Substitutes for nonylphenol surfactants)

Sung Hun Jung[pc]

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Recently, various chemicals have been found to interfere with the endocrine system of animals. In particular, research results have shown that reproductive disturbances occur in animals in the wild. Therefore, SFC, a manufacturer specializing in surfactants, selected a group of candidate substances that could be substituted and developed substances for nonylphenol surfactants known as substances that act as environmental hormones. In order to realize the interfacial performance resulting from the aromatic structure of nonylphenol, the improvement of the interfacial performance of the hydrophobic group was studied by appropriately adding alkylene oxide to the fatty alcohol. In addition, various surfactants manufactured by SFC were reviewed to select alternative candidates. We collaborated with the university research institute to select low-toxic candidate materials by screening potential toxicity and in vivo dynamics of alternative candidate materials at high speed, and provided information on the stability of surfactants and in vivo dynamics. It mass-produced nonylphenol ethoxylate substitute materials that act as environmental hormones and is used for all industries such as paint, ink, cosmetics, artificial leather, fiber, metal, rubber, etc.

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SS-4

Physical and biological property of 1,4-bis(2-ethylhexyl) cyclohexane-1,4-dicarboxylate

Myungik Yoo^{PC}

Hanwha Solutions Chemical Division, PVC Tech Center, Korea

Plasticizers are additives used as plastic softeners. Most plasticizers are used for PVC(Polyvinylchloride) and are designed to be suitable for PVC. ECO-DEHCH(Ecofriendly plasticizer DEHCH), the world's first commercialized in Hanwha Solution, is a plasticizer with a cyclohexane structure and has physical and chemical characteristics similar to phthalate-based plasticizers like DINP. The Bleeding characteristics, which have the most influence on the human body, were relatively more than phthalate, but showed less than other alternative phthalate plasticizers. In addition, ECO-DEHCH showed good results in various toxicity tests such as skin sensitization, acute eye irritation/corrosion, acute dermal irritation/corrosion and Haemocompatibility. ECO-DEHCH is currently conducting chronic toxicity and carcinogenicity tests.

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Special Session

Special Session 1

ESG special session on climate risk and biodiversity (TCFD VS TNFD)

Date & Time : Oct. 19 (Wed) 16:10 - 17:50
Room : Grand Ballroom 1+2+3

Chair: Prof. Won Seog Park
Chung-Ang University, Korea

16:10 - 16:40	S1-1	**[Keynote Speaker]** **Biodiversity conservation and ESG** Min Hwan Suh (National Institute of Biological Resources, Korea)
16:40 - 17:10	S1-2	**[Keynote Speaker]** **Environmental regulations and ESG** Do Hyung Kim (Yoon & Yang LLC, Korea)
17:10 - 17:40	S1-3	**[Keynote Speaker]** **ESG in a business context: How can companies positively contribute towards ESG improvements** Nando Hoffmann (Carlsberg, Switzerland)
17:40 - 17:50	Panel discussion	**[Panel member]** **TCFD vs TNFD** Chan woo Kim (Gyeongsang National University, Korea) Jay Hyuk Rhee (Korea University, Korea) Yong Sik Ok (Korea University, Korea)

S1-1

Biodiversity conservation and ESG

Min Hwan Suh[pc]

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Recently, there has been a heated debate regarding ESG in business management and investment. However, biodiversity has not been discussed well although it is one of significant environmental aspects. Meanwhile, the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) reports that 25% of species on earth are on the brink of extinction. As many scholars warn a sixth mass extinction is underway, global biodiversity is severely threatened. In December 2022, the 15th Conference of the Parties to the Convention on Biological Diversity (CBD) is planned to adopt the Post-2020 Global Biodiversity Framework (GBF). The GBF includes global targets by 2030, some of which need to be achieved by businesses. It implies companies that are dedicated to considering ESG factors must take into account biodiversity conservation. The CBD was opened for signature at the UN Conference on Environment and Development in 1992 and as of now, the CBD has 196 parties. From the mid-1990s, Korea started to agree on international agreements regarding biodiversity, such as the CITES and the Ramsar Convention, along with the CBD. Moreover, Korea began to legislate biodiversity conservation. Furthermore, biodiversity research institutes were established from the mid-2000s and they have conducted full-scale research on biodiversity protection and conservation since then. This presentation showed what efforts Korea had made to protect and conserve biodiversity and how fast-changing the situation regarding biodiversity conservation both at home and abroad was. In addition, this presentation aimed to help business adopt ESG-friendly practices and protect and conserve biodiversity in a parallel manner by showing cases where conflicts between biodiversity conservation and development had been involved.

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S1-2

Environmental regulations and ESG

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ESG is an important issue in business management and investment by a company. ESG is an acronym for environment, society and governance, which are non-financial factors that are distinct from the financial performance of business and company operations. There is still no clear legal definition and also no internationally standardized evaluation criteria or indicators. Although environmental, social, and governance are all important factors for businesses, the environmental pillar is especially important because it carries regulations and risks. Environmental regulations can be divided into traditional areas, such as emission control of pollutants, and new areas, namely environmental information disclosure. In Korea, an environmental regulation that requires disclosure of ESG-related information has already been adopted, such as the mandatory and phased disclosure of environmental information from 2022. In this regard, all important environmental indicators, e.g. greenhouse gas emissions, and waste and water resource management, are subject to the information disclosure regulation. Meanwhile, according to the Global Risks Report 2022, biodiversity loss is considered the second most serious threat over the next decade after the climate crisis. Although biodiversity is one of the most important environmental indicators, it is still difficult to use biodiversity as an ESG evaluation indicator in Korea because the subject of review and analysis is more diverse and complex than that of climate change indicators. However, various discussions on biodiversity and ESG are in progress in the international community. For example, the Nature-Related Financial Information Disclosure Task Force (TNFD) published the TNFD Framework Guidelines in June 2022. And the Post-2020 Global Biodiversity Framework (GBF) will be finalized in the 15th Convention on Biological Diversity (CBD). Therefore, the Korean government and companies should seek ways to protect biodiversity through ESG management.

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S1-3

ESG in a business context: How can companies positively contribute towards ESG improvements

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Private organizations have been a great catalyst for change and contributing to improving overall quality of life. If we want private businesses to improve their ESG impact, we need to understand the underlying incentives and decision-taking structures. Examples from Carlsberg Switzerland will be presented to illustrate both the progress and current challenges that businesses face when dealing with ESG issues. This will serve as an example to investigate possible future actions for businesses, regulatory authorities, and consumers.

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Special Session 2

Development of integrated models for climate change adaptation

Date & Time : Oct. 19 (Wed) 16:10 - 17:50
Room : Grand Ballroom 4

Chair: Dr. Young-Il Song
Korea Environment institute, Korea

16:10 - 16:20	S2-1	**Development of integrated model for climate change impacts** Young-Il Song (Korea Environment institute, Korea)
16:20 - 16:40	S2-2	**Projecting temperature-related mortality by SSP scenarios** Ho Kim (Seoul National University, Korea)
16:40 - 17:00	S2-3	**Application of a forest integrated model for climate change adaptation** Mina Hong (Korea University, Korea)
17:00 - 17:20	S2-4	**Gridded projection of crop production using process-based models** Kwang Soo Kim (Seoul National University, Korea)
17:20 - 17:40	S2-5	**Assessment of climate change impact on wildlife habitat** Changwan Seo (National Institute of Ecology, Korea)
17:40 - 17:45	S2-6	**Development of a forest carbon model for climate change adaptation** Hyung-Sub Kim (Korea University, Korea)
17:45 - 17:50	S2-7	**Development of crop suitability model for climate change adaptation** Shinwoo Hyun (Seoul National University, Korea)
17:50 - 17:55	S2-8	**Development of a pest risk model for climate change adaptation** Jinsol Hong (Korea University, Korea)

S2-1

Development of integrated model for climate change impacts

Young-Il Song[pc] and Songmi Park

Korea Environment Institute, Republic of Korea

Climate change effects on natural eco-system and socio-economic system in a complex of ways while influencing each other. Due to the rising threat of Climate Change, adaptation has become a time-ticking challenge. For that reason, many countries develop the National Adaptation Plans (NAPs) to cope with climate risks. In the planning process of the NAPs, it is necessary to figure out the impacts and vulnerabilities of climate change scientifically from a holistic and integrated perspective. It is also necessary to enhance the capability to deal with various risks systematically. In this context, it is essential to develop the core technology to achieve these objectives. Since 2011, Korean government is implementing NAP not only to minimize potential damages from climate change but also to exploit beneficial opportunities. Meanwhile research project for development on “Model Of inTegrated Impact and Vulnerability Evaluation (MOTIVE) of climate change” was launched on 2014 to develop an integrated models evaluating the impacts and vulnerabilities due to climate change. The integrated models developed from the projects will be used to support the NAP process with providing scientific information. This research aims at developing the followings, Developing sectoral integrated models including water, health, agriculture, forest, ecosystem, marine Developing integrated model for climate change assessment using meta models Development of integrated model for climate change assessment using meta models will be presented.

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S2-2

Projecting temperature-related mortality by SSP scenarios

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It is widely accepted that the dose-response curve between temperature-mortality is U-shaped: mortality risk is higher in the hot as well as cold temperature ranges. Because of the warming trend of global temperature change, it is generally expected that mortality burden due to cold temperature will be slowly decreased but heat impact will be sharply increased. So total mortality burden due to temperature will be increased. We estimated county (Si-Gun-Gu)-level temperature -mortality curves by DLNM (distributed-lag non-linear model). We projected future county-specific temperature-related morality by three scenarios: SSP125, SSP245, and SSP585.

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S2-3

Application of a forest integrated model for climate change adaptation

Mina Hong[p1,3], Moonil Kim[2], Cholho Song[3], Jiwon Kim[1], Minwoo Roh[1],
Hyung-Sub Kim[1], and Woo-Kyun Lee[c1]

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The issue of climate change is recognized as a global issue and affects all areas of our lives, including the environment, economy, and society. Recent research in climate change adaptation areas has been actively discussed for risk based adaptation policies. Thus, discussions for establishing research and policies in the adaptation field to cope with climate change are being actively conducted. IPCC AR6 also emphasized the importance of adaptation measures for the forest sector to respond to climate change. Forests contribute significantly to climate change mitigation activities as a carbon sink. In this study, forest changes due to climate change were predicted through the 'Korean Forest Integrated Model,' which is a process-based model that interconnects the forest growth model, tree species distribution model, forest fire model, landslide model, and forest carbon model. As a result of the analysis, the stand volume was 165 m^3 as of 2020s, 204 m^3 in the scenario where the current climate maintenance and forest disasters do not occur in the 2050s, and 175 m^3 in the scenario where the climate change scenario (RCP8.5) and forest disasters are applied. At this time, it was analyzed that the decrease in growth would be alleviated if forest management was implemented. It was estimated that climate change would have a negative impact on forest resources, ecology, and health. Therefore, it was found that a management strategy for each sector that could minimize the negative impact was needed. The results of this study are meaningful in that they predicted the effects of climate change on forests from various angles, and are expected to contribute to responding to the new climate regime by supporting the establishment of forest management plans that enhance the ability to adapt to climate change.

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S2-4

Gridded projection of crop production using process-based models

Kwang Soo Kim[pc1,2] and Shinwoo Hyun[1]

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Crop productivity under future climate conditions would be affected by spatial variation in temperature and precipitation. The objective of this study was to develop a gridded crop simulation system that supports spatial and temporal assessments of climate change impact on crop production. Decision Support System for Agrotechnology Transfer (DSSAT), which is a process-based crop model, was chosen for the gridded simulation system. Gridded weather data such as the outputs of numerical weather models were used as inputs to the simulation system. Crop management conditions for the baseline scenario were identified analyzing the outcome of crop growth simulations under a set of management conditions. Crop yield data obtained from the simulations and the observations for a recent period, e.g., 2001~2015, were compared to determine the variable of importance for crop management options using random forest. Rice and soybean simulations were performed from 2001 to 2050. It was found that spatial and temporal changes in crop yield differed by region and crop in the future. In the southern provinces, rice yield was projected to be lower than that in the northern regions in Korea. The application of adaptation measures such as shifting transplanting date resulted in higher yield. There was no clear difference in soybean yield between southern and northern provinces. For example, Jeonnam and Gangwon had greater soybean yield than other provinces during the period from 2020-2050. Shift of planting date was highly effective for Jeonnam province although such an adaptation measure did not improve yield for Gangwon. These results suggest that the gridded simulation systems would be useful for impact assessment of climate change on crop production and evaluation of adaptation measures over space and time period, which merits further evaluation studies using a diverse set of weather input data as well as crop management conditions.

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S2-5

Assessment of climate change impact on wildlife habitat

Changwan Seo[pc1], Do-Hun Lee[1], Da-Jeong Choi[1], Gwang-Il Cheon[1], Joo-Young Joo[1], and Man-Seok Shin[2]

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Climate crisis have tremendously and widely influenced ecosystem, and must be so crucial for survival of wildlife in the near future. Distribution of wildlife will shift to another suitable habitat or shrink due to Climate change, and will change species composition of ecosystem. We set protected areas such as national park, DMZ, Baekdudaegan as study area. We simulated the distribution of species which are elements of ecosystem under climate change and examined the change of species in ecosystem. The result showed that species composition was expected to be changed differently according to the ecological and geological characteristics of ecosystem.

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S2-6

Development of a forest carbon model for climate change adaptation

Hyung-Sub Kim[P], Sanggeun Kwon, and Yowhan Son[C]

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Forests mitigate climate change by absorbing atmospheric carbon dioxide through photosynthesis. However, climate change again affects forest carbon absorption by changing temperature and precipitation, challenging to understand the climate mitigation role of forests. A forest carbon model is a key tool to help understand this complex interaction between forests and climate changes by formulating interrelated ecological processes. From 2014 to 2020, we developed a forest carbon model, called the Forest Biomass and Dead organic matter Carbon (FBDC), under the Model Of InTegrated Impact and Vulnerability Evaluation of climate change (MOTIVE) project. In the first phase of the MOTIVE project, the FBDC estimated the future climate mitigation role of South Korean forests with the impacts of climate change on forests. In the second phase of MOTIVE from 2022 to 2028, the FBDC will be further modified to assess the climate change risks on forests and to support decision makings on climate change adaptation strategies.

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S2-7

Development of crop suitability model for climate change adaptation

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Migration of crop cultivation as a climate change adaptation should be preceded by assessment of suitable regions. Climate suitability of a crop has been evaluated using a model which is developed based on a fuzzy logic system. Still, the model is not enough to simulate the suitability of perennial crops which require a chilling period to induce flowering. The object of this study was to integrate the suitability model with the vernalization process, which represents the promotion of the flowering process after prolonged cold temperature. The process would make the growing season and calculation of suitability be delayed by dormancy during the cold period. In this study, Chill Days Model was used to simulate the vernalization process, which accumulates chill days during rest and anti-chill days during quiescence. Although the degree days should be calculated based on daily minimum and maximum temperature, the process was modified to use monthly weather data to match with the temporal scale of the suitability model. Different parameter sets are required for each crop to determine the chilling requirement and the threshold of degree days. The parameter sets were reported in previous studies for some major fruit trees in South Korea. Further studies to validate the integrated model and determine the parameters for additional crops should be performed, which would be helpful for evaluating the crop suitability for perennial crops under climate change conditions.

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S2-8

Development of a pest risk model for climate change adaptation

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For the last 7 years, the MOTIVE project (Model Of InTegrated Impact and Vulnerability Evaluation of climate change) has conducted climate change impact assessments on Korea. For the pest model, the potential distribution, and the number of generations of 11 major agricultural pests were predicted. Now, the second phase of the MOTIVE project has begun, focusing on climate change risk assessment and adaptation. This study reviewed Korean R&Ds to manage pest risk and categorized the national scale adaptation strategies for pest risk reduction. In the second phase of the MOTIVE project, there is a need to improve the currently developed models and revise the effectiveness of current pest control strategies under future climates.

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Special Session 3

The role of small and medium-sized enterprises (SMEs) in Korea's advanced environment

Date & Time : Oct. 20 (Thu) 11:30 - 13:10
Room : Grand Ballroom 1+2+3

Chair: Prof. Baik-Ho Kim
Hanyang University, Korea

11:30 - 11:45	S3-1	**Sustainable business and research: A case study of Blue Carbon** Sung Joon Song (GeoSystem Research Corporation, Korea)
11:45 - 12:00	S3-2	**A case study on the implementation of ESG in small and medium enterprises - Focus on the case of INTIN** Yujin Lee (Intin Inc., Korea)
12:00 - 12:15	S3-3	**Commercialization by using hygiene and safety(KC) certified products and high-efficiency equipment certified pumps** Jae Kun Kim (Sung Jin IND, Korea)
12:15 - 12:30	S3-4	**Introduction: The past, present, and future of ESG management in LS Cable & System** Jungin Shin (LS Cable & System, Korea)
12:30 - 12:45	S3-5	**Application of nonpoint pollution reduction facilities to secure water friendly space** Eunmi Gwon (Ecostar Co. Ltd., Korea)
12:45 - 13:00	S3-6	**Review of environmental studies utilizing aquatic organisms** SeongDae Moon (NeoEnBiz Co., Korea)
13:00 - 13:15	S3-7	**The eco-friendly control of cyanobacterial blooms using highly refined hydrogen peroxide** Nam Kwon (Hansol Chemical, Korea)

S3-1

Sustainable business and research: A case study of Blue Carbon

Sung Joon Song[pc1,2]

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Many global companies are paying great attention to environment, Society, and governance and striving for ESG management for sustainable growth and survival. Among them, climate change and carbon neutral (=Net Zero) have recently become big issues, the impact of company on the natural environment is gradually increasing. In the present presentation, Geosystem Research Corporation introduces examples of influence in consideration of climate change, carbon emission, environmental pollution control, ecosystem and biodiversity, etc. In particular, we would like to focus on blue carbon. Our expert group in marine environment accurately grasps the current state of the ecosystem, and performs the task of quick diagnosis and evaluating the environmental impact and habitat health caused by various human activities. Recently, we are contributing to the expansion of blue carbon, a carbon capture in the marine and fishery for the carbon neutral. Blue carbon refers to carbon stored in coastal ecosystems, and 28 countries are using the blue carbon as a means of reducing greenhouse gas emissions. Unfortunately, a large portion of the coastal area in Korea is artificial, not natural. The absorption capacity of blue carbon will be greatly improved if the coastal areas are built to adapt to climate change according to the Korean situation. We investigate the suitable target sites for the Korean living shore-line, evaluate carbon absorption capacity, and tracks changes between marine environment and organisms. In addition, we introduce the researches on seedings and plantings of vegetation using aquaponics system, and non-destructive monitoring for sustainable business.

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S3-2

A case study on the implementation of ESG in small and medium enterprises - Focus on the case of INTIN

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ESG management, which means environmental, social, and governance of a company, has recently become an essential requirement among companies. INTIN Inc., a digital healthcare company, also cannot avoid this change. INTIN Inc., a small and medium-sized company, is increasing investor attractiveness through the introduction of the ESG management system and building trust in the community and consumers who consume it's products and services. First, INTIN Inc. uses environmentally friendly, recyclable raw materials and plans to implement 100% recyclable packaging by 2023. Through the strengthening of ESG capabilities of executives and employees, eco-friendliness is considered in all areas of R&D, manufacturing, production, and marketing. Second, for social factors, INTIN Inc. changes the paradigm of disease diagnosis and treatment, contributing to the problem of low birth rate through changes in the medical system and inventory of adult awareness through the sperm tester and ovulation tester. The respiratory diagnostic treatment system contributes to the prevention of infectious diseases and the resolution of health inequality by improving medical accessibility. Third, external audits are being conducted for governance and transparent management, and the ESG diagnostic evaluation project of the Daegu Chamber of Commerce and Industry was conducted to evaluate ESG diagnosis. ESG management will be enhanced through ESG management consulting support projects next year. The introduction of ESG management in small and medium-sized enterprises may still feel unfamiliar. However, it is now an essential area for survival, and is not an option. Compared to ESG activities at the government and large companies, difficulties such as lack of information and cost burden exist in establishing ESG activities at small and medium-sized enterprises. Despite these difficulties, if ESG is strategically introduced and used in the company's internal management goals, it will provide global competitiveness and create new business opportunities.

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S3-3

Commercialization by using hygiene and safety(KC) certified products and high-efficiency equipment certified pumps

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In general, the material of the pumps used in water supply facilities before KC sanitary and safety certification was a cast-type pump. As a result of this, a lot of rust is generated and complaints are increasing, so we have introduced the sanitary and safety (KC) certification for water supply, which is a legally mandatory certification, to lay the foundation for the supply of safe tap water to the public and is implementing it. In addition, by applying inverter control system to pumps and motors that have obtained high efficiency equipment certification products, energy (power amount) is reduced. In addition to the water supply and heating sectors, the application of the above system to the chemical, general industries, and agriculture sectors is expected to contribute to the development of national industries.

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S3-4

Introduction: The past, present, and future of ESG management in LS Cable & System

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In recent years, ESG is in the spotlight. Simply, the environment refers to environmental protection activities that take into account climate change, deforestation, and limited resources. Corporate economic activities and social values must develop together. In the face of COVID-19, ESG management that adds social responsibility to sustainable management has been emerged as ESG evaluation, ESG investment, ESG fund, ESG management, ESG information disclosure, etc. Just by looking at the various keywords with ESG, it can be seen that ESG has permeated the overall management of the corporate. LS cable & System also declared ESG management in June 2021 and has been actively conducting ESG management activities. This work will introduce the trends (past-present-future) related to ESG management in LS cable & System and the progress of recycling research related to the environment. In addition, as a researcher, I would like to consider the meaning of ESG management and the direction to go forward.

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S3-5

Application of nonpoint pollution reduction facilities to secure water friendly space

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The terrace land on the river in highly developed-urban area can be used for various purposes, like training space, walkway, ecological park, so, it has cherished value to citizen as water friendly area. Meanwhile, combined sewer overflow(CSO) or separate sewer overflow(SSO) were located in near terrace land on the river to discharge sewage that overflow in rainy season(Storm water runoff). Storm water runoff from CSOs or SSOs contains debris and sediment on the botton of sewer pipe, it can highly effect on water quality of urban stream. As a results, hundreds of thousands of fish can be founded dead, bad smell and damage to the landscape can be occurred. Finally, the value of terrace land on river as a water friendly area becomes disappeared. When it rains, sediment in sewage or pollutants on the road surface can be washed out with storm water runoff. It is called nonpoint pollutants and is cause of over 70% of pollution load in public water bodies. In this articles, the rapid up-flow filtration system for nonpoint pollutants to enhance value of terrace land on the river will be introduced. And the case study of these system operation will be analyzed with the effect on water quality and ecological value of the stream.

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S3-6

Review of environmental studies utilizing aquatic organisms

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Chemicals have improved the quality of human life. However, the exposure of living organisms and the environment to the processes of manufacturing, distribution, use, and disposal of chemicals has induced risks. The number of newly discovered chemical substances is increasing every year, and limitations in assessing their risks by chemical analysis alone persist. Accordingly, international organizations and developed countries are using various bioassays to evaluate the environmental hazards and risks of chemical substances. The risk assessment of a chemical in the environment determines whether the standard concentration has been exceeded. The most convenient way of making this determination is by comparing the predicted environmental concentration (PEC) with the predicted no-effect concentration (PNEC). At present, the PNEC is generally derived using the toxicity values of aquatic organisms, and its level is set to a very low risk value. This paper briefly introduces research examples of ecotoxicity evaluation, including those deriving environmental guidelines for each medium using aquatic organisms, among the various studies conducted by a small business enterprise (NeoEnBiz). In addition, the paper introduces various applications of such research outcomes, such as deriving the fishery damage rate using living organisms, performing ballast water bioassays, and conducting impact assessments of renewable energy development.

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S3-7

The eco-friendly control of cyanobacterial blooms using highly refined hydrogen peroxide

Nam Kwon^{PC}, Jiho Shin, and Jisu Kim

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While cyanobacteria decrease natural water quality, only few methods are known for rapid suppression of cyanobacterial blooms. Among those methods, hydrogen peroxide, which is decomposed into H_2O and O_2 in aquatic system, has been studied and considered as one of the highly promising algicide for cyanobacteria. Despite of numerous studies for application of H_2O_2 to laboratory and water supply resource in other countries, little is known about moderate H_2O_2 dosage and its toxicity for aquatic organisms in Korean reservoirs, however. In this study, we provide the chemical properties of highly refined H_2O_2 compound and its toxicity in aquatic organisms, including *Aliivibrio fischeri, Daphnia magna, Danio rerio*. Furthermore, we also afford the evaluation of H_2O_2 as an algicidal reagent in both laboratory and reservoir. In the laboratory condition, the cyanobacterial *microcystis aeruginosa* population, in which initial cell density is from 10,000 to 100,000 cells/mL, decreased by 100% within 72 hours, suggesting 0.35ppm H_2O_2 is sufficient concentration for suppression of *cyanobacteria.* In the case of the application of H2O2 to Korean reservoir, the cyanobacterial population was decreased by 100% within a few days. In addition, no toxicity toward other organisms was observed. Our results afford experimental insights into the application of hydrogen peroxide as an algicide for cyanobacteria.

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Special Session 4

Environmental protection and remediation

Date & Time : Oct. 20 (Thu) 11:30 - 13:10
Room : Grand Ballroom 4

Chair: Prof. Man-Young Jung
Jeju National University, Korea

11:30 - 12:00	S4-1	**[Keynote Speaker]** **Behaviors of conjugative plasmids in different environments** Masaki Shintani (Shizuoka University, Japan)
12:00 - 12:30	S4-2	**[Keynote Speaker]** **Cellular physiology and kinetics govern the substrate competitiveness of ammonia oxidizers** Christopher J. Sedlacek (University of Vienna, Austria)
12:30 - 12:50	S4-3	**Genomic and physiological characterizations of a novel Thermoplasmatales reveal their ecological niches in acidic and thermophilic environments** So-Jeong Kim (Korea institute of Geoscience and Mineral Resources, Korea)
12:50 - 13:10	S4-4	**Kinetics and community analysis of groundwater microbes in Jeju island** Man-Young Jung (Jeju National University, Korea)

S4-1

Behaviors of conjugative plasmids in different environments

Masaki Shintani[pc1,2,3]

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Plasmids are ones of the mobile genetic elements to transmit different genes including antibiotic resistance genes. Thus, it is important to understand which plasmids are truly spread in nature. Various conjugative plasmids were obtained by exogenous plasmid capture in biparental mating and/or triparental mating methods from different environmental samples in Japan1). Based on phylogenetic analyses of their whole nucleotide sequences, new IncP/P-1 and PromA-like plasmids that could be classified into novel subgroups were obtained. There were two large clades of IncP/P-1 plasmids, clade I and II. Several plasmids in clades I and II were reported to carry clinically highly relevant ARGs (e.g., colistin or ESBL resistance). The host range of plasmids of clade II was different from that of clade I. The host ranges of PromA group plasmids were broad and they could be transferred to different and distinct classes of *Proteobacteria*. Nevertheless, there were no previously known accessory genes on these PromA plasmids. These findings indicate the presence of 'hitherto-unnoticed' plasmids in nature, which would have important roles in the exchange of various genes, including antibiotic resistance genes, among different bacteria in nature.

1)Hayakawa et al., 2022, Applied and Environmental Microbiology, in press. doi:10.1128/aem.01114-22

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S4-2

Cellular physiology and kinetics govern the substrate competitiveness of ammonia oxidizers

Christopher J Sedlacek[pc1], Man-Young Jung[2,3], Petra Pjevac[1,4], Holger Daims[1,5], and Michael Wagner[1,5,6]

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In contrast to previous assumptions, ammonia-oxidizing archaea (AOA) are not always superior competitors for substrate, when compared with ammonia-oxidizing bacteria (AOB) or complete ammonia oxidizers (comammox). Here, we highlight how both cellular physiological properties and substrate kinetics together govern the competitiveness for substrate among a wide variety of ammonia oxidizers. The first step of nitrification, ammonia oxidation, is performed by three, often co-occurring guilds of chemolithoautotrophs: the AOB, AOA, and comammox. Substrate kinetics are considered to be a major nichedifferentiating factor between these guilds, but to date few AOA strains have been kinetically characterized. Here, the ammonia oxidation kinetic properties of 12 AOA representing all major cultivated phylogenetic lineages were determined using microrespirometry and compared with previously determined values for AOB and comammox species. Members of the genus Nitrosocosmicus have the lowest affinity for both ammonia and total ammonium of any characterized AOA, and these values are similar to previously determined ammonia and total ammonium affinities of AOB. In addition, Nitrosocosmicus species were among the worst competitors for ammonia or total ammonium. The substrate affinity and competitiveness for substrate of all ammonia oxidizers investigated correlated with their cell surface area to volume ratios. Lastly, our kinetic measurements across a range of pH values supports the hypothesis that —like for AOB—ammonia and not ammonium is the substrate for the ammonia monooxygenase enzyme of AOA and comammox. Together, these facilitate predictions and interpretation of ammonia oxidizer community structures and provide a robust basis for establishing testable hypotheses on competition between AOB, AOA, and comammox.

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S4-3

Genomic and physiological characterizations of a novel Thermoplasmatales reveal their ecological niches in acidic and thermophilic environments

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Alphabet-plasmas are classified as Thermoplasmatales and their most clones and metagenomic bins were detected in acid mine drainage and acidic hot springs. However, due to a lack of cultivation, their physiologies and metabolisms remain unclear. Here, we isolated a Thermoplasmatales strain AK from an acidic and geothermal mud volcano. 16S rRNA gene and phylogenomic based analyses revealed that the isolate was located between A and B-plasmas clades. The genome (1.67 Mbp) contained the genes contributed to carbon cycling by degrading proteins and amino acids and produce ATP via aerobic respiration. The genome of strain AK did not contain canonical genes coding for TCA cycle but candidate genes were included. The genome lacked biosynthetic pathway for some amino acids. Strain AK could utilize yeast extract, beef extract, tryptone and peptone as sole substrate based on cultivation experiments. It represented that they take up proteins and amino acids produced by other organisms like scavengers. These results expand our understanding of alphabet-plasma by revealing their ecological role.

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S4-4

Kinetics and community analysis of groundwater microbes in Jeju island

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Nitrification, the oxidation of ammonia (NH_3) via nitrite (NO_2^-) to nitrate (NO_3^-), is a vital process of the global biogeochemical nitrogen cycle and plays a significant role in fertilizer loss in industrial agriculture, eutrophication, and the production of greenhouse gas N_2O. Various groups of nitrifiers play a significant role in the groundwater, but their correct abundance with physiological mysteries still raised concerns. This study analyzed the nitrifying microbial community in various groundwater samples from Jeju Island, Korea. In addition, each major ammonia-oxidizing bacteria (AOB), archaea (AOA), and nitrite-oxidizing bacteria (NOB) were enriched from the different groundwater samples. We also identified the substrate kinetic properties of the enriched nitrifying culture and compared them to the microbial consortium of the groundwater samples to understand their adaptation strategy. Finally, we also analyzed human-originated bacteria in growundwater samples to estimate how significantly organic pollutants were contaminated in groundwater. Therefore, this study provides essential information on the physiological and biochemical characteristics of various nitrifying microorganisms and links to the survival strategies of the microbiomes in the nitrogen cycle.

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Special Session 5

The role of liberal education in the age of environmental crisis

Date & Time : Oct. 20 (Thu) 11:30 - 13:10
Room : Sydney

Chair: Prof. Eungbin Kim
Yonsei University, Korea

11:30 - 12:00	S5-1	**[Keynote Speaker]** **Successes and failures in response to the climate crisis in Germany, and the tasks of the church** Markus Dröge (Evangelischen Kirche Berlin-Brandenburg-schlesische Oberlausitz, Germany)
12:00 - 12:30	S5-2	**The three dimensions of ecological spirituality and liberal arts education** Ick-sang Shin (Sungkonghoe University, Korea)
12:30 - 13:00	S5-3	**Soil ecosystem responses to soil heating and wetting in maritime Antarctic regions** Dockyu Kim (Korea Polar Research Institute, Korea)
13:00 - 13:10	Q&A	Hak Chol Kim (Yonsei University, Korea)

Co-organized by Korean Theology Forum for Climate Crisis and Research Institute for Liberal Education, Yonsei University.

S5-1

Successes and failures in response to the climate crisis in Germany, and the tasks of the church

Dr. Dr. h.c. Markus Dröge[pc]

Evangelical Church Berlin-Brandenburg-Silesian Upper Lusatia, 10249 Berlin, Germany

The lecture first describes the self-understanding of the Protestant Church in Germany in the challenges that the climate crisis poses to Christians. How has the church developed its stance since the mid-1970s? What theological and ethical positions does it take? How does it understand its role? In a second step, the goals the church has set for itself and the measures it intends to take to achieve these goals are outlined. The climate concepts for the congregations and institutions of the church are of particular importance here. The third step describes the successes, failures and dilemmas to date. Finally, the tasks that the Protestant Church in Germany sees ahead are outlined.

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S5-2

The three dimensions of ecological spirituality and liberal arts education

Ick Sang Shin[pc]

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In the era of climate crisis, ecological thinking is becoming important in all academic disciplines. In particular, in theology, there is a tendency to pursue systematic theological explanations by accepting ecological thinking from the three perspectives of the story of creation, soteriology, and apocalypse. In this study, 1) These trends are reconstructed and introduced into three dimensions of eco-spirituality, and these three are to be synthesized from the perspective of Messiah concept. 2) By applying the three dimensions of eco-spirituality synthesized in this way to the actual orientation of liberal arts education in the posthuman situation, I would like to examine and suggest the possibility of forming the ideology and goal of liberal arts education based on ecological thinking.

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S5-3

Soil ecosystem responses to soil heating and wetting in maritime Antarctic regions

Dockyu Kim[pc1], Namyi Chae[2], Mincheol Kim[1], Soon Gyu Hong[1], Eungbin Kim[3],
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A large amount of soil organic matter (SOM) accumulates in maritime Antarctic tundra due to low microbial decomposition rates in cold environments. Humic substances (HS) are the largest constituents of SOM and perform the vital functions of carbon storage and supply in soil ecosystems. Microbial decomposition supplies HS-derived small compounds to the ecosystem as bioavailable carbon nutrients, which are ultimately emitted to the atmosphere as CO_2 and CH_4. Recent rapid air temperature increases across the tundra regions have prolonged permafrost thawing and snow melting periods, resulting in increased soil temperature and water content (the main terrestrial ecological factors). Due to the higher soil temperature and humidity with HS's structural flexibility, HS microbial decomposition might abruptly increase under rapid climate warming, and the resulting HS metabolites will possibly accelerate the changes in vulnerable Antarctic ecosystems that are already occurring. We investigated the effects of warming- and topography-induced higher soil temperatures and water contents on the microbial communities and functions, to answer the consequential effects on plant-microbe interactions in maritime Antarctic terrestrial ecosystem. We expect that the results of physiological and ecological studies can improve the accuracy of biological response models to predict the future of Antarctic ecosystem change.

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Special Session 6

Paradigm shift and challenge for cooperation for effective public communication of science and technology

Date & Time : Oct. 20 (Thu) 14:10 - 15:50
Room : Grand Ballroom 1+2+3

Chair: Prof. Eungbin Kim
Yonsei University, Korea

14:10 - 14:30	S6-1	**What is ‘SCIENCE’ for you?** Eungbin Kim (Yonsei University, Korea)
14:30 - 14:50	S6-2	**Trends in environmental education of science museum** Joon-Young Choi (Busan National Science Museum, Korea)
14:50 - 15:10	S6-3	**The importance of introductory chapter for classes of general biology for liberal education** Soo Chul Chang (Yonsei University, Korea)
15:10 - 15:30	S6-4	**Science, taking it to public: sow your own kind of seeds** Sojeng Yim (PIEXO2, Korea)
15:30 - 15:50	Panel Discussion	

Co-organized by KOFAC(Korea Foundation for the Advancement of Science&Creativity) and Research Institute for Liberal Education, Yonsei University.

S6-1

What is ‘SCIENCE’ for you?

Eungbin Kim[pc]

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When asked what science is, many point to scientific knowledge. However, science encompasses a much larger scope including scientific thinking. It was after the 17th century scientific revolution that science began to exert important values for mankind. Science has been the driving force behind new civilizations and cultures from the beginning. One of the best reasons for studying science is the scientific literacy, which can be defined as the knowledge of science, as well as the scientific framework by which people make decisions based on facts, not on opinion or hearsay. Scientific literacy enables you to learn new scientific knowledge on your own and develop the skills necessary for your future career, let alone be a consumer. One major obstacle to be overcome is that scientific knowledge is often a complex concept that is difficult to explain to everyone. Therefore, it is imperative that science communication plays its mediating role effectively.

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S6-2

Trends in environmental education of science museum

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The Science Museum, which has established itself as a representative venue for informal science education, provides various education according to the target and subject. While global environmental problems and the importance of environmental education are increasing day by day, science museums are also aware of the need for eco-environmental education and are trying them in various ways. This study discusses the direction and trends of sustainable environmental education in the science museum through various examples of eco-environmental education conducted at the Busan National Science Museum.

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S6-3

The importance of introductory chapter for classes of general biology for liberal education

Soo Chul Chang[PC]

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In our country, many lecturers tend to skipped introductory chapter in classes of general biology for liberal education of university. This study was carried out to point out that such attitude can miss very efficient and important approach in performing the course. It is well known that many general biology text books were designed to stand out their strengths and important principles in introductory chapters. Such strengths and principles are demonstrated in descriptions of life, themes of biology, and scientific methods. This means that lecturers should regard introductory chapter as an essential part to be given lesson. In introductory chapter, the importance of biological themes such as cells, genetic information, interaction with other individuals, regulation, relationship between structure and function, hierarchical structure, and evolution can be provided to students in very efficient ways. Among these themes, evolution is the most fundamental. Also point to be stressed is that these themes should be working as principles among various and huge amount of biological features. Keeping these themes in minds thru introductory chapter, it seems to be possible that students reach higher performance in studying biology than before.

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S6-4

Science, taking it to public: sow your own kind of seeds

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In recent years, even in Korea, there has been a growing awareness that science communication for the public is as important as scientific research. Most obviously, public demands on science communication have been increased in both quantitative and qualitative aspects. However, for now, the supply from the scientist and science communicator cannot meet such demand from both quantitative and qualitative aspects. In this talk, comparing the conventional science communication and recent new attempts, it is expecting that the clues for the direction in which future science communication should go through. Most importantly, each science communicator should develop his/her own way of communication, thus increasing the diversity of scientific communication.

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Special Session 7

Diverse aspects of omics in ecological studies

Date & Time : Oct. 20 (Thu) 14:10 - 15:50
Room : Grand Ballroom 4

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

14:10 - 14:35	S7-1	**[Keynote Speaker]** **Understanding the plankton community based on microscope and DNA sequencing approaches** Jun Yang (Chinese Academy of Sciences, China)
14:35 - 15:00	S7-2	**Freshwater microalgae omics approaches for Korean ecological studies** Jang-Seu Ki (Sangmyung University, Korea)
15:00 - 15:25	S7-3	**Exploration of antibiotic resistome and microbiome profiles of fish farm effluents in Jeju** Tatsuya Unno (Jeju National University, Korea)
15:25 - 15:50	S7-4	**Whole genome phylogeny of *Microcystis* with a focus on the toxic genotype** Zhun Li (Korea Research Institute of Bioscience and Biotechnology, Korea)

S7-1

Understanding the plankton community based on microscope and DNA sequencing approaches

Jun Yang[pc]

Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, 361021, China

Microeukaryotic plankton and bacterioplankton are critical components of aquatic microbial food webs and play essential roles in the structure and function of aquatic ecosystems. Understanding the processes and mechanisms that community dynamics and assembly of these microorganisms is one of major goals in both pure and applied microbial community ecology. Plankton communities normally consist of few abundant and many rare species, yet little is known about the ecological pattern and role of rare planktonic species. We found the rare bacterioplankton subcommunity had a distinct biogeographical pattern in inland waters that was reasonably similar to the abundant bacteria. However, local processes and factors play the most important role in structuring rare bacterial subcommunity, with regional factors explaining more variation in abundant bacteria. Both deterministic and stochastic processes significantly influenced eukaryotic plankton community assembly, and the stochastic pattern was particularly pronounced for rare taxa. Stochastic processes are sufficient in shaping substantial variation in rare plankton metacommunity in a river-reservoir system across different hydrographic regimes. Co-occurrence network analysis revealed that keystone taxa mainly belonged to rare species, which may play fundamental roles in network persistence following a cyanobacterial bloom event. Both warming and decline in water level can boost cyanobacterial dominance in subtropical reservoirs. The long-term observations revealed that the cyanobacterial biomass cycle created distinct niches between persistent bloom, non-bloom, decrease and increase of cyanobacteria, and therefore associated with distinct eukaryotic plankton patterns. These findings provide a new perspective for the ecological significance of rare plankton in changing aquatic ecosystems, clarifying the contribution of microbial interactions in plankton food web theory.

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S7-2

Freshwater microalgae omics approaches for Korean ecological studies

Jang-Seu Ki[PC], Taehee Kim, Han-Sol Kim, Quynh Thi Nhu Bui,
Jaeyeong Park, and Jeongmin Shin
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Microalgae are considered to be a good bio-indicator for environmental changes, because of their high diversity and sensitive response to water qualities. In addition, microalgae react sensitively at physiological and biochemical levels in response to exposure to toxic contaminants, and thus when they are used as influence indicators, it is possible to accurately detect biological harmful effects of each pollutant. Recently, various molecular techniques and omics have been applied to study on microalgae in aquatic ecosystems. In the present study, we presented ecological research using microalgae omics technique that applied to Korean ecological research. Microalgal-targeting omics has been mainly used for biodiversity analysis using DNA barcoding. With this method, the molecular diversity of cyanobacteria and microeukaryotic phytoplankton have been identified in Korean freshwaters. In addition, genomics, including molecular cloning and transcrtiptomics, have been applied to study on microalgae molecular biology. This include toxicogenomics and molecular biomarker to target the freshwater green algae *Closterium ehrenbergii*. The omics approaches in freshwater algae are in infancy, when compared to other organisms; thus, their wide applications are challenging in understanding molecular ecology of aquatic communities and toxicological impacts.

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S7-3

Exploration of antibiotic resistome and microbiome profiles of fish farm effluents in Jeju

Tatsuya Unno[pc]

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There are more than 200 fish farms in the coastal area on Jeju island. Most of these fish farms operate flow-through system in which seawater is directly pumped in and out. To prevent infectious disease, fish feeds often contain subtle amount of antibiotics. Recent studies have reported these antibiotics could trigger antibiotic resistance to marine bacteria. To investigate whether fish farm effluents contain antibiotic resistant bacteria, we performed metagenomic sequencing to reveal antibiotic resistome profile. In addition, we performed 16S rRNA gene sequencing to reveal microbial communities in fish farm effluents. Samples were collected from six fish farm effluents and three non-fish farm areas as a control. Our results showed antibiotic resistance genes were far more prevalent in fish farm effluents compared to non-fish farm samples. Moreover, summer samples showed higher abundance of fecal bacteria, indicating fecal pollution. Finally, our results indicate many of ARGs are carried by plasmids, suggesting high potential in transmission. The study presents current situation of antibiotic resistance gene discharge from fish farms and warns immediate actions to prevent dissemination of antibiotic resistant bacteria.

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S7-4

Whole genome phylogeny of *Microcystis* with a focus on the toxic genotype

Zhun Li[pc]

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Blooms of the harmful cyanobacterium *Microcystis* are increasing worldwide. Some *Microcystis* strains produce harmful toxins such as microcystin, impacting drinking water quality. Despite the importance of understanding the bloom mechanisms that influence cyanobacterial toxin production, the genetic features of toxic and non-toxic *Microcystis* are largely unknown. In this study, we performed a whole genomic analysis of 17 newly sequenced genomes from single *Microcystis* colony based cultures. We identified 24 *Microcystis* clusters of genomic similarity, four of which correspond to monophyletic clades containing at least three newly sequenced genomes. We observed that *Microcystis* genomes lacking the microcystin cluster (*mcy*) usually contained another gene cluster instead. For example, strain M23 lacked *mcy* but instead had genes related to the biosynthesis of anabaenopeptins (apn). However, some genomes (e.g. M3, M9, M22) contain a complete microcystin biosynthetic gene cluster (*mcyA-J*).

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Special Session 8

Linking international perspectives for advances in environmental research

Date & Time : Oct. 20 (Thu) 16:10 - 17:50
Room : Grand Ballroom 4

Chair: Prof. Ikju Park
Kyungpook National University, Korea

16:10 - 16:25	S8-1	**Understanding genomic structures, evolutionary event, and expression response of saxitoxin biosynthesis gene *sxtA* in the toxic marine dinoflagellate *Alexandrium pacificum* (group IV)** Quynh Thi Nhu Bui (Sangmyung University, Korea)
16:25 - 16:40	S8-2	**Effective control of harmful *Microcystis* blooms using *Paucibacter aquatile* DH15: from lab-scale to field research** Ve Van Le (Korea Research Institute of Bioscience & Biotechnology, Korea)
16:40 - 16:55	S8-3	**Sediment physicochemical properties and microbial community structure determine *Zostera marina* litter-derived carbon dynamics during litter decomposition** Zhaxi Suonan (Pusan National University, Korea)
16:55 - 17:10	S8-4	**In vivo toxic effects of *Nemopilema nomurai* jellyfish venom in zebrafish (*Danio rerio*)** Ramachandran Loganathan Mohan Prakash (Gyeongsang National University, Korea)
17:10 - 17:25	S8-5	**Inhibitory efficacy of myricetin against *Nemopilema nomurai* jellyfish venom metalloproteinase using computational approach** Ravi Deva Asirvatham (Gyeongsang National University, Korea)
17:25 - 17:40	S8-6	**Environmental identification of *Amaranthus* species using Visible-Near-Infrared (Vis-NIR) spectroscopy and machine learning methods** Subramani Pandian (Rural Development Administration, Korea)
17:40 - 17:55	S8-7	**Predicting the impact of climate change on the habitat distribution of famine weed (*Parthenium hysterophorus*) globally and locally in South Korea** Anil Poudel (Hankyong National University, Korea)

S8-1

Understanding genomic structures, evolutionary event, and expression response of saxitoxin biosynthesis gene *sxtA* in the toxic marine dinoflagellate *Alexandrium pacificum* (group IV)

Quynh Thi Nhu Bui[P], Han-Sol Kim, and Jang-Seu Ki[C]

Department of Biotechnology, Sangmyung University, Seoul 03016, South Korea

The dinoflagellate Alexandrium is known to produce saxitoxins (STXs), causing paralytic shellfish poisoning (PSP). STXs biosynthesis is directly catalyzed by eight enzymes encoded in their corresponding *sxt* core genes. Of them, sxtA is a core gene participating in the initial step of STXs biosynthesis; however, its gene coding structure and evolutionary history have yet to be fully elucidated in dinoflagellates. Herein, we determined the full-length sequence of sxtA from toxic dinoflagellate Alexandrium pacificum (Alex05), characterized their domain structures, resolved evolutionary events, and evaluated transcriptional responses under varying salinity. The *Ap*sxtA was 5031 bp in length and was encoded on the genome without intron. Phylogenetic analysis showed that ApsxtA formed a clade with sxtA of toxic dinoflagellates and cyanobacteria. STXs eq was highest (35.8 fmol/cell) in the exponential phase at 30 psu. At that time, GTX4 and C2 were predominant but were replaced by GTX1 and NeoSTX in the stationary phase. *ApsxtA* expression level was induced, and its patterns were similar in all tested conditions. However, PCA showed that the *ApsxtA* gene transcriptional level was not statistically correlated with toxin contents and salinity. These suggest that *A. pacificum* may produce the highest amount of toxins at optimal salinity, but *sxtA* may be only minimally affected by salinity, even under high salinity stress.

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S8-2

Effective control of harmful *Microcystis* blooms using *Paucibacter aquatile* DH15: from lab-scale to field research

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As a result of global warming and eutrophication, *Microcystis* blooms are increasing globally, causing water quality deterioration. Cyanobactericidal bacteria have attracted much attention in the research community as a vehicle for controlling *Microcystis* blooms because of their ecological safety. Herein, we evaluated the algicidal activity of *Paucibacter aquatile* DH15 in lab-scale and scale-up field experiments. Strain DH15 was observed to control the growth of *M. aeruginosa* through mechanisms related to oxidative stress and damage to the cell wall, membrane, organelles, and photosynthetic systems. The algicidal activity of DH15 (2.1×10^4 CFU/ml) against *M. aeruginosa* (2×10^6 cells/ml) was 94.9% within 36 h of exposure. In a mesocosm experiment (1000 L), strain DH15 showed great potential to control outbreaks of *Microcystis* blooms without secondary pollution: (1) DH15 reduced natural *Microcystis* cell density by 90.7% within two days; (2) microcystins released by *Microcystis* death decreased to the control level in four days; (3) during the cyanobactericidal processes, the physicochemical parameters of water quality remained safe for other aquatic organisms; and (4) the cyanobactericidal processes promoted the growth of eukaryotic microalgae, replacing cyanobacteria. The cyanobactericidal processes accelerated turnover rates, decreased stability, and altered the functional profile of the microbial community. Network analysis demonstrated that this process resulted in more complex interactions between microbes. Collectively, our findings highlighted that strain DH15 could be considered a promising candidate for controlling *Microcystis* blooms in an eco-friendly manner.

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S8-3

Sediment physicochemical properties and microbial community structure determine *Zostera marina* litter-derived carbon dynamics during litter decomposition

Zhaxi Suonan[P], Seung Hyeon Kim, Hyegwang Kim, Fei Zhang, and Kun-Seop Lee[C]

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Seagrass litter material is an important source of sediment organic carbon contributing to the long-term blue carbon storage in coastal ecosystems. However, the organic carbon dynamics of both above- and below-ground *Zostera marina* litter materials during decomposition remain unclear. This study aimed to investigate the decomposition process of *Z. marina* above- and below-ground litter materials during the different phases of decomposition. Two distinct mass loss phases of *Z. marina* above- and below-ground litter materials existed with an initial rapid leaching phase of the labile litter component and a slow remineralization phase of the refractory litter component. The lower decomposition rates of *Z. marina* below-ground litter materials guaranteed the higher litter mass remaining. Carbon accumulations of *Z. marina* below-ground litter materials in muddy study sites were higher than those in sandy study sites due to sediment oxygen variability attributing to differences in sediment characteristics (e.g. dry bulk density, water content, and organic matter) between sandy and muddy sediments. High sediment nutrient availability appeared to provide exogenous inorganic nutrient resources to sediment microbes accelerating the microbial breakdown of *Z. marina* above-ground litter materials, which resulted in relatively lower litter mass remaining and litter-derived carbon burial in muddy sediments of study sites. The significant dissimilarities in microbial community structure between the sandy and muddy sediments offered an alternative explanation for the different decomposition patterns of *Z. marina* above- and below-ground litter materials among the study sites. Our results suggested that site-specific physicochemical sediment properties associated with different sediment microbial compositions potentially influence *Zostera marina* litter-derived carbon dynamics during decomposition.

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S8-4

In vivo toxic effects of *Nemopilema nomurai* jellyfish venom in zebrafish (*Danio rerio*)

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Nemopilema nomurai venom (NnV) has been previously described for its various kinds of toxicity in many organisms. However, the mechanism of its toxicity has been rarely understood yet. The present work is the first report demonstrating some novel toxic effects of NnV on zebrafish (*Danio rerio*) as an alternative vertebrate model for jellyfish venom study. In this model, NnV appears to cause severe hemorrhagic and inflammatory responses in the cardiopulmonary regions of zebrafish. Besides these effects, NnV also altered the swimming behavior of zebrafishes, accompanied by a significant downregulation of acetylcholinesterase (AChE) activity in the brain tissues. The histopathological changes have also been illustrated in *Danio rerio* upon various organs which corresponds to an increase in lactate dehydrogenase (LDH) activity in the tissues. NnV also significantly altered the glutathione S-transferase (GST) activity in cardiopulmonary and in brain tissues of *Danio rerio*. SDS-PAGE revealed many protein bands of NnV showing various sizes which could be detected by silver staining. Taken together, we propose *Danio rerio* is an excellent animal model for investigating jellyfish venom toxicology study. Likewise, our present findings would suggest a useful tool for developing an effective treatment and discovering the mechanism of action for jellyfish venom poisoning.

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S8-5

Inhibitory efficacy of myricetin against *Nemopilema nomurai* jellyfish venom metalloproteinase using computational approach

Ravi Deva Asirvatham^{p1,2}, Ramachandran Loganathan Mohan Prakash[1,2],
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Around the world, jellyfish stings cause various problems in public health. *Nemopilema nomurai*, a scyphozoan jellyfish contains millions of nematocysts in their tentacles causing many toxinological effects. Although, *Nemopilema nomurai* venom (NnV) is a cocktail of several toxins, the earlier finding reveals that metalloproteinase activity is one of the key components in the jellyfish venom, which is responsible for the toxic effects in animal model. Therefore, we consider that, identifying some potential metalloproteinase inhibitor (MPI) would neutralize the venom toxicities. So, our aim is to find a specific MPI against NnV using computational approach. Therefore, we have screened numerous primary polyphenol compounds to see its ability to inhibit the metalloproteinases. The NnV metalloproteinases were retrieved from transcriptomic data and protein sequences were modeled by ab initio modeling. Among many polyphenol compounds, myricetin shows the highest docking score with NnV metalloproteinase. Together, molecular dynamics analysis reveals the accurate binding orientation of phenolic principles were in the binding pockets of (NnV) metalloproteinase. Hence, we conclude that myricetin might be a plausible NnV-MPI as a remedy against the envenomation caused by scyphozoan jellyfish stings.

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S8-6

Environmental identification of *Amaranthus* species using Visible-Near-Infrared (Vis-NIR) spectroscopy and machine learning methods

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Visible-near-infrared (Vis-NIR) spectroscopy in combination with chemometric techniques, was used for the feasibility of quick and non-destructive method of identification of plant species. The main goal of this study would be to classify six different *Amaranthus* sp. in different geographical regions of South Korea using a handheld spectrometer in the field. Spectra were obtained from the adaxial side of the leaves at 1.5 nm intervals in the Vis-NIR spectral range between 400 and 1075 nm. The obtained spectra were assessed with four different preprocessing methods in order to detect the optimum preprocessing method with high classification accuracy. Preprocessed spectra of six *Amaranthus* sp. were used as input for the machine learning-based chemometric analysis. All the classification results were validated using cross-validation to produce robust estimates of classification accuracies. The different combinations of preprocessing and modeling were shown to have a classification accuracy of between 71% and 99.7% after the cross-validation. Considering the high number of spectra involved in this study, the growth stage of the plants, varying measurement locations, and the scanning position of leaves on the plant are all important. We conclude that Vis-NIR spectroscopy, in conjunction with proper preprocessing and machine learning approaches, can be utilized in the field to efficiently categorize *Amaranthus* sp. for effective weed management and/or monitoring of their culinary applications.

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S8-7

Predicting the impact of climate change on the habitat distribution of famine weed (*Parthenium hysterophorus*) globally and locally in South Korea

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The famine weed (Parthenium hysterophorus) is one of the world's worst noxious invasive weeds. It can seriously threaten agriculture, native biodiversity, ecosystem services, and human beings. The invasion of P. hysterophorus may be further exacerbated due to the increasing temperature and elevated carbon dioxide regime. Therefore, it is necessary to predict the potential distribution of P. hysterophorus to identify the areas prone to invasion and adopt preventive measures. In this study, we used a maximum entropy modeling approach and estimated global and local distribution in South Korea under current and future climate change. Its distribution is relatively high in Australia, South America, and Oceania, and the invasion hotspots are concentrated at 35° north and south of the equator under the current climate. However, by 2081–2100, the change in suitable habitats would be maximum in Europe, and the invasion extend up to 65° N latitudes. In South Korea, currently, it has invaded a small portion of the country (2.24%), particularly in the six administrative divisions (ADs). However, by 2081–2100, the invasion would expand across the whole country (except Incheon), increasing its area by 3,344.54% more than the current invasion. Also, the ADs in the southern and central regions showed very high suitability compared to the northern part. This study revealed that climate change is likely to aggravate the habitat suitability of P. hysterophorus globally and in South Korea, and the habitat expansion occurs in a northward direction by shifting the climatic barrier. Thus, it is essential to conduct control and management activities to prevent further expansion into the new area.

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Special Session 9

Exploration of organic substances in various environmental systems by analytical science and technology

Date & Time : Oct. 20 (Thu) 16:10 - 17:50
Room : Sydney

Chair: Dr. Kyoung-Soon Jang, Dr. Jong Bok Seo
Korea Basic Science Institute, Korea

16:00 - 16:25	S9-1	**[Keynote Speaker]** **Dissolved organic matter and microbial processes on mountainsides** Jianjun Wang (Chinese Academy of Sciences, China)
16:25 - 16:45	S9-2	**Biogeochemical cycling of dissolved organic matter and the associated environmental effects in typical lakes in China** Yongqiang Zhou (Chinese Academy of Sciences, China)
16:45 - 17:05	S9-3	**Smart fertilizer developments using plant lignin and coal-derived humic substances** Jong-Rok Jeon (Gyeongsang National University, Korea)
17:05 - 17:25	S9-4	**Particulate matter 2.5's cellular toxicology and its natural modulators** Byeong-Churl Jang (Keimyung University, Korea)
17:25 - 17:45	S9-5	**Microfluidic platforms for environmental screening applications** Hyun Soo Kim (Kwangwoon University, Korea)

S9-1

Dissolved organic matter and microbial processes on mountainsides

Ang Hu[1,2], Mira Choi[3], Andrew J. Tanentzap[4], Kyoung-Soon Jang[3], Jinfu Liu[1,5], Jay T. Lennon[6], Yongqin Liu[7,8], Janne Soininen[9], Xiancai Lu[10], Yunlin Zhang[1], Ji Shen[11], and Jianjun Wang[pc1,8]

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Dissolved organic matter (DOM) is one of the largest pools of carbon in aquatic ecosystems, and interlinked with microbes in nature. It remains open questions: (1) how to quantify DOM-microbe associations and disentangle the interactive and independent effects of global change drivers. (2) Individual DOM molecules have unique functional traits, but how their assemblages vary deterministically under global change remains poorly understood. Here, we examine DOM and associated bacteria in 300 aquatic microcosms deployed on mountainsides that span contrasting temperature and nutrient gradients. We firstly develop a framework called Energy-Diversity-Trait integrative analysis (EDTiA) to examine the associations between DOM and bacteria along temperature and nutrient gradients. DOM-bacteria associations depend strongly on molecular traits of DOM, with negative correlations as molecules are more biolabile such as high H/C ratio. Using bipartite networks, we demonstrate that specialization is higher for negative than positive DOM-bacteria associations indicative of decomposition and production, respectively. Nutrient enrichment promotes specialization of positive associations, while decreases specialization of negative associations particularly at warmer temperatures in the subtropical region. Secondly, based on molecular trait dimensions of reactivity and activity, we partition DOM composition into labile-active, recalcitrant-active, recalcitrant-inactive and labile-inactive fractions, and quantify relative influences of deterministic and stochastic processes governing the assembly of each. At both subtropical and subarctic study sites, the assembly of labile or recalcitrant molecules in active fractions is primarily

governed by deterministic processes while stochastic processes are more important for the assembly of molecules within inactive fractions. Surprisingly, the importance of deterministic selection increases with global change gradients for recalcitrant molecules in both active and inactive fractions, and this trend is paralleled by changes in the deterministic assembly of microbial communities and environmental filtering, respectively. Together, our findings reveal that molecular traits will influence DOM-microbe associations and wider carbon cycling under global change.

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S9-2

Biogeochemical cycling of dissolved organic matter and the associated environmental effects in typical lakes in China

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Lakes receive and actively process terrestrial dissolved organic matter (DOM) and play an important role in the global carbon cycle. Urbanization results in elevated inputs of nonpoint source DOM to headwater streams. Retention of water in lakes allows time for alteration and transformation of the chemical composition of DOM by microbial and UV radiation. Yet, it remains unclear how anthropogenic and natural drivers impact the composition and bio-lability of DOM in non-pristine lakes. We used optical spectroscopy, Fourier transform ion cyclotron mass spectrometry, stable isotopic measurements, and laboratory bio-incubations to investigate the chemical composition and bio-lability of DOM across two large datasets of lakes associated with a large gradient of urbanization in lowland Eastern China, encompassing a total of 99 lakes. We found that increased urban land use, gross domestic product, and population density in the catchment were associated with an elevated trophic level index, higher chlorophyll-*a*, higher bacterial abundance and a higher amount of organic carbon with proportionally higher contribution of aliphatic and peptide-like DOM fractions, which can be highly bio-labile. Catchment area, water depth, lake area : catchment area, gross primary productivity, $\delta^{18}O$-H_2O, and bacterial abundance, however, had comparatively little linkage with DOM composition and bio-lability. Urban land use is currently intensifying in many developing countries, and our results anticipate an increase in the level of bio-labile aliphatic DOM from nonpoint sources and accelerated carbon cycling in lake ecosystems in such regions.

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S9-3

Smart fertilizer developments using plant lignin and coal-derived humic substances

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Humic substances (HSs) are stabilized organic matter in soil, and versatile organic moieties of HSs are involved in microbial respiration, metal bioavailability, soil fertility, and plant nutrient immobilization. In spite of the complex organic structures of HSs, key structure-function relationship has been deciphered, thus encouraging their use in several application areas. HSs are structurally supramolecular assemblages whose components are reversely disaggregated in response to small organic acids. Given that plant roots can secret a variety of organic acids whose compositions are related to plant stress status, HS architecture could be used to encapsulate plant nutrients whose quantity released is modulated with the plant status. In addition, HSs are able to acidify mineral surfaces, thus facilitating mineral dissolution which coincides with the supply of plant nutrients. This property would be very useful to modify the dissolution kinetics of new ceramic-based ferilizers. Here I introduce how physicochemical and stuructural features of HSs are harnessed to fabricate new types of fertilizers which show the better performances on plant nutrition and stress tolerance. I also discuss how plant lignin could be an alternative to HSs.

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S9-4

Particulate matter 2.5's cellular toxicology and its natural modulators

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Particulate matter (PM), a major component of air pollution, induces significant adverse health effects. PM is classified into PM0.1, PM2.5, and PM10, based on the aerodynamic diameter of fine particles of 0.1, 2.5, and 10 mm, respectively. The PM2.5-induced cellular toxicology (cell growth inhibition and death, inflammation, fibrosis, and wound) and its molecular and signaling mechanisms are not fully understood. In addition, natural and synthetic substances that inhibit PM-induced cellular toxicology are limited. Thus, it is necessary to understand the PM's cellular toxicology and identify new material that inhibits it. This review will describe the effect and mode of action of PM2.5D (diesel PM2.5) on growth inhibition of lung epithelial cells. This review will also describe the effect and mode of action of PM2.5U (urban PM2.5) on induction of inflammatory cyclooxygenase-2 (COX-2) or fibrogenic type 1 collagen expression in adipocytes, microglial cells, and lung epithelial cells. Finally, this review will describe several newly identified natural substances that inhibit the PM2.5D-induced cytotoxicity and the PM2.5U-induced COX-2 or type 1 collagen expression in the cells, along with their molecular and signaling mechanisms to control it.

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S9-5

Microfluidic platforms for environmental screening applications

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Microfluidics, a technology that can accurately control extremely small amount of liquid samples, together with various micro/nano fabrication technologies, enable the concept of lab-on-a-chip systems. The lab-on-chip concept, which is building an entire life science or chemistry lab on a chip, allows integration of multiple functional components into a single system that can perform all the necessary steps for a particular procedure, such as from sample preparation to sample analysis, with minimum manual intervention. We are interested in solving grand challenge problems in the broad area of environment through the use of microfluidic system technologies. Two of our research themes will be presented; 1. Microsystems that allow for high-throughput screening of microbial libraries in the environmental samples, and 2. Microsystems that enable environmental toxin analysis/control.

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Special Session 10

Diversity of the undiscovered taxa in Korea

Date & Time : Oct. 21 (Fri) 09:30 - 11:10
Room : Grand Ballroom 1+2+3

Chair: Prof. Jong-Seok Park
Chungbuk National University, Korea

09:30 - 09:50	S10-1	**[Keynote Speaker]** **Coleoptera inventory projects: past, present, and future** Victoria Bayless (Louisiana State University, USA)
09:50 - 10:05	S10-2	**Novel species of the genus *Metschnikowia* isolated from Alnus Ambrosia Beetle *Xylosandrus germanus*** Minji Bang (Seoul Women's University, Korea)
10:05 - 10:20	S10-3	**Morphological and molecular analysis of the novel species belong to genus *Monochaetia* isolated from *Moechotypa diphysis*** Seong-Keun Lim (Kyungpook National University, Korea)
10:20 - 10:35	S10-4	**New record of two *Tintinnopsis* species (Protozoa: Ciliophora: Tintinnida) from Korean coastal waters** Ji Hye Moon (Gangneung-Wonju National University, Korea)
10:35 - 10:50	S10-5	**Diversity and assemblage structure of litter-dwelling beetles in different sizes of islands using a sifting method** Ui-Joung Byeon (Chungbuk National University, Korea)

S10-1

Coleoptera inventory projects: past, present and future

Victoria Bayless^{pc} and Chris Carlton

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The order Coleoptera is the largest order of insects, containing over 380,000 described species globally, This represents more than one third or all described animal species. There are ~ 4,821 described species in Korea and ~30,000 in the US. Beetles are often used in both natural areas and agricultural environments as an indicator species for research and conservation. The history, results, and current progress of a project to document total beetle diversity in Great Smoky Mountains National Park USA is presented. In total, we documented 2,527 species from an area approximately 522,000 acres (211,000) hectares in size. We expect to add to this number slowly in anticipation of about 3000 total species. The role of citizen science and professional specialists from around the world was critical to the success of the project. We discuss the possibility of a comparable project in Korea and offer some suggestions about how to approach the project.

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S10-2

Novel species of the genus *Metschnikowia* isolated from Alnus Ambrosia Beetle, *Xylosandrus german*

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Department of Bio & Environmental Technology, College of Natural Science, Seoul Women's University, Seoul 01797, Republic of Korea

Two yeast strains SK21-476^T and SK20-698, representing a novel Ascomycota yeast species were isolated from Alnus Ambrosia Beetle, *Xylosandrus germanusinin* Republic of Korea. Molecular phylogenetic analysis of the internal transcribed spacer (ITS) region and 26S rRNA D1/D2 domains showed that they belonged to the genus *Metschnikowia* of order *Saccharomycetales* and the closet known relative being *Metschnikowia kofuensis*. The strain SK21-476^T differed by 4 nucleotide substitutions with no gap in the D1/D2 domain of the LSU rRNA gene and 11 nucleotide substitutions with 2 gaps in the ITS region. Therefore, the results of phylogenetic analyses and the phenotypic characteristics showed that both strains are reproductively isolated from other *Metschnikowia* species. The name *Metschnikowia jejuensis* sp. nov. is proposed to accommodate these both strains, with strain SK21-476^T designated as the type strain

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S10-3

Morphological and molecular analysis of the novel species belong to genus *Monochaetia* isolated from *Moechotypa diphysis*

Seung-Keun Lim[P1], Soo-Min Hong[1], Seung-Yeol Lee[c1,2], and Hee-Young Jung[1,2]

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In this study, the fungal strain designated KNUF-6L2F was isolated from a specimen of *Moechotypa diphysis* in Kangwon province in Korea. Phylogenetic analyses based on a concatenated dataset of DNA sequences of ITS region and partial gene sequences of beta-tubulin (TUB) and elongation factor (TEF) showed that the strain belongs to the same clade together with other *Monochaetia* species but represented a different species than the ones previously described. Morphologically, the novel strain produced olivaceous-colored 4-septated conidia and shorter apical-appendage (4–12 μm) compared with the closely related *M. ilicis,* which produces brown-colored 4-septated conidia and an apical-appendage of 10–20 μm. The novel strain also differed from *M. ilicis* by colony color and size on PDA. The detailed morphological descriptions and the phylogenetic analyses of the closely related species support that the strain KNUF-6L2F represents a novel species in the genus *Monochaetia.*

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S10-4

New record of two *Tintinnopsis* species (Protozoa: Ciliophora: Tintinnida) from Korean coastal waters

Ji Hye Moon[P] and Jae-Ho Jung[c]

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For the investigation of ciliate diversity in Korea, we collected net-tow samples from Korean coastal waters. Using microscopic examination of the samples, we found two unrecorded *Tintinnopsis* species. To assure their identification, we studied their morphology. As a result, we identified the two species as *Tintinnopsis fimbriata* Meunier, 1919 and *T. kiaochowensis* Yin, 1956. *Tintinnopsis fimbriata* is characterized by the size (60–70 × 35–40 μm) and shape (stout campanulate) of the lorica. Its lorica consists of two parts: an obconical collar (about 10 μm high) and a globular bowl (on average 44.0 × 33.6 μm) merging into a cylindroidal posterior process (about 10.5 × 7.5 μm). *Tintinnopsis kiaochowensis* is characterized by the size (85–95 × 65–70 μm) and shape (bumpy) of the lorica. Its lorica composed of irregular collar (35–40 × 45– 72 μm; 2.5–3.5 spiral turns) and a conical bowl (on average 50 × 65 μm) with rounded posterior end.

** This work was supported by grants from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR202231206).

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S10-5

Diversity and assemblage structure of litter-dwelling beetles in different sizes of islands using a sifting method

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We studied litter-dwelling beetles among different sizes of islands to understand how beetle diversity and structure change across islands that were connected to bridges. We also investigated environmental factors that may affect diversity and relative abundance of litter-dwelling beetles. Such factors included soil temperature, atmospheric temperature, humidity, soil pH, forest type, altitude, canopy cover, island size, distance from mainland, and number of bridges to the islands. Sampling was conducted in May and July 2022 on nine islands in South Korea, using a sifting method. We collected a total of 3,345 beetles, representing 37 families and 175 species. As a result of regression analysis, beetle species richness and abundance showed a decreasing trend with an increasing island size. However, rarefaction curves predicted that medium-sized islands would have the highest species richness. Beetle assemblage composition was affected by all environmental factors, of which location was the most significant factor. The islands within each location presented only slight differences in assemblage composition. The community structure of litter-dwelling beetles was not determined by single environmental factor, but was determined by the complex relationships of various environmental factors. Continuous researches between litter-dwelling beetles and various environmental factors will provide a better understanding of species distribution in modern islands connected to bridges.

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Special Session 11

Post 2020, the conservation strategy of wild plants seed in Baekdudaegan National Arboretum

Date & Time : Oct. 21 (Fri) 09:30 - 11:10
Room : Grand Ballroom 4

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

09:30 - 09:40	Introduction	Sun Hee Hong (Hankyong National University, Korea)
09:40 - 10:00	S11-1	**Conservation strategy for wild plant seeds in Baekdudaegan National Arboretum, Republic of Korea** Chae Sun Na (Baekdudaegan National Arboreutm, Korea)
10:00 - 10:20	S11-2	**An external perspective on seed collection strategy of Baekdudaegan National Arboretum** Gyu Yong Chung (Andong National University, Korea)
10:20 - 10:40	S11-3	**Industrial values of wild plant** Yeong-Su Kim (Baekdudaegan National Arboreutm, Korea)
10:40 - 11:00	S11-4	**A corporate perspective on the conservation of useful wild plants in the cosmetic industry** Jin Young Lee (Amorepacific R&I Center, Korea)
11:00 - 11:10	Q&A	Sun Hee Hong (Hankyong National University, Korea)

S11-1

Conservation strategy for wild plant seeds in Baekdudaegan National Arboretum, Republic of Korea

Chae Sun Na[PC]

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The best way to conserve the genetic resource of plants is through their seeds. Therefore, seed banks have been created and operate globally to conserve all plant genetic resources, from crops to wild plants. Svalbard Global Seed Vault has been opend to duplicate crop seeds from seed banks in 2008. Among these, the Baekdudaegan National Arboretum is unique as it comprises two important facilities, the Baekdudaegan Global Seed Vault (BGSV) and the Baekdudaegan Wild Plant Seed Bank (BWSPB), that work in conjunction for the conservation and research of wild plant seeds. In the BWSPB, we collect wild plant seeds from Korea and other collaborative nations to compile large-scale data such as storage behavior, dormancy, and chemical properties to maintain seed viability during storage and to find further useful conservation strategies. The viable seeds collected by the BWSPB are preserved in the BGSV. The BGSV is also working towards creating their own global network for the preservation of wild plant seeds collected worldwide. With these facilities, Baekdudaegan National Arboretum would contribute to the new Post-2020 Global Biodiversity Framework and finally succeed in unifying nations toward the conservation of wild plants for our future generations.

** This study was carried out with the support of ‘R&D Program for Forest Science Technology (Project No. “FTIS 2021399B10-2225-CA02” and “FTIS 2021400B10-2225-CA02”)’ provide by Korea Forest Service (Korea Forestry Promotion Institute).

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S11-2

An external perspective on seed collection strategy of Baekdudaegan National Arboretum

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An external perspective on the seed collection strategy of Baekdudaegan National Arboretum can be divided into two categories: first, region and taxonomic group, and second, conservation and utilization. The primary target of the regional aspect of the collection strategy should be the entire Baekdudaegan region of South Korea and other regions with species diversity hot spots such as Ulleungdo should be included. In the case of overseas, it is recommended to collect seeds from the Amr region, which includes Jilin and Heilongjiang in China, Primorsky Krai and Sakhalin in Russia, and Hokkaido in Japan. Next, it would be good to consider collecting seeds from eastern North America, where distributed disjunct genera of vascular plants in eastern Asia. Finally, countries that are vulnerable to climate crisis should be targeted.

In terms of the taxonomic aspect of the collection strategy, it is necessary to prioritize Korean endemic and rare plants in the domestic case, and it is suggested to proceed overseas focusing on the genus endemic to East Asia. In the conservation aspect, it is necessary to consider the taxa vulnerable to the climate crisis. In addition to the collection strategy, information on the anatomical structure of seeds and information related to seed germination characteristics should be continuously constructed as a part of the seed research of Baekdudaegan National Arboretum. It is necessary to strengthen the network through publicity on the importance of seeds and continuous joint research with related researchers. Lastly, Baekdudaegan National Arboretum is the only institution in the world that has both a seed bank and a seed vault and is expected to become a mecca for worldwide seed research.

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S11-3

Industrial values of wild plant

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Seeds are a repository of genetic information and are the most efficient resource to conduct research on plant conservation and utilization. As conservation and utilization of biodiversity has been gaining increasing attention worldwide, many countries are implementing different strategies to conserve and utilize these biological resources. Approximately 4500 vascular plant species are native to Korea, with more than 600 species having several industrial applications. Although the global market size of the bioindustry is exceeding 300 trillion won and the annual growth rate is more than 7%, the size of the domestic bioindustry is only approximately 1% of the global market. Thus, increasing the utilization of native plants in Korea is necessary because more than 70% of the biological resources used in the bioindustry of Korea depend on imports. Various plant parts, such as seeds, leaves, roots, and berries are used as raw materials in different industries, such as food, cosmetic, and pharmaceutical industries. Among these plant parts, seeds can serve as an effective raw material. As native plant seeds not only have economic value, but also ecological, environmental, and sociocultural values, they can be used to discover new values that can promote the conservation and utilization of native plants. It is said that, "seeds are semiconductors in the agricultural sector." Moreover, seeds are important base raw materials for agriculture and other bio-industrial sectors. The value of the domestic seed market has been steadily increasing since 2015 and it was approximately 650 billion won in 2021, with vegetable and fruit seeds accounting for approximately 75% of the value, and forest seeds accounting for 3.5% (23 billion won). Thus, studying the characteristics of native plant seeds in Korea is important to reduce the import dependence of the domestic bioindustry market and consequently, revitalize the market. Accordingly, the Baekdudaegan National Arboretum has been collecting seed information, including information on the characteristics of the native plant seeds in Korea, through the "Native Plant Seed Information Database Project" since 2021. This initiative can not only assist in establishing sovereign rights on the native biological resources of Korea, but also in discovering their value as a biological resource and supplying this information to the public.

Keywords: Native seed, Biodiversity, Industrialization, Baekdudaegan National Arboretum

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S11-4

A corporate perspective on the conservation of useful wild plants in the cosmetic industry

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Cosmetics are made from a variety of naturally-derived ingredients. In addition to oils, waxes, and pigments for making basic formulations, active extracts that can solve customers' skin concerns are obtained from various plants. Therefore, cosmetic companies have been conducting a lot of research to apply various plants for a long time. In particular, in order to discover new ingredients with skin effects, cosmetic companies are interested in many wild plant materials. Recently, as awareness of biodiversity reduction due to climate change and environmental destruction has been strengthened, as a responsible corporate citizen, cosmetic companies are contemplating the sustainable supply of raw materials used in product production. In addition, it is also necessary to respond to the growing interest-sharing movement for the use of genetic resources in the international community. Therefore, the conservation of domestic native plants is important by providing industrial opportunities to domestic companies in terms of securing original natural resources.

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Oral Presentation

General Oral Presentation

Date & Time : Oct. 20 (Thu) 14:10 - 15:50
Room : Sydney

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

14:10 - 14:25	GS-1	**Understanding stand dynamics of natural and managed temperate forests under climate change in South Korea** Moonil Kim (Pyeongtaek University, Korea)
14:25 - 14:40	GS-2	**Population dynamics of Antarctic scallop *Adamussium colbecki* (Smith, 1902) in Tera Nova Bay, Antarctica** Sun Kyeong Choi (Jeju National University, Korea)
14:40 - 14:55	GS-3	**A new strategy of metal biochar fabrication** Dong-Wan Cho (Korea Institute of Geoscience and Mineral Resources, Korea)
14:55 - 15:10	GS-4	**Notes on small jellyfish in Korean waters; not moon-like or giant, but ecologically important and often problematic** Jinho Chae (Marine Environmental Research & Information Laboratory, Korea)
15:10 - 15:25	GS-5	**Species-specific eDNA analysis of the index species in soil ecosystem, *Allonychiurus kimi* (Collembola: Onychiuridae)** Yun-Sik Lee (Korea University, Korea)
15:25 - 15:40	GS-6	**Adsorption properties of the polyethylenimine-modified industrial biomass waste-based adsorbent for removal of harmful cyanobacterial species and cyanotoxin from aqueous solution** Sok Kim (Korea University, Korea)
15:40 - 15:50	Q&A	

GS-1

Understanding stand dynamics of natural and managed temperate forests under climate change in South Korea

Moonil Kim[pc1,2], Nick Strigul[3], Elena Rovenskaya[2], and Youngjin Ko[4]

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During the past century, several afforestation and reforestation projects were implemented globally. Yet, it remains uncertain if planted forests will be similar to extant natural forests. The primary objective of this study was to improve our understanding of temperate forest dynamics, including diameter and height distribution dynamics, by simulating planted and natural forests in Korea using the Perfect Plasticity Approximation with Simple Biogeochemistry (PPA-SiBGC) model. We used the 5th Korean national forest inventory (NFI) data to estimate the coefficients of functions for simulating forest dynamics. In addition, we developed growth modifiers for the PPA-SiBGC model that reflect climate- and site-specific conditions on an individual tree-level. We selected thirty plots in the NFI data and simulated forest dynamics for the period 1981-2015. Based on validation approaches comparing model predictions to 6th Korean NFI data, we found that the PPA-SiBGC model can effectively explain horizontal and vertical forest dynamics. In our results, forest structural dynamics differed significantly between coniferous and broad-leaved forests and between planted and natural forests. Coniferous forest dynamics were closer to mixed forests than to broad-leaved forests. This property of coniferous forests was more apparent in planted than natural forests, likely attributable to their homogeneous nature. The relative abundance of dominant tree species, or the mean ratio of their basal area to the basal area of all trees for each coniferous plot with the exception of saplings, differed significantly between planted and natural forests. However, this difference was not observed for broad-leaved forests. The results of our study can be used to develop a specialized management strategy for these forest types in East Asia to ensure their resilience.

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GS-2

Population dynamics of Antarctic scallop *Adamussium colbecki* (Smith, 1902) in Tera Nova Bay, Antarctica

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Antarctic scallop *Adamussium colbecki* is one of the main marine invertebrates around Jang Bogo Antarctic Research Station (JBS) in Terra Nova Bay, Antarctica. The main purposes of the present study were to evaluate the population distribution, the morphological characteristics, and the growth of the Antarctic scallop. The density of Antarctic scallops at JBS increased with water depth (6m < 13m <25m). In the morphometric study of 389 Antarctic scallops collected between February and March 2018-2019, the shell height of the Antarctic scallop showed a clear correlation with the various length-weight parameters. A comparison of external vs. X-ray bands in 66 individuals showed a clear linear correlation ($Y = 0.9581X + 0.4074$, $R^2 = 0.9857$). The growth equation for the Antarctic scallop was derived from the von Bertalanffy growth function using height-at-age data estimated by external analysis of 389 individuals: Height = 115.40 mm ($1 - e^{-0.0640t}$). The age of the Antarctic scallops at JBS varied up to 20 years old, and the initial growth of this species was delayed compared to the previous studies. In addition, the gonadal weight and gonadal index of the Antarctic scallop showed distinct differences based on the shell height of 50mm. In this study, the shell height of 9-year-old Antarctic scallops was estimated to be approximately 50 mm, suggesting that the sexual maturation of Antarctic scallops is delayed by 2-3 years compared to the previous study. These results suggest that the change in the mortality rate of young Antarctic scallops may have a significant impact on population growth due to delayed sexual maturation.

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GS-3

A new strategy of metal biochar fabrication

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For past few years, biochar has gained a great deal of interest for its versatile utility in agricultural/ environmental applications. To further increase the functionality of biochar, metallic oxides/metal incorporation on biochar matrix (*i.e.*, metal biochar) with surface precipitation has been recently studied. However, surface precipitation method using commercial chemicals inevitably causes the increase in fabrication cost and secondary environmental pollution. Furthermore, pyrolysis method for fabricating biochar is regarded an energy-intensive process due to energy input to heating at 400 °C or higher, and therefore achieving the value-added resources for during pyrolysis is highly desirable as a feasible compensation way. To address these problems, one-step pyrolytic process (*i.e.*, co-pyrolysis of solid minerals and organics), which could enhance the production of oil compounds or syngas (H_2 and CO) from thermochemical conversion, was newly considered as alternative method for metal biochar fabrication. This work introduced a few case studies for new strategy of metal biochar fabrication.

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GS-4

Notes on small jellyfish in Korean waters; not moon-like or giant, but ecologically important and often problematic

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Moon- and Nomura's jellyfish (*Aurelia coerulea* and *Nemopilema nomurai*, respectively) cause a lot of damage to mankind, and have therefore been highly noted and studied in depth. However, besides these two species, there are many other jellyfish species that need to be studied in Korea. *Carybdea brevipedalia*, a cubozoan medusa, the only species of the box jellyfish distributed in Korean waters, is strongly venomous. Hydromedusae are the most widespread and diverse representatives of gelatinous plankton. Even though the body sizes of cubozoan and hydrozoan medusae are generally much smaller than those of the scyphozoan jellyfish species above mentioned and have only been studied a little comparatively, many species in Korean waters are able to bloom (*Rathkea octopunctata*, *Sarsia tubulosa*, Spirocodon saltatrix, *Aequrea coerulescens*, etc) and are extremely venomous (*Gonionemus vertens*, *Olindias formosus*, *Physalia* physali, *Apolemia* sp., etc.). Several species of the hydromedusae are also known as non-indigenous (*Blackfordia virginica* and *B. polytentaculata*, which also bloom) and/or potentially non-native (*Turritopsis lata*, *Turritopsis* sp. *Nemopsis* sp, etc). We have recently observed their possible expansion of distribution and/or northward shift, and thus I shortly discuss the current state of research on the small species of jellyfish and the future study.

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GS-5

Species-specific eDNA analysis of the index species in soil ecosystem, *Allonychiurus kimi* (Collembola: Onychiuridae)

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Collembola is abundant and has significant roles in the soil ecosystem. Therefore, the phenotypic endpoints of Collembola population or community have been used as an effective bioindicator for assessing soil quality. Since the identification and counting the collembolans in the soil is a laborious and costly procedure, environmental DNA (eDNA)-based biomonitoring was proposed as an analysis tool of collembolan species found in the soil. In this study, standard primer sets for the species-specific eDNA analysis using *Allonychiurus kimi,* a soil bioindicator species was selected. Then, the primers were tested for specificity and sensitivity from the soil samples. Two different eDNA samples were tested: 1) eDNA samples were extracted from the soil with *A. kimi* individuals (intra-organismal eDNA). 2) the samples from the soil without *A. kimi* individuals (extra-organismal eDNA). The two primers were confirmed in their sensitivity and specificity to the two types of eDNA samples selected. C_t-values from both intra- and extra-organismal eDNA showed the significant correlations to the number of inoculated *A. kimi* (adj. $R^2 = 0.7453 - 0.9489$). These results suggest that in excretion, egg, and other exuviae had a significant effect on eDNA analysis from soil samples taken. Furthermore, our results suggest consideration of variables for other inorganic environmental factors that should be considered when analyzing eDNA collected from soil.

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GS-6

Adsorption properties of the polyethylenimine-modified industrial biomass waste-based adsorbent for removal of harmful cyanobacterial species and cyanotoxin from aqueous solution

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Contamination of water resources such as lakes, rivers, and reservoirs by harmful algal blooms (HABs) has been greatly concerned due to its negative impacts on the environments as well as human health. Although various conventional water treatment methods applied to counteract HABs, the development of safe and efficient HABs treatment methods are still demanded since the conventional methods are based on the algicidal mechanism, which can accelerate discharge of cyanotoxins from harmful cyanobacterial species. In the present study, we applied adsorption method for remediation of HABs contaminated aqueous solution. To utilize in an adsorptive HABs treatment, the industrial biomass waste-based adsorbent was fabricated through the biomass immobilization using polysulfone and surface modification using polyethylenimine (PEI). The prepared PEI-modified adsorbent evaluated its adsorption properties on harmful cyanobacterial species (Microcystis aeruginosa) and cyanotoxins (microcystin-LR) from solution. The utilized PEI-modified adsorbent could efficiently remove M. aeruginosa cells from aqueous medium without inducing of cell destruction. In addition, it showed potential as an adsorbent which could remove microcystin-LR efficiently and rapidly from HABs occurred aqueous solution. Consequently, the adsorptive HABs treatment method using PEI-modified adsorbent may be suggested as an efficient and safe solution for remediation of HABs contaminated waterbodies.

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Student Oral Presentation 1

Date & Time : Oct. 20 (Thu) 08:30 - 09:40
Room : Grand Ballroom 1+2+3

Chair: Prof. Ikju Park
Kyungpook National University, Korea

08:30 - 08:40	ST-01	**Differential susceptibility to arsenic in glutathione S-transferase omega 2 (*GST-O2*)-targeted freshwater water flea *Daphnia magna* mutants** Eunjin Byeon (Sungkyunkwan University, Korea)
08:40 - 08:50	ST-02	**Bacterial species diversity of family Burkholderiaceae colonizing midgut of *Riptortus pedestris* (Hemiptera: Alydidae) and symbiotic effects of the bacteria on *R. pedestris*** Do-Hun Gook (Gachon University, Korea)
08:50 - 09:00	ST-03	**Morphology and phylogenetics of *Paraamphidinium jejuensis* gen. nov., a new species of sand-dwelling dinoflagellates from Jeju Island** Su-Min Kang (Jeju National University, Korea)
09:00 - 09:10	ST-04	**Individual-based phenology modeling of *Haemaphysalis longicornis*** Jaejun Song (Korea University, Korea)
09:10 - 09:20	ST-05	**Population genetics and ecological niche modelling of three dung beetles in Mongolia: Predicting future genetic diversity and distribution under climate change** Changseob Lim (Korea University, Korea)
09:20 - 09:30	ST-06	**Metabarcoding analysis of the stomach contents of the introduced voracious predator fish (Cyprinidae: *Erythroculter erythropterus*) in the Nakdong River from Korea** Hee-kyu Choi (Sangji University, Korea)
09:30 - 09:40	ST-07	**Molecular characterization of two dopamine receptor in *Haemaphysalis longicornis*: dopamine receptor (D1) and invertebrate specific D1-like dopamine receptor (InvD1L)** Seoyul Hwang (Kyungpook National University, Korea)

ST-01

Differential susceptibility to arsenic in glutathione *S*-transferase omega 2 (*GST-O2*)-targeted freshwater water flea *Daphnia magna* mutants

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To examine the role of glutathione *S*-transferase omega class (*GST-O2*) genes in the biotransformation and detoxification in *Daphnia magna*, various in vivo endpoints, arsenic speciation, enzymatic activities, and gene expression pathways related to arsenic metabolism were investigated in wild-type (WT) and *GST-O2*–targeted mutant (MT) fleas produced by CRISPR/Cas9. Sensitivity to arsenic in MT fleas was higher than in WT fleas. Also, the reduction rate of arsenate (As^{V}) to arsenite (As^{III}) in the MT group was significantly lower and led to accumulation of higher arsenic concentrations, resulting in decreased protection against arsenic toxicity. Relative mRNA expression of other GST genes in the *GST-O2*–targeted MT group generally increased but the enzymatic activity of GST decreased compared with the WT group. Oxidative stress on arsenic exposure was more strongly induced in the MT group compared with the WT group, resulting in a decrease in the ability to defend against toxicity in *GST-O2*–targeted mutant *D. magna*. Our results suggest that *GST-O2* plays an important role in arsenic biotransformation and detoxification functions in *D. magna*.

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ST-02

Bacterial species diversity of family Burkholderiaceae colonizing midgut of *Riptortus pedestris* (Hemiptera: Alydidae) and symbiotic effects of the bacteria on *R. pedestris*

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and Doo-Hyung Lee[C]
Department of Life Sciences, Gachon University, Gyeonggi-do, South Korea

Riptortus peedestris (Hemiptera: Alydidae) can establish endosymbiosis with free-living bacteria belonging to Burkholderiaceae in soil, where *R. pedestris* would be exposed to extremely diverse microbiota in nature. This environmental acquisition by the insect is predicted to be largely affected by environmental factors over the course of co-evolution, compared to vertical transmission of the symbionts. Under this circumstance, it is important to address bacterial species diversity and further evaluate symbiotic effects of those species on *R. pedestris* in order to better understand evolutionary and ecological associations between the two groups. In laboratory conditions, 2nd instar nymphs were provided with field-collected soil and reared to adult. Then, bacteria colonizing in the midgut of *R. pedestris* were cultured and subject to species identification based on 16S rRNA. From the experiments, 41 out of 51 *R. pedestris* adults were detected to harbor single bacterial species. Among *R. pedestris* detected with single bacterial species, 92.7% were found to harbor bacteria belonging to genus *Caballeronia* in their midguts: the most dominant species was *C. jiangsuensis* (46.3%), followed by *C. megalochromosomata* (22.0%), and *C. insecticola* (7.3%). From the symbiotic effect evaluation with the most dominant species (*C. jiangsuensis*), it was revealed that these bacteria significantly and positively affected development, body length and reproduction of *R. pedestris*, compared to individuals with no symbiosis established. Our study characterized for the first time the bacterial species diversity establishing endosymbiosis with *R. pedestris* from field-collected soil. This information can serve as basis to better understand how the environmental acquisition trait has been shaped during the course of evolution and its ecology.

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ST-03

Morphology and phylogenetics of *Paraamphidinium jejuensis* gen. nov., a new species of sand-dwelling dinoflagellates from Jeju Island

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Genus *Amphidinium* Claperéde & Lachmann (1859) is an unarmored dinoflagellates distributed worldwide in a variety of habitats. It has traditionally been classified into small left-facing epicone and position of cingulum, however, morphology and molecular systematics of this genus have been recently refined. Novel genera such as *Togula*, *Apicoporus*, *Prosoaulax* and *Testudodinium* have been established and modified from *Amphidinium* genus. Sand samples were collected from Pyoseon beach of Jeju Island in April 2020. An isolate of unarmored dinoflagellate was established in clonal culture from the sand samples. Light and electron microscopic examination revealed that the epicone is very small and embedded in the hypocone and a faint apical groove at the point where the base meets the cingulum in sessile form of cells. The hypocone is large and oval. The sulcus is observed in tear drop shape and pyrenoid is absent. The cells are 35.0 – 38.0 μm in length, 27.0 – 30.0 μm in width. The isolate most closely resembles *A. mootonorum*. Maximum-Likelihood and Bayesian phylogenetic analysis based on rRNA sequences revealed that it forms a clade with *A. mootonorum* and is divided into different group from *Amphidinium* sensu stricto. Based on morphological and molecular data, we proposed to established new genus *Paraamphidinium* gen. nov. and described *Paraamphidinium jejuensis* sp. nov. and transferred *A. mootonorum* to *Paraamphidinium mootonorum* com. nov.

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ST-04

Individual-based phenology modeling of *Haemaphysalis longicornis*

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The *Haemaphysalis longicornis* (Asian longhorned tick) is a three-host Ixodid tick species which originated from East Asia. They are a major vector of several tick-borne diseases and considered as invasive in New Zealand and Australia. Recently, they are receiving attention because of their introduction to North America. This species has two reproduction types: bisexual and parthenogenetic races. They have some differences in ecological traits and distribution. Especially, only parthenogenetic races were detected in the invaded ranges, e.g., Australia, and New Zealand. Such distribution pattern is expected to be explained with the phenological differences between the reproduction types. Because blood feeding on a host animal is essential to the development of each stage, questing behavior can affect the seasonal dynamics. Therefore, life cycle process including the host-tick interactions was difficult to be modeled in the collective approach. In this study, an individual-based model to simulate the daily tick development was designed with the NetLogo system. The model was tested and validated with the tick collection data by Korea Disease Control and Prevention Agency. According to the model simulation, the incomplete development until the beginning of winter in some regions can limit the survival of the bisexual race. Our study suggests that the physiological differences between the reproduction types should be considered to predict the outbreak period and the potential invasion range of the *H. longicornis*.

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ST-05

Population genetics and ecological niche modelling of three dung beetles in Mongolia: Predicting future genetic diversity and distribution under climate change

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Climate change is considered as a major threat to biodiversity. Despite the ecological importance of dung beetles, the current status of this group such as genetic diversity, distribution, and the potential impact of climate change have not been fully investigated. Here, we investigate the genetic diversity, population structure, and distribution of three dung beetles *Colobopterus erraticus*, *Cheironitis eumenes*, and *Gymnopleurus mopsus*, and predict future genetic diversity and distribution of these species under future climate change scenarios (SSP245, SSP370, and SSP585) in Mongolia. Ecological niche modelling was performed to estimate current and future distribution of three species. Population genetic analyses using mitochondrial *COI* sequences were conducted to estimate genetic diversity and population structures of three species. *Colobopterus erraticus* and *G. mopsus* exhibit high genetic diversity whereas *C. eumenes* presents moderate genetic diversity. Under future climate change, the distribution of *C. erraticus* and *G. mopsus* will shift their distributional ranges to the west and north, respectively. In contrast, the distribution of *C. eumenes* will expand to north. Although an apparent loss in haplotypes was predicted to *C. erraticus* and *G. mopsus*, genetic diversity of mtDNA will be maintained due to the high frequency of unique haplotypes and low divergence of mtDNA. We also highlight the importance of conservation action on the central region of Mongolia which could be a climate refuge and corridor for dung beetles in the future.

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ST-06

Metabarcoding analysis of the stomach contents of the introduced voracious predator fish (Cyprinidae: *Erythroculter erythropterus*) in the Nakdong River from Korea

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The introduced species often negatively affects native populations, which can lead to cascading changes in ecological communities and whole ecosystems. In particular, the artificial introduction of new predator fishes in freshwater ecosystems might drive unintended competition with native predators, resulting in the decrease in the community-level species diversity as well as within-species genetic diversity. *Erythroculter erythropterus* (Cyprinidae) is a large carnivorous fish, originally distributed in the Geum River and Han River basins in Korea, but was introduced into the Nakdong River during early 2000s. This species is known to be highly migratory and predatory, and is currently disturbing the entire food web dynamics as a top predator by expanding its distribution throughout the whole Nakdong River basins. However, its primary prey species and feeding ecology remain largely unknown. In this study, we investigated the stomach contents of *E. erythropterus* by using NGS (next generation sequencing)-based metabarcoding analysis (stomach samples: N=31) at nine sites in the Nakdong River between June and October 2021. A total of 17 fish species were identified as prey and relative frequencies of DNA reads were 28.31%, 16.06%, 15.36%, 5.76% for *Opsariichthys uncirostris*, *Hemibarbus* spp., *Squalidus* spp., and *Lepomis macrochirus*, respectively. The results of metabarcoding analysis were largely consistent with those of the fish community survey by traditional sampling methods. This study will help to advance our understanding of the feeding ecology of the introduced species of *E. erythropterus* and thus inform on effective management of native fish populations or community in the Nakdong River.

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ST-07

Molecular characterization of two dopamine receptor in *Haemaphysalis longicornis*: dopamine receptor (D1) and invertebrate specific D1-like dopamine receptor (InvD1L)

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Dopamine, as a paracrine and/or autocrine factor, is the most effective biogenic amine that induces tick salivary secretion. The salivary glands of ticks are composed of three types of acini (Type-I/-II/-III), which function in different physiological roles in salivary secretion and production of saliva contents. In particular, type-II and type-III acini play critical roles in salivary secretion. In previous studies, two distinct dopamine receptors, dopamine receptor (D1) and invertebrate specific D1-like dopamine receptor (InvD1L), were highly expressed in type II and III acini and function in collecting saliva via inward fluid transport and expelling collected saliva via pumping/gating, respectively. Putative dopamine receptors of *Haemaphysalis longicornis* were identified by BLAST search against the *H. longicornis* genome. We confirmed the full-length ORF of two distinct dopamine receptors, Haelo-D1 and Haelo-InvD1L, with lengths of 1278 bp (426aa) and 1369 bp (467aa), respectively. Phylogenetic analysis revealed that Haelo-D1 and Haelo-InvD1L were orthologous to D1 and InvD1L of *Ixodes scapularis*. Transcripts of D1 and InvD1L were profiled from different developmental stages, i.e., eggs, larvae, nymph, and adults. The molecular function of two dopamine receptors was analyzed by Ca^{2+} and cAMP mobilization assay using a heterologous expression system in CHO or HEK293 cells. Further studies, such as RNA interference (RNAi), are required to expand our knowledge about the physiological function of *H. longicornis* D1 and InvD1L in tick salivary secretion.

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Student Oral Presentation 2

Date & Time : Oct. 20 (Thu) 08:30 - 09:40
Room : Grand Ballroom 4

Chair: Dr. Yongeun Kim
Korea University, Korea

08:30 - 08:40	ST-08	**The strategies of designating Marine Protected Areas to protect seagrass habitats have a positive effect on the increase in the seagrass meadows area** Tae Hyeon Kim (Jeju National University, Korea)
08:40 - 08:50	ST-09	**Morphology, phylogeny, and fatty acid composition of a new useful euglenoid *Eutreptiella* sp. (KCTC 19016P) from Korean coastal waters** Sungmo Kang (Korea Research Institute of Bioscience and Biotechnology, Korea)
08:50 - 09:00	ST-10	**Species identification of Tilapia (*Oreochromus* spp.) and potential habitat prediction** Ju Hyoun Wang (Sangji University, Korea)
09:00 - 09:10	ST-11	**The effects of nitrogen sources and water temperatures on the growth of *Ulva ohnoi* causing green tides on Jeju Island in Korea** Yejin Heo (Jeju National University, Korea)
09:10 - 09:20	ST-12	**Endocrine disruption by low concentration bisphenols in *Bombina orientalis*** Jenny Lee (Hanyang University, Korea)
09:20 - 09:30	ST-13	**Comparative population genetics using GBS and DNA barcodes revealed the origin of differential grasshopper, *Melanoplus differentialis*, in the Republic of Korea** Jiseok Kim (Kyungpook National University, Korea)
09:30 - 09:40	ST-14	**How a widespread Korean freshwater fish, *Zacco koreanus* has evolved unique genetic lineages: different ecotypes or cryptic species?** Yu Rim Kim (Sangji University, Korea)

ST-08

The strategies of designating Marine Protected Areas to protect seagrass habitats have a positive effect on the increase in the seagrass meadows area

Tae Hyeon Kim[p1], Young Baek Son[2], and Sang Rul Park[c1]

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Seagrasses are specialized marine flowering plants that form meadows in shallow habitats adjacent to the foreshore. Seagrasses play important roles in coastal ecosystems such as carbon sequestration, mitigating climate, supporting biodiversity, and providing coastal protection services. Despite their importance, seagrass meadows worldwide are steadily decreasing mainly due to anthropogenic pressures. A common strategy for protecting and managing ecosystems is to designate them as marine protected areas (MPAs). In order to protect seagrass, it is important to ascertain the effects of MPAs on seagrass habitat. In this study, we assessed the spatial distribution and the biological and ecological characteristics of seagrass *Zostera marina* meadows at Tokkiseom, located on the northeastern coast of Jeju Island, which was designated as an MPA in December 2016. The aim of this study was to examine the direct and indirect effects of MPAs on seagrass meadows by comparing before and after the MPA designation. In April 2015, the area of the *Z. marina* meadows measured using GPS was 4,438 m^2. After being designated as an MPA, the area of the *Z. marina* meadows increased rapidly, and in October 2019, three years after being designated as an MPA, it increased by about three times to 14,026 m^2. In order to see the spatial change of the seagrass habitat over time, the seagrass habitat in this study site was photographed and calculated using a drone every month from May 2021. In addition, this study provides biological parameters and environmental factor data to compare changes in seagrass habitat. Our results demonstrate the possibility that the designation of an MPA affects the increase in the *Z. Marina* meadows area and can be an effective strategy to protect seagrass.

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ST-09

Morphology, phylogeny, and fatty acid composition of a new useful euglenoid *Eutreptiella* sp. (KCTC 19016P) from Korean coastal waters

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Euglenoids are the primary producers of useful fatty acids that can be used in animal feed, functional foods, and biofuels. Euglenoids are mostly found in freshwater habitats. However, few of them are reported in marine ecosystems. Therefore, the isolation and identification of various marine useful euglenoids are necessary. In this study, the morphology, molecular phylogeny, and fatty acid composition were investigated to identify an unspecified euglenoid strain (KCTC 19016P) isolated off the coast of Korea. The vegetative cells were longitudinally spindle-shaped, 23.7 ± 2.9 μm in length and 7.6 ± 0.5 μm in width, and narrowed at the anterior part to a truncated apex, tail-like extension at the posterior end. Cells contained numerous chloroplasts. An eyespot was present in the anterior part of the cell. Two flagella were unequal in length. The pellicular striations of the cells, which cannot be seen with a light microscope, were easily visible in the FE-SEM. The maximum growth rate was 0.5, and the doubling time was 1.37 day^{-1} in the exponential growth phase. The phylogenetic analyses based on the nuclear SSU (nSSU) and chloroplast SSU (cpSSU) rRNA sequences revealed that *Eutreptiella* sp. (KCTC 19016P) was nested within the genus *Eutreptiella* and closely related to *E. pomquetensis* (AJ532398). The omega-3 fatty acid content in total fatty acid was 37.61 ± 1.27%, of which alpha-Linolenic acid (ALA), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) was 4.07 ± 2.01%, 19.29 ± 0.63%, and 11.5 ± 0.12 %, respectively. These findings indicate that this new isolate could be a potential candidate in the field of aquaculture.

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ST-10

Species identification of Tilapia (*Oreochromus* spp.) and potential habitat prediction

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Species of tilapia (*Oreochromis* spp.) are very difficult to distinguish morphologically due to the similarities in phenotypes and the presence of many hybrids. The study investigated the tilapia population living in Dalseo Stream in Korea by morphological identification and molecular genetic identification using haplotypes previously registered in NCBI for clearer species identification. Morphological analysis identified two species, *O. niloticus* and *O. aureus*, and showed a distinct difference between the gill rakers ($p < 0.001$). As a result of genetic species identification, two haplotypes were identified with a genetic distance of 8% between the haplotypes. The Neighbor Joining tree reconstruction showed haplotype 1 formed one clade with *O. niloticus* living in the Philippines, and haplotype 2 formed one clade with *O. aureus*, an African original population. Therefore, we check the distribution of habitats at home and abroad of *O. niloticus* and *O. aureus*, which are invasive species, and to provide data for population management by predicting the potential habitat distribution of tilapia populations in Korea.

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ST-11

The effects of nitrogen sources and water temperatures on the growth of *Ulva ohnoi* causing green tides on Jeju Island in Korea

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Massive blooms of green macroalgae called 'green tides' generally occur except in summer at the temperate regions, due to the high water temperature. However, in Jeju Island, this phenomenon outbreaks throughout the year and induces severe damage to the coastal ecosystems. To determine the main cause of this phenomenon, we sampled some *Ulva* spp. in Jeju Island, and *Ulva ohnoi* was observed as the dominant species. Thus, in this study, the physiological characteristics and growth rates of *U. ohnoi* which is considered the main causative species of green tides on Jeju Island were measured at different nitrogen sources and water temperatures. We incubated for 14 days at water temperatures from winter to summer gradually at 5 points and light conditions were 100 μmol photons m^{-2} s^{-1} (12L:12D). Culture medium was renewed daily and comprised of 4 treatments (1. Control, 2. NH-100 μM NH_4^+, 3. NO-100 μM NO_3^-, 4. NHNO-100 μM NH_4^+ + 100 μM NO_3^-, 10 μM PO_4^{3-} was added except control to prevent inhibition of growth). We measured the nutrient concentrations in the culture medium, growth rates, and the effective quantum yield. As a result, *U. ohnoi* uptakes nutrients in the culture medium over 90%. Daily growth rate based on fresh weight and surface area was the highest at 27.5°C and lowest at 12°C. And in nutrient treatments, the control showed the lowest growth rate and there were no significant differences between the experimental treatments. Effective quantum yield remained respectively constant except for the control. These results show that when high concentrations of nutrients are supplied continuously, *U. ohnoi* can grow in a wide range of water temperatures including 33°C, the highest in summer of temperate zone. This study means that green tides consisting of *U. ohnoi* can occur year-round on Jeju Island.

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ST-12

Endocrine disruption by low concentration bisphenols in *Bombina orientalis*

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Bisphenol A (BPA) is an estrogenic endocrine disruptor used in household goods, water bottles, water pipe and can coatings, and thermal paper manufacture. BPA binds to estrogen receptors and causes growth inhibition, reproductive abnormalities, and changes in nervous system dysfunction. Recently, use of bisphenol F (BPF) and bisphenol S (BPS) as alternatives to BPA has been increasing. Present study aimed to evaluate developmental toxicity and endocrine disruption effects of BPA and its analogues at environmentally relevant concentration (~1000 nM) in *Bombina orientalis* embryos. At ~1000nM, BPA, BPF, and BPS did not affect embryonic survival, malformation, and growth. In the liver of stage 45 tadpoles, vitellogenin (*vtg*) mRNA, a biomarker for estrogenic endocrine disruption, was significantly increased in 100 nM BPA group and 1000 nM BPF group but no significant change in *vtg* mRNA was found in 1000 mM BPS group. In liver, *vtg* transcription is regulated by the estrogen signal, which requires estrogen receptor α (ERα) and/or estrogen receptor β (ERβ). ERα mRNA and protein were abundantly expressed in adult female liver whereas no visible expression of ERα was found in tadpole liver. By contrast, ERβ was highly expressed in stage 45 tadpole liver. These suggest that BPA and BPF may induce *vtg* transcription by binding to ERβ in stage 45 tadpole liver. Though BPA and BPF at low concentrations (~1000 nM) didn't affect the survival, malformation, and growth of *Bombina* embryos, they could induce estrogenic endocrine disruption in tadpoles.

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ST-13

Comparative population genetics using GBS and DNA barcodes revealed the origin of differential grasshopper, *Melanoplus differentialis*, in the Republic of Korea

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Invasive species are unintentionally introduced into new ecosystems and cause various damage to agricultural environments. The differential grasshopper, *Melanoplus differentialis*, was firstly reported from Onsan port, Ulsan, Korea in 2018. To identify the origin of the *M. differentialis* population in Korea, the genetic variations were analyzed using DNA barcodes and GBS (Genotyping-By-Sequencing) analysis. The differential grasshoppers were collected from Ulsan, Korea and North America including eight states in the U.S. and two states in Mexico. The haplotypes and genetic variations among populations in Korea and North America were analyzed by using concatenated mitochondrial genes: NADH dehydrogenase subunit 2 (ND2), mitochondrial cytochrome oxidase subunit I (CO I), mitochondrial cytochrome oxidase subunit II (CO II), and cytochrome B (CytB) as well as SNPs (single nucleotide polymorphism) obtained from GBS analysis. The populations in North America were mainly divided into Southern and Northeastern U.S. *M. differentialis* individuals in Korea were clustered into one clade, of which three were also grouped with Southern U.S. populations. The analysis based on mitochondrial genes revealed that populations in Mississippi and Mexico were genetically close to the Northeastern U.S. in population. Whereas the analysis using SNPs selected by GBS analysis showed that both populations were closely clustered with populations in the Southern U.S. Taken together, we suggest that the Korea population collected from Ulsan, Korea was introduced from the Southern U.S., including Texas.

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ST-14

How a widespread Korean freshwater fish, *Zacco koreanus* has evolved unique genetic lineages: different ecotypes or cryptic species?

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The formation of major river/stream basins on the Korean Peninsula has been greatly influenced by geological processes and glacial activity, and they have become geographically isolated over time. This led to allopatric speciation as a result of limited gene flow and diversifying selection among environmentally different river basins, resulting in the evolution of approximately 67 Korean indigenous freshwater fish species. *Zacco koreanus* is a Korean endemic freshwater fish that is widely distributed in the upper and middle streams of most rivers, and has been suggested to be classified into three ecotypes according to morphological characteristics related to the patterns of their geographical distributions. In this study, using mitochondrial DNA cytochrome oxidase I (COI) and control region (CR), and 9 microsatellite loci we developed, we attempted to determine the phylogenetic relationships and population genetic structure among geographically separated five river basins [Han River (HR; Population (N) = 11), East-flowing river (ER; N = 4), Geum River (GR; N = 2), Nakdong River (NR; N = 8) and Seomjin River (SR; N=1)]. We further assessed quantitatively the morphology of the populations from the five rivers based on previously reported ecotype characteristics to test whether they have ecologically diversified. We found four relatively well-separated clades with clade 1 containing HR and ER, clade 2 with GR, clade 3 with NR, and clade 4 containing NR and SR. Nevertheless, some populations were admixed with non-native individuals of other lineages, which may probably result from artificial translocation by humans. This study identified the genetic population structure of *Z. koreanus*, which is one of the widely distributed freshwater fishes in Korea, and the findings will shed an intriguing insight into understanding how Korean freshwater fishes have evolved in response to geographically isolated major river/stream environments.

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Young Scientist & Student Oral Presentation 3

Date & Time : Oct. 20 (Thu) 16:10 - 17:50
Room : Grand Ballroom 1+2+3

Chair: Dr. In-Hyun Nam
Korea Institute of Geoscience and Mineral Resources, Korea

16:10 - 16:23	YS-01	**Establishment of ultrasonic stimulation method for promoting the growth of *Haematococcus lacustris*** Sang-Il Han (Korea Atomic Energy Research Institute, Korea)
16:23 - 16:36	YS-02	**Epigenetic plasticity enables copepods to cope with ocean acidification** Young Hwan Lee (Sungkyunkwan University, Korea)
16:36 - 16:49	YS-03	**Environmental identification of *Amaranthus* species using Visible-Near-Infrared (Vis-NIR) spectroscopy and machine learning methods** Subramani Pandian (National Institute of Agricultural Sciences, Korea)
16:49 - 17:02	YS-04	**Potential global invasion risk of small hive beetle, *Aethina tumida*, considering host distribution** Jinsol Hong (Korea University, Korea)
17:02 - 17:15	YS-05	**Strategies for natural ecosystem conservation and management in Korea National Parks** Jeong Eun Kim (Korea National Park Research Institute, Korea)
17:15 - 17:25	ST-15	**Recent trends and temporal changes in growth and abundance of temperate seagrass *Zostera marina* in Jeju Island, Korea** Kyeonglim Moon (Jeju National University, Korea)
17:25 - 17:35	ST-16	**Characterization of clade compositions of *Burkholderia* bacteria in soil and *Riptortus pedestris* (Hemiptera: Alydidae) in South Korea** Joo-Young Kim (Gachon University, Korea)
17:35 - 17:45	ST-17	**The development of research on Environmental, Social, and Governance (ESG): A bibliometric analysis** Sachini Supunsala Senadheera (Korea University, Korea)
17:45 - 17:55	ST-18	**Molecular understanding of the common cordgrass *Spartina anglica*: from a global perspective to its invasion of Korean coasts** Buhari Lawan Muhammad (Sangmyung University, Korea)

YS-01

Establishment of ultrasonic stimulation method for promoting the growth of *Haematococcus lacustris*

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In this study, ultrasonication at a frequency of 40 kHz was used to shorten the sonication period and enhance the growth of *Haematococcus lacustris*. The effects of ultrasound output and treatment interval were examined to confirm the optimal conditions. Under optimal conditions (20 W and 15-day cycle), the maximum cell density and chlorophyll content were 66.75×10^4 cells mL^{-1} and 36.54 mg g^{-1}, respectively, which were increased by 50.00% and 39.01%, respectively, compared to the control. Transmission electron microscopy analysis showed that ultrasonication caused tiny cracks in the W4 and W6 strata but did not disrupt the inner W2 layer. Additionally, RT-qPCR analysis showed that ultrasonication upregulated cell division and nitrogen uptake. No differences were detected in the composition or quantity of fatty acids. This study demonstrates a novel ultrasonic approach for enhancing the growth of *H. lacustris*.

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YS-02

Epigenetic plasticity enables copepods to cope with ocean acidification

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Plasticity enhance species fitness and survival under climate change. Ocean acidification poses a potential threat to copepods, a major zooplankton group that serves as a key link between the lower and higher trophic levels in the marine environment, yet the mechanisms underlying different adaptive responses remain poorly understood. Here we show that although elevated CO_2 can exert negative effects on reproduction of *Paracyclopina nana*, multigenerational plasticity can enable recovery after three generations. By integrating the methylome and transcriptome with the draft genome, and undertaking DNA methylation treatments, we demonstrate the vital role of epigenetic modifications in ocean acidification responses and identify regions associated with reproductive resilience. Our results demonstrate that DNA methylation might play an important role in enhancing species fitness of copepods and that failing to consider phenotypic plasticity could lead to overestimation of species' vulnerabilities.

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YS-03

Environmental identification of *Amaranthus* species using Visible-Near-Infrared (Vis-NIR) spectroscopy and machine learning methods

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Visible-near-infrared (Vis-NIR) spectroscopy in combination with chemometric techniques, was used for the feasibility of quick and non-destructive method of identification of plant species. The main goal of this study would be to classify six different *Amaranthus* sp. in different geographical regions of South Korea using a handheld spectrometer in the field. Spectra were obtained from the adaxial side of the leaves at 1.5 nm intervals in the Vis-NIR spectral range between 400 and 1075 nm. The obtained spectra were assessed with four different preprocessing methods in order to detect the optimum preprocessing method with high classification accuracy. Preprocessed spectra of six *Amaranthus* sp. were used as input for the machine learning-based chemometric analysis. All the classification results were validated using cross-validation to produce robust estimates of classification accuracies. The different combinations of preprocessing and modeling were shown to have a classification accuracy of between 71% and 99.7% after the cross-validation. Considering the high number of spectra involved in this study, the growth stage of the plants, varying measurement locations, and the scanning position of leaves on the plant are all important. We conclude that Vis-NIR spectroscopy, in conjunction with proper preprocessing and machine learning approaches, can be utilized in the field to efficiently categorize *Amaranthus* sp. for effective weed management and/or monitoring of their culinary applications.

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YS-04

Potential global invasion risk of small hive beetle, *Aethina tumida*, considering host distribution

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In order to understand the potential invasion risk of a parasitic pest, it is also necessary to understand the availability of the host organisms. In this study, three bee hosts are considered to understand the global invasion risk of the small hive beetle (SHB), *Aethina tumida*. SHB is a beekeeping pest that is native to sub-Saharan Africa, and this species has invaded various countries since the late 90s. SHB feeds on pollen, honey, and even host bee larvae during adult and larval periods, causing devastation to the infested beehive. Honeybee, *Apis mellifera*, is known to be the main host for SHB; however, some other bombus species are also known to be hosts for SHB. In this study, the potential distribution of SHB is modeled using a Species Distribution Model. Also, potential distributions of the three host species (*A. mellifera*, *B. impatiens*, *B. terrestris*) are modeled and considered to assess the potential invasion risk of SHB on a global scale. Compared to the potential distribution of SHB, host species cover wider environmental and geographical spaces. This study shows that the potential SHB invasion will not be limited by its host availability.

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YS-05

Strategies for natural ecosystem conservation and management in Korea National Parks

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National Park Research Survey is an activity to investigate the overall status of National Parks such as natural ecosystems, landscapes, culture, and human social environment. The main purpose is to obtain basic information and data necessary for park management and to provide the information to the public. Species surveys were conducted from 1991 to 2018 (1st to 3rd survey), and habitat surveys are being conducted from 2019 to the present (4th survey) to establish a scientific park management system by evaluating of natural resource distribution and conservation status. As the biodiversity conservation policy and park management paradigm change, the National Park's unique analysis and evaluation system is recently developed and used for park management to protect the natural ecosystem of the National Park. It has been applied since 2020 (4th survey) by improving the survey system that can simultaneously conduct species and habitat surveys and monitoring, after compensating for the shortcomings of the previous point random sampling survey method. In preparation for the 5th National Park Research Survey, we suggest a plan to maximize the utilization of data between professional investigators and park managers to establish a National Park conservation management plan and to contribute to the preservation of national biodiversity.

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ST-15

Recent trends and temporal changes in growth and abundance of temperate seagrass *Zostera marina* in Jeju Island, Korea

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As anthropogenic activities and natural events linked to global climate changes increase in coastal regions, there is concern that crucial seagrass meadows that provide important ecosystem services are significant decline globally. Increasing sea surface temperature (SST) due to global climate change can have lethal impacts on growth and survival of temperate seagrass species. Although Jeju Island is strongly affected by increase of SST driven by climate change, few data on changes in abundance are available for temperate seagrass, *Zostera marina* in Jeju Island. Morphological trait, shoot density, biomass and leaf productivity of *Z. marina* were investigated in Tongbatarl lagoon located on east coast of Jeju Island from February 2013 to September 2022. Additionally, we measured environmental parameters such as water temperature, underwater irradiance and inorganic nutrients in water column and sediment pore water at study sites. The annual mean SST (SST_{mean}) during study period and the mean SST during the summer (SST_{max}) and winter (SST_{min}) season were calculated for each year. Gradual decrease in morphological traits, total biomass, and productivity of *Z. marina* was observed during 2013-2021. The SST_{max} reached 27.7 to 29.8°C during the recent year (2016-2021). These results showed that growth and abundance of *Z. marina* was intimately related with high summer SST can be controlled the growth of *Z. marina*. Our findings suggest vulnerability in *Z. marina* population of the Jeju Island to climate changes and emphasize the necessity of effective management action for preserve of seagrass meadows.

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ST-16

Characterization of clade compositions of *Burkholderia* bacteria in soil and *Riptortus pedestris* (Hemiptera: Alydidae) in South Korea

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and Doo-Hyung Lee[c]

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Symbiosis between *Riptortus pedestris* (Hemiptera: Alydidae) and *Burkholderia* bacteria is a representative example of environmental symbiont acquisition in nature. In every generation, *R. pedestris* is known to acquire its gut symbionts from soil; however, because soil harbors extremely diverse microbes including a variety of *Burkholderia* clades such as SBE, PBE, and BCC, symbiont acquisition of *R. pedestris* is thought to be largely affected by bacterial diversity in soil. Therefore, we investigated *Burkholderia* clade compositions from soil across South Korea and also *R. pedestris* when the insects were provided with the field-collected soil. Also, wild *R. pedestris* adults were surveyed to characterize their *Burkholderia* compositions. From the field survey, 88% of soil samples were detected with the genus *Burkholderia*, and 91% of nymphs successfully acquired *Burkholderia* bacteria from the soil samples. Interestingly, the triple clade consisting of SBE+ PBE+BCC was the most dominant composition in soil, whereas nymphs reared on the soil samples were found most frequently to harbor single clade such as BCC. Similar to the laboratory results, 81% of wild adults harbored the genus *Burkholderia*, and single BCC clade was most frequently detected from those adults. Finally, 29% and 47% of the reared and wild *R. pedestris* were detected with unidentified *Burkholderia* clade, which does not belong to any of SBE, PBE, or BCC clade. This study provides baseline information to better understand ecological associations between *R. pedestris* and *Burkholderia* in different clades.

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ST-17

The development of research on Environmental, Social, and Governance (ESG): A bibliometric analysis

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Investment in environmental, social, and governance (ESG) significantly influences a company's financial aspects that drive sustainability. This study sample covers the data of 981 articles obtained from the Scopus database spanning over 141 journals from 2001 to 2021 and uses quantitative bibliometric analysis to discover present and future research directions of ESG. This analysis evaluates prolific research elements, such as authors, citations, journals, institutions, countries, regions, possible links between ESG and corporate performance and trends while focusing on the environmental pillar. With the emergence of the term ESG in 2006, the number of publications on this topic has almost doubled every year since 2017. With this exponential increase in the number of publications, the world is expected to give greater consideration to the concept of ESG, including green investing, circular economy, and RE100. This study highlights the key findings during the past decade including the importance of and tendency for ESG investing and revealing the less well-specified metrics of the governance pillar compared to those of the environmental and social pillars.

"This abstract is adapted from the author's recently accepted paper, Senadheera, S. S., Gregory, R., Rinklebe, J., Farrukh, M., Rhee, J. H., Ok, Y. S. (2022). The development of research on Environmental, Social, and Governance (ESG): A bibliometric analysis. Sustainable Environment, 7, 2125869. https://doi.org/10.1080/27658511.2022.2125869"

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ST-18

Molecular understanding of the common cordgrass *Spartina anglica*; from a global perspective to its invasion of Korean coasts

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Spartina anglica, C. E. Hubbard (also named *Sporobolus anglicus*), arose in the late nineteenth-century in Southern England following interspecific hybridization between *S. alterniflora* and *S. maritima,* which produced a sterile hybrid, *S.* × *townsendii*. Subsequent whole genome duplication of the hybrid gave rise to a vigorous allopolyploid *S. anglica*. The species is an aggressive, aquatic alien plant that has rapidly spread and colonized a wide range of mudflats worldwide, out-competing native plants and causing detrimental ecological changes. The evolutionary and adaptive success of *S. anglica* is due to the immediate genetic redundancy caused by the duplicated genomes. However, this aspect of *S. anglica* is complicated and poorly understood. Furthermore, *S. anglica* has recently invaded the Korean coasts, but its molecular status and invasion pathway remain elusive. In our study, we used the nuclear ITS and *Waxy* genes in conjunction with multiple chloroplast DNA (*trnK* intron + *matK*, *rps16-trnK*, *rps16* intron, *trnV-ndhC*, *trnT-trnL*, *trnL-trnF*, *ndhF*, *ccsA*, *rbcL,* and *ycf3*), to investigate the hybrid origin, evolutionary changes, and population genetics structure of *S. anglica* invading Korean coasts. Our results revealed for the first time the phylogenetic hybrid origin of *S. anglica* and significant evolutionary changes following its allo-polyploid formation. Moreover, the results highlighted the molecular status and genetic structure of the Korean *S. anglica*. Our study revealed widespread genetic variations within *S. anglica* population, which could have contributed to its success and diversification. This may aid in a better understanding of the molecular status of *S. anglica* globally as well as on the Korean coasts.

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Poster Presentation

■ Poster Presentation

	Schedule	Topics	Poster Presentation
Poster Presentation A	Set-up : Oct. 19, 13:00 Removal: Oct. 20, 13:00	1, 2, 3, 4, 5	Oct. 20, 11:10 ~ 11:30
Poster Presentation B	Set-up : Oct. 20, 14:00 Removal: Oct. 21, 12:00	6, 7, 8, 9	Oct. 20, 17:50 ~ 18:10

■ Poster Topics

1. 유해생물 (Harmful organisms)
2. 바이오에너지 (Bioenergy)
3. 동물생태·분류·유전 (Animal ecology, classification, genetics)
4. 식물생태·분류·유전 (Plant ecology, classification, genetics)
5. 미생물생태·분류·유전 (Microbial ecology, classification, genetics)
6. 생물다양성 및 생물모니터링 (Biodiversity and Biomonitoring)
7. 생태독성 및 환경호르몬 (Ecotoxicity and environmental hormones)
8. 재난분석과학 (Disaster Analysis Science)
9. 기타 (Others in Environmental Biology)

■ Poster Presentation Layout

Poster Presentation A	Poster Presentation B
P1-01 ~ P1-09 P2-01 P3-01 ~ P3-11 P4-01 ~ P4-09 P5-01 ~ P5-14	P6-01 ~ P6-30 P7-01 ~ P7-06 P8-01 P9-01 ~ P9-03

Poster Presentation

1. 유해생물 (Harmful organisms)

P1-01 **Species composition and seasonal population dynamics of ticks (Acari: Ixodidae) as a vector of SFTS virus from 2019 to 2021 in Gyeonggi-do, South Korea**
Young Min Jung, Do-Hun Gook, Minhyung Jung, Jung-Wook Kho, Soowan Kim, Joo-Young Kim, and Doo-Hyung Lee (Gachon University, Korea)

P1-02 **Development of cyanobacteria control and recovery strategy using adsorption and desorption**
Jeong Sik Choi, Yun Hwan Park, Sok Kim, Jino Son, Jaewon Park, and Yoon-E Choi
(Korea University, Korea)

P1-03 **Development of harmful alga control technology using bio-derived materials**
Yun Hwan Park, Jeong Sik Choi, Jooeun Chung, Jaewon Park, Sok Kim, and Yoon-E Choi
(Korea University, Korea)

P1-04 **Thermotaxic diel vertical migration of the harmful dinoflagellate *Cochlodinium* (*Margalefidinium*) *polykrikoides*: response to marine heatwaves**
Young Kyun Lim, Jin Ho Kim, HyeJoo Ro, and Seung Ho Baek
(Korea Institute of Ocean Science and Technology, Korea)

P1-05 **Development of cyanobacteria control strategy based on Chitosan adsorbents for industrial application**
Yun Hwan Park, Kyoung Suk Han, Woo Seok Han, Chung Ju Kim, and Sungho Yun
(Korea University, Korea)

P1-06 **Development of adsorption-based cyanobacteria control strategy using PEI-Cotton with additional modification of bacterial culture medium**
Yun Hwan Park, Kyoung Suk Han, Woo Seok Han, Chung Ju Kim, and Sungho Yun
(Korea University, Korea)

P1-07 **Physiological characteristics and habitat prediction analysis of the golden apple snail *Pomacea canaliculata* wintering individuals**
Jung Soo Han, I Chan Shin, and Hwang Goo Lee (Sangji University, Korea)

P1-08 **Identification and expression of a novel saxitoxin synthesis gene *sxtB* from the harmful marine dinoflagellate *Alexandrium catenella***

Han-Sol Kim, Quynh Thi Nhu Bui, Sofia Abassi, and Jang-Seu Ki (Sangmyung University, Korea)

P1-09 **Removal property of cyanotoxin microcystin-LR in an aqueous phases by isolated bacteria from soli environment**
Joo Eun Chung, Jung Sik Choi, Yun Hwan Park, Sok Kim, and Yoon-E Choi (Korea University, Korea)

2. 바이오에너지 (Bioenergy)

P2-01 **Study of biomass and fucoxanthin productivity from *Nitzschia palea* HY1**
Hyunji Won, Eunmi Ro, Baik ho Kim, Seungbeom Seo, and EonSeon Jin (Hanyang University, Korea)

3. 동물생태·분류·유전 (Animal ecology, classification, genetics)

P3-01 ***Acrotrichis grandicollis* (Mannerheim, 1844) and *Acrotrichis similaris* Sundt, 1969 new to Korea (Coleoptera: Ptiliidae)**
Taeyoung Jang and Jong-Seok Park (Chungbuk National University, Korea)

P3-02 **A new species of the genus *Trissemus* Jeannel (Staphylinidae: Pselaphinae: Goniaceritae) from Korea**
Yeon-Jae Choi, Sun-Jae Park, Seung-Gyu Lee, and Jong-Seok Park (Chungbuk National University, Korea)

P3-03 **Diversity of Chironomidae larvae (Diptera) in drinking water treatment plants (DWTPs)**
Jae-Won Park and Ihn-Sil Kwak (Chonnam National University, Korea)

P3-04 **Possibility of new species known as *Lourinia armata* (Claus, 1866) from Korean waters**
Jinwook Back and Heejin Moon (National Marine Biodiversity Institute of Korea)

P3-05 **New record of *Pleuronema marinum* Dujardin, 1841 (Protozoa, Ciliophora) from South Korea**
Jeong Hyeon Yeo, Ji Hye Choi, Atef Omar, and Jae-Ho Jung (Gangneung-Wonju National University, Korea)

P3-06 **Creating a pond environment to induce behavior enrichment of captive bred storks, *Ciconia boyciana***
Sungchae Moon, Jae Beom Yoo, Na Hee Kwon, Young Sook Nam, and Yun Seob Moon
(Korea National University of Education, Korea)

P3-07 **The first observation of bitterling's spawning events in a small mussel, *Corbicula fluminea* as a novel host in the Nakdong River basin from Korea**
Jin Kyu Seo, Hee-kyu Choi, and Hyuk Je Lee (Sangji University, Korea)

P3-08 **Integrative taxonomy uncovers new *Culicoides* Latreille, 1809 (Diptera: Ceratopogonidae) biting midge species from Dokdo Island South Korea**
Wongyu Lee and Yeon Jae Bae (Korea University, Korea)

P3-09 **Environmental factors affecting calling activities of black-spotted pond frogs (*Pelophylax nigromaculatus*) in South Korea**
Jaeyoung Seo, Sera Kwon, Kyo Soung Koo, and Yikweon Jang (Ewha Womans University, Korea)

P3-10 **A close look for the genetic and morphological differences between Kumkang fat minnow (*Rhynchocypris kumgangensis*) and a new species, Deogyu fat minnow (*Rhynchocypris deogyensis*) from Korea**
Soon Young Hwang, Ji Young Kim, Jae Goo Kim, Soonku So, and Hyuk Je Lee (Sangji University, Korea)

P3-11 **Population genetic structures and demographic expansion of exotic jellyfish *Carybdea brevipedalia* in Korean coasts inferred from mitochondrial *COI* analysis**
Buhari Lawan Muhammad, Yoseph Seo, Jinho Chae, and Jang-Seu Ki (Sangmyung University, Korea)

4. 식물생태·분류·유전 (Plant ecology, classification, genetics)

P4-01 **The complete chloroplast genome sequences of eight *Orostachys* species: comparative analysis and assessment of phylogenetic relationships**
Ha-Rim Lee, Kyung-Ah Kim, Ha-Lam Kang, Yoo-Jung Park, Sung-Mo An, Yoo-Bin Lee, and
Kyeong-Sik Cheon (Sangji University, Korea)

P4-02 **The complete chloroplast genome sequences of *Adenophora lamarckii* (Campanulaceae): comparative analysis with congeneric species**
Yoo-Jung Park, Halam Kang, Sung-Mo An, Ha-Lim Lee, Yoo-Bin Lee, Kyung-Ah Kim,
and Kyeong-Sik Cheon (Sangji University, Korea)

P4-03 **Antioxidant activity of ten lamiaceae plant seed extracts**
JunHyeok Kim, Hee Ho Lee, Chung Youl Park, Hyun Min Kim, Young Ho Jung, Da Hyun Lee, Kyeongmin Kim, Sae Hyun Kim, and Chae Sun Na (Baekdudaegan National Arboretum, Korea)

P4-04 **Plant virus detection using next generation sequencing (NGS) in South Korean wild plants**
Chung Youl Park, Da Hyun Lee, Young Ho Jung, Hyeon Min Kim, Kyeong Min Kim, JunHyeok Kim, and Chae Sun Na (Baekdudaegan National Arboretum, Korea)

P4-05 **Microbial diversity analysis of *Bupleurum latissimum* Nakai from Ulleung-do of South Korea using nxt generation sequencing**
Kyeung Min Han, Mi Na Choi, Jung Hun Pi, Sea Hyun Kim, Yeong Su Kim, and Chae Sun Na (Baekdudaegan National Arboretum, Korea)

P4-06 **Chloroplast genome mapping of crop wild relatives of *Allium* using reference genome of *Allium* genus**
Kyeongmin Kim, Chung Youl Park, Do Hyun Kim, Da Hyun Lee, Hyeon Min Kim, Jun Hyeok Kim, Gyu Young Chung, and Chae Sun Na (Baekdudaegan National Arboretum, Korea)

P4-07 **CRISPR based gene editing system for breeding of pre-harvest sprouting tolerant *Brassica napus* (L.)**
Soo-In Sohn, Subramani Pandian, Young-Ju Oh, and Eun-Kyoung Shin
(National Institute of Agricultural Sciences, Korea)

P4-08 **Identification of transgenic canola (*Brassica napus* L.) and their hybrids with *B. juncea* using visible-near infrared spectroscopy**
Soo-In Sohn, Subramani Pandian, Eun-Kyoung Shin, and Young-Ju Oh
(National Institute of Agricultural Sciences, Korea)

P4-09 **Effect of four different environmental raster resolutions on species distribution modelling of alien plants in South Korea**
Ga Eun Kim, Yong Ho Lee, Ji Yeon Yun, Sue Hyuen Choi, Seung Hwan Kim, and Sun Hee Hong
(Hankyong National University, Korea)

5. 미생물생태·분류·유전 (Microbial ecology, classification, genetics)

P5-01 **Identification of fungal species collected from insects belonging to orders of Coleoptera, Hemiptera, and Dermaptera in Korea**
Soo-Min Hong, Seong-Keun Lim, Seung-Yeol Lee, and Hee-Young Jung
(Kyungpook National University, Korea)

P5-02 **Utilization and applicable technology using biological resources isolated from costal and island area**
Jae-Hyoung Joo, Kira Moon, Jae-Cheol Lee, Byung Hee Chun, Nakyeong Lee, Seunghui Song, Sung Moon Lee, Yun Ji Kim, WonWoo Lee, Aslan Hwanhwi Lee, and Kyung Min Choi
(HONAM National Institute of Biological Resources, Korea)

P5-03 ***Mucilaginibacter straminoryzae* sp. nov., isolated from periphyton**
So-Ra Ko, Ve Van Le, Mingyeong Kang, Hee-Mock Oh, and Chi-Yong Ahn
(Korea Research Institute of Bioscience & Biotechnology, Korea)

P5-04 **The inhibitory effect of biological nitrification inhibitors on the nitrification activity of three different groups of ammonia-oxidizing microorganisms in co-culture**
Seongwook Kim, Yun Ji Choi, Saem Han, Min-Ju Kang, and Man-Young Jung
(Jeju National University, Korea)

P5-05 **Morphology, phylogeny, and fatty acid composition of a new useful euglenoid Eutreptiella sp. (KCTC 19016P) from Korean coastal waters**
Sungmo Kang, Ki-Hyun Kim, Namhyun Chung, and Zhun Li
(Korea Research Institute of Bioscience and Biotechnolog, Korea)

P5-06 **Distribution of sand-dwelling dinoflagellate species in Pyoseon Beach of Jeju Island during spring and summer season 2022**
Su-Min Kang and Jin Ho Kim (Jeju National University, Korea)

P5-07 **Study for lactic acid bacterial diversity of environmental samples in Jeju Island**
Hina Ayub and Man-Young Jung (Jeju National University, Korea)

P5-08 **Study on the physiological characterization of comammox bacterium *Nitrospira inopinata* under acidic conditions**
Yun Ji Choi, Saem Han, and Man-Young Jung (Jeju National University, Korea)

P5-09 **Diversity and adaptation strategies of nitrifying microorganisms in the groundwater sources of Jeju Island**
Saem Han, and Man-Young Jung (Jeju National University, Korea)

P5-10 **Comparative genomics and physiology of novel *Brachybacterium* sp. unveiling its metabolic potential**
Adeel Farooq, Myunglip Lee, Seam Han, and Man-Young Jung (Jeju National University, Korea)

P5-11 **Activity variations of ammonia and methane oxidizers at various copper concentrations**
Min-Ju Kang, Miye Kwon, and Man-Young Jung (Jeju National University, Korea)

P5-12 **Phylogenetic analysis of bacterial diversity in the marine sponge, *Callyspongia confoerderata* and *Spirastrella insignis* collected from Jeju**
So Hyun Park, Ji Young Kim, and Moon Soo Heo (Jeju National University, Korea)

P5-13 **Morphology and molecular phylogenetic position of three new epilithic diatom species of Han River from Korea**
Liyao Jiang, In-Hwan Cho, Chen Yi, Byeong-Hun Han, Young-Hyo Kim, and Baik-Ho Kim
(Hanyang University, Korea)

P5-14 **Characterization of an extracellular protease EcpZ-1 from *Pseudoalteromonas* sp. strain SiA1**
Kyuwon Jeon, Dockyu Kim, and Eungbin Kim (Yonsei University, Korea)

6. 생물다양성 및 생물모니터링 (Biodiversity and Biomonitoring)

P6-01 **Coastal warming heightens direct impacts of seawater temperature on nutrients near aquaculture farms**
Yoonja Kang, Jae Hyung Lee, and Dong-Hun Lee (Chonnam National University, Korea)

P6-02 **Wild hybridization between Native *Mauremys reevesii* and invasive *Mauremys sinensis* in South Korea**
Kyo Soung Koo, Eun Sol Kim, Ji Hee Park, Kayoung Yun, Hae Jun Baek, and Yikweon Jang
(Ewha Womans University, Korea)

P6-03 **Size distribution and their energy flux in belowground food web**
June Wee, Hyun-Gi Min, Yun-Sik Lee, Taewoo Kim, Yongeun Kim, and Kijong Cho
(Korea University, Korea)

P6-04 **Management and role of the Baekdudaegan Global Seed Vault**
Chihyeon Song, Hayan Lee, Jinki Kim, Minsun Kim, Suna Kang, and Kee Hwa Bae
(Baekdudaegan National Arboretum, Korea)

P6-05 **Effect of apple snail (*Pomacea canaliculata*) on aquatic invertebrates in rice fields**
Jinu Eo, Soon-Kun Choi, So-Jin Yeob, and Min-Kyeong Kim
(National Institute of Agricultural Sciences, Korea)

P6-06 **eDNA metabarcoding analysis of compositional variation in the gut content of filter feeder *Polypedilum* (Chironomidae) in the weirs and streams**
Boobal Rangaswamy, Chang-Woo Ji, Won-Seok Kim, Jae-Won Park, Yong-Jun Kim, and Ihn-Sil Kwak (Chonnam National University, Korea)

P6-07 **Discovery of exotic turtle leeches and cases of parasitism on invasive and native species in South Korea**
Eun Sol Kim, Kyo Soung Koo, Ji Hee Park, and Yi kweon Jang (Ewha Womans University, Korea)

P6-08 **Trend analysis of YouTube videos related to exotic amphibians and reptiles in South Korea**
Taeeun Um, Kyosung Koo, Eunsol Kim, Narin Park, Younji Kim, and Yikweon Jang (Ewha Womans University, Korea)

P6-09 **Experiment on the food preference for invasive and native turtles in South Korea**
Jihee Park, Kyo Soung Koo, and Yikweon Jang (Ewha Womans University, Korea)

P6-10 **Distributional shifts of Canopy-forming algae in Korea under climate change**
Sun Kyeong Choi and Sang Rul Park (Jeju National University, Korea)

P6-11 ***Bemicia tabaci* density prediction using machine learning algorithms in tomato greenhouses**
Taechul Park, SoEun Eom, Kimoon Son, Ji-won Jeong, Mincheol Kim, and Jung-Joon Park (Gyeongsang National University, Korea)

P6-12 **Geostatistical analysis for *Frankliniella occidentalis* in commercial hot pepper greenhouse using variogram models**
SoEun Eom, Taechul Park, Kimoon Son, Ji-won Jeoing, Mincheol Kim, and Jung-Joon Park (Gyeongsang National University, Korea)

P6-13 **Monitoring the movement of native *Mauremys reevesii* and invasive *Trachemys scripta elegans* in Geumho Reservoir, South Korea, using GPS-based Telemetry**
Hakyung Kang, Kyo Soung Koo, and Yikweon Jang (Ewha Womans University, Korea)

P6-14 **Characteristic analysis of invasive turtles inhabiting Jinju Geumho reservoir according to period and habitation environment**
Kayoung Yun, Jeongmin Oh, KyoSoung Koo, and Yikweon Jang (Ewha Womans University, Korea)

P6-15 **Population management of American Bullfrog using calling behavior and territoriality during breeding season**
Minkyung Kwak, Kyo Soung Koo, and Yikweon Jang (Ewha Womans University, Korea)

P6-16 **Restored ecological role of Chilbal-do (Island) based on adaptive restoration**
Dae Seung Jeon, Yang Mo Kim, Gwang Gyun Kim, Dong Sun Ahn, Jong Hwan Kim, Jae Kook Jung, and Hang Hwa Hong (Dadohaehaesang National Park Western Office, Korea)

P6-17 **Biomass and species variation of *Ulva* spp. exposed to different nutrient gradients in Jeju Island, Korea**
SeongBin Ham, Kyeonglim Moon, Young Baek Son, and Sang Rul Park (Jeju National University, Korea)

P6-18 **Distribution and historical records of diatom assemblages in surface and sediment cores from the Yellow and Bohai seas**
Hanna Bae, Jinsoon Park, Sung Joon Song, and Jong Seong Khim (GeoSystem Research Corporation, Korea)

P6-19 **First record of the invasive ascidian *Microcosmus squamiger* Michaelsen, 1927 (Ascidiacea: Pyuridae) in Jeju Island, South Korea**
Chang-Ho Yi, Seung-Hyun Lee, Ji Min Kim, and Seongjun Bae (Marine Biodiversity Institute of Korea, Korea)

P6-20 **Analysis of habitat characteristics of odonata climate-sensitive biological indicator species (CBIS) and candidate species**
Chae Hui An, Jung Soo Han, and Hwang Goo Lee (Sangji University, Korea)

P6-21 **A study on habitat characteristics and food sources of brown dipper (*Cinclus pallasii*)**
Chul Woo Park, Jung Soo Han, Hwang Goo Lee, and Jun Kil Choi (Sangji University, Korea)

P6-22 **Spatial variation of the microalgae in the Han River and its tributaries with focusing on the correlation with water quality**
Taehee Kim, Han-Sol Kim, Quynh Thi Nhu Bui, Ha-eun Lee, and Jang-Seu Ki
(Sangmyung University, Korea)

P6-23 **Prediction of habitat distribution changes of endangered conifer *Abies nepholepis* Maxim. on climate change scenarios using MaxEnt model**
Da Hyun Lee, Jun Gi Byeon, Young Ho Lee, and Chae Sun Na (Baekdudaegan National Arboretum, Korea)

P6-24 **Inhabitation status of the dominant Cyprinid fish species (*Zacco platypus* and *Zacco koreanus*) population in the Seom River**
Ji Hye Bae, Ju Hyoun Wang, Jung Soo Han, Chae Hui An, Wan Ok Lee, Jun Kil Choi, and Hwang goo Lee
(Sangji University, Korea)

P6-25 **Phytoplankton community differences between lake and river sections of the Han River (Korea): Paldang Reservoir and Seongsan bridge stations**
Taehee Kim, Yeon-Su Lee, Buhari Lawan Muhammad, Ha-Eun Lee, and Jang-Seu Ki
(Sangmyung University, Korea)

P6-26 **Effect of three different environmental raster scales on species distribution modelling of alien plants in the South Korea**
Ji Yeon Yun, Yong Ho Lee, Ga Eun Kim, Sue Hyuen Choi, Seung Hwan Kim, and Sun Hee Hong
(Hankyung National University, Korea)

P6-27 **Analysis of soil seed bank in four different biotopes**
Sue Hyuen Choi, Yong Ho Lee, Ga Eun Kim, Ji Yeon Yun, Seung Hwan kim, and Sun Hee Hong
(Hankyung National University, Korea)

P6-28 **Correlation between the occurrence of harmful cyanobacteria in the Namhan River basin and environmental factors**
Young Hyo Kim, In Hwan Cho, Byeong Hun Han, Ha Kyung Kim, and Baik Ho Kim (Hanyang University, Korea)

P6-29 **The effect of monsoon rainfall patterns on epilithic diatom communities in the stream and river, Korea**
In Hwan Cho, Young Hyo Kim, Ha Kyung Kim, Eun A Hwang, and Baik Ho Kim (Hanyang University, Korea)

P6-30 **Seasonal features of benthic diatom community of the lower Han River**
Byeong-Hun Han, Chen Yi, In-Hwan Cho, Young-Hyo Kim, Liyao Jiang, and Baik-Ho Kim
(Hanyang University, Korea)

7. 생태독성 및 환경호르몬 (Ecotoxicity and environmental hormones)

P7-01 **Gene responses in *Zacco platypus* fish as a biomarker to applications for lake environmental monitoring**
Won-Seok Kim, Kiyun Park, and Ihn-Sil Kwak (Chonnam National University, Korea)

P7-02 **Functional diversity of the microbial community in an abandoned mine**
Taewoo Kim, June Wee, Yong Ho Lee, Sun-Hee Hong, and Kijong Cho (Korea University, Korea)

P7-03 **Short- and long-term single and combined effects of microplastics and chromium on the freshwater water flea *Daphnia magna***
Haksoo Jeong, Young Hwan Lee, Alaa El-Din H. Sayed, Chang-Bum Jeong, Bingsheng Zhou,
Jae-Seong Lee, and Eunjin Byeon (Sungkyunkwan University, Korea)

P7-04 **Applicability of *Brassica juncea* as bioindicator for As contamination in soil near the abandoned mine area**
Eunji Chae and Jeong-Gyu Kim (Korea University, Korea)

P7-05 **Modification of arsenic contaminated *Phragmites japonica* biochar with silicon and the stabilization of arsenic**
Hyun-Gi Min and Jeong-Gyu Kim (Korea University, Korea)

P7-06 **Qualitative status and quantitative analysis of pesticide residues of wild bird carcasses collected from islands of Marine National Park**
Jae Hoon Kim, Hyun A Jeon, Bo Yeon Hwang, and Woo Hyun Kim (National Park Service, Korea)

8. 재난분석과학 (Disaster Analysis Science)

P8-01 **Novel electrochemical PMI marker biosensor based on quantum dot dissolution using a double-label strategy**
Bongjin Jeong, Rashida Akter, Jeonghyun Oh, Gyu Ri Kim, Chang-Geun Ahn, Jong-Soon Choi, and Md. Aminur Rahman (Korea Basic Science Institute, Korea)

9. 기타 (Others in Environmental Biology)

P9-01 **Evaluation of drought damage by the growth stage of maize in Saemangeum reclaimed land**
Yang Yeol Oh, Hee Kyoung Ock, Su Hwan Lee, Hak Sung Lee, Kwang Seung, Lee, Bo Seong Seo, Kang Ho Jung, Jin Hee Ryu, Sung Yung Yoo, and Tae Wan Kim (National Institute of Crop Science, Korea)

P9-02 **Characterization of three novel *CAs* related to photosynthetic reactions under different pH in the marine dinoflagellates *Prorocentrum minimum***
Jeongmin Shin, Ha-eun Lee, Han-sol Kim, and Jang-Seu Ki (Sangmyung University, Korea)

P9-03 **Implementation of fuzzy logic in a system dynamics model: An application to the Korean rice production systems**
Yongeun Kim, Yun-Sik Lee, June Wee, Jinsol Hong, and Kijong Cho (Korea University, Korea)

P1-01

Species composition and seasonal population dynamics of ticks (Acari: Ixodidae) as a vector of SFTS virus from 2019 to 2021 in Gyeonggi-do, South Korea

Young Min Jung[P], Do-Hun Gook, Minhyung Jung, Jung-Wook Kho, Soowan Kim,
Joo-Young Kim, and Doo-Hyung Lee[c]
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Ticks are one of the medically important vectors which transmit diseases to human including Severe Fever with Thrombocytopenia Syndrome (SFTS). In South Korea, a total of 638 SFTS patients have been recorded from 2019 to 2021 with a mean case-fatality rate of 16.3%. Given that there is no vaccine for SFTS currently available, prevention of SFTS is important and this can be achieved by monitoring and managing the SFTS virus vectors. Therefore, this study reports a recent three-year (2019 – 2021) field survey using CO_2 bait traps to characterize the species composition of the SFTS-vector ticks and their seasonal abundance in diverse landscapes in a Gyeonggi-area, South Korea. In addition, the minimum infection rate of SFTS virus in the ticks was estimated by performing reverse transcription PCR and nested PCR from RNA virus. From the field survey, the Asian longhorned tick (*Haemaphysalis longicornis* Neumann) was the most dominant species accounting for 96% and 99% of adult and nymphal ticks collected, respectively. With regard to seasonal population dynamics, *H. lomgicornis* nymphs peaked in April, June, and May in 2019, 2020, and 2021, respectively; *H. longicornis* adults peaked in July, June, and June in 2019, 2020, and 2021, respectively. Overall, the total number of collected ticks was highest in 2021 followed by 2019 and 2020, whereas the MIR of SFTS virus was highest in 2020 yielding 0.96 and no SFTS virus was detected in 2021. The results of our study can serve as baseline information to improve the management programs against the medically-important ticks and better understand the ecology of *H. longicornis* in newly-invaded countries such as the United States.

** This work was supported by a grant from vector surveillance programs under the climate change, the Korea Disease Control and Prevention Agency (code 4800-4851-304).

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P1-02

Development of cyanobacteria control and recovery strategy using adsorption and desorption

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Harmful algal bloom (HAB) derived by overgrowth of cyanobacterial species in water resources can cause severe problems. Various methods have been applied to suppress HABs, but conventional methods only offer a temporary solution and contribute to accelerate cyanotoxins to be discharged by the cell destruction or lysis. In addition, it is not easy to recover cyanobacterial cells by conventional methods. Therefore, to control *M. aeruginosa* and utilize it as energy resources, suggestion of new approaches that do not cause cell destruction and can easily separate cyanobacteria is demanded. In this study, adsorption strategy using diethylenetriamine-modified cotton fiber (DETA-cotton) was investigated to control the target cells in aqueous phase. Desorption process was performed to analyze total lipid and fatty acid contents for potential use as bio-energy resources. Our adsorption-based approach might provide feasible solution not only to counteract environmental issue HABs but also to recover energy-resources from the harmful cyanobacterial species.

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P1-03

Development of harmful alga control technology using bio-derived materials

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Harmful algal bloom (HAB) can cause severe water pollution since some microalgae secrete toxic compounds, such as microcystin-LR (from the Microcystis species) and anatoxin-a (from the Anabaena species). Thus, it is essential to devise a method urgently to suppress HAB. Different methods have been adopted to suppress HAB, including sedimentation, the use of an oxidizing agent or algicide treatment, and UV sterilization. However, these methods only offer a temporary solution and contribute toward causing additional secondary problems in the aquatic ecosystem. Therefore, this study aims to control cyanobacteria by using an adsorbents that has undergone surface modification using bio-derived materials. Our adsorption technique has unique advantages over traditional adsorption technique. First, we designed a novel 'adsorbents' made from cotton fiber. In addition, further PEI (polyethyleneimine) modifications of functional groups on the surface of sorbent were performed to enhance the capability of 'PEI-Cotton fiber'. After PEI modification, an additional surface modification was performed using materials derived from natural enemies (*Daphnia magna*) of *Microcystis aeruginosa* and bacteria existing in nature. As a result, it was confirmed that the sorbents subjected to additional modification using *D. magna* culture medium, shown 99% removal rate within 24hours. The cyanobacterial control technology using biological materials is a kind of eco-mimicry technology and is expected to minimize the impact on the ecosystem.

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P1-04

Thermotaxic diel vertical migration of the harmful dinoflagellate *Cochlodinium* (*Margalefidinium*) *polykrikoides*: response to marine heatwaves

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The harmful dinoflagellate *Cochlodinium polykrikoides*, a species that causes mass mortality of farmed fish, uses diel vertical migration (DVM) as an ecological strategy. In summer 2018, a bloom of *C. polykrikoides* occurred on the southern coast of Korea when the surface water temperature exceeded 29°C, as a result of a marine heatwave. To understand the effect of high temperature conditions on the DVM of *C. polykrikoides*, vertical profiles of environmental variables and abundance of *C. polykrikoides* were investigated through a 48 h field survey. In addition, a thermally stratified environment (6–12°C difference between the surface and bottom layers) was established in a laboratory study to investigate the effect of temperature difference on the DVM of *C. polykrikoides*. In the field, most of the *C. polykrikoides* population was at a depth of 3–6 m during the day, and only the water temperature at 0 m was not correlated with weighted mean depth of *C. polykrikoides*, suggesting the usage of DVM to avoid high temperature stress. Based on our field and laboratory results, we found that there was a trend of greater DVM velocity by thermotaxis when moving from “unfavorable” water temperature (30°C hot and 12°C cold) to “favorable” water temperature for growth (optimal 24°C) of *C. polykrikoides*. Our findings suggest that thermotaxic DVM is an important ecological strategy used by *C. polykrikoides* to optimize environmental conditions for growth through vertical positioning and changing migration velocity. However, we also propose that the increase in water temperature as a result of global warming may have negative impact on *C. polykrikoides*, such as the decrease of the suitable habitats and of photosynthetic efficiency by the limitation of DVM range.

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P1-05

Development of cyanobacteria control strategy based on Chitosan adsorbents for industrial application

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Microcystis aeruginosa is one of the predominant species responsible for cyanobacterial-harmful algal blooms (Cyano-HABs) in water bodies. Cyano-HABs pose a growing number of serious threats to the environment and public health. Therefore, the demand for developing safe and eco-friendly solutions to control Cyano-HABs is increasing. In the previous study, the adsorptive strategy using chitosan was applied to remove *M. aeruginosa* cells from aqueous phases. Using a simple immobilization process, chitosan could be fabricated as a fiber sorbent (chitosan fiber, CF). By application of CF, almost 89% of cyanobacterial cells were eliminated, as compared to those in the control group. Field emission scanning electron microscopy proved that the *M. aeruginosa* cells were mainly attached to the surface of the sorbent, which was correlated well with the measurement of the surface area of the fiber. We tested the hypothesis that massive applications of the fabricated CF to control Cyano-HABs might cause environmental damage. However, the manufactured CF displayed negligible toxicity. For this adsorption-based removal strategy to be applied to actual environment, a 50-liter reactor was designed by analyzing the fluid behavior. Removal efficiency was evaluated using the chitosan sorbents prepared in this 50-liter reactor, and it was confirmed that *Microcystis aeruginosa* was controllable even at large scale reactors. In the future, we plan to conduct research on various application methods for the expanded application and practical use of the research.

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P1-06

Development of adsorption-based cyanobacteria control strategy using PEI-Cotton with additional modification of bacterial culture medium

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Microcystis aeruginosa is one of the predominant species responsible for cyanobacterial-harmful algal blooms (Cyano-HABs) in water bodies. Cyano-HABs pose a growing number of serious threats to the environment and public health. Therefore, the demand for developing safe and eco-friendly solutions to control Cyano-HABs is increasing. In the previous study, we applied an adsorption-based strategy for the removal of a harmful cyanobacterial species, *Microcystis aeruginosa*, using cotton fiber. Considering the negatively charged surface properties of *M. aeruginosa* cells in aqueous phases, aminated cotton fibers were prepared through polyethyleneimine (PEI) modification on the pristine cotton fibers. Our results indicate that the application of PEI-cotton fibers for the removal of *M. aeruginosa* cells could be suggested as a feasible, effective, and eco-friendly method of harmful algal bloom (HAB) control in water resources. In this study, additional surface modification was performed using a culture medium of bacteria, which has cyanobacteria lysis properties. Cyanobacteria removal efficiency was evaluated on lab scale using Bio-PEI-Cotton with additional surface modification. For industrial application of adsorption-based cyanobacteria removal technology, environmental conditions were arbitrarily simulated in a 50-liter reactor, and removal experiments were conducted each condition. Additionally, a removal experiment was conducted in a 15-ton reactor using Nakdong river water provided by the National Water Industry Cluster, and as a result, it was confirmed that field application was possible.

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P1-07

Physiological characteristics and habitat prediction analysis of the golden apple snail *Pomacea canaliculata* wintering individuals

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Pomacea canaliculata has a high protein content and has been used as a food resource in many countries. This was introduced in Korea as a food in 1983. Since then, it has been distributed on a national scale to be used for eco-friendly farming methods due to its high weeding effect. When *P. canaliculata* was initially distributed, it was expected that there would be no problem with population control *and* spread as it could not adapt to the winter climate of Korea. However, due to the influence of climate change, it was confirmed that it is possible to survive during four seasons in some parts of Korea. It was also expected that the range of wintering areas would be expended. According to a report from the rural development administration in 2021, it was confirmed that *P. canaliculata* wintering in southern regions such as Goheung and Wando in Jeollanam-do province. However, there is insufficient information about wintering because there are no studies so far that were conducted. Therefore, this study was carried out to identify the physiological characteristics of *P. canaliculata* identified in the wintering regions and to identify potential wintering habitats through SDM (species distribution modeling) analysis. For the survey point, the area of the agricultural promotion zone where *P. canaliculata* were found in the literature was selected, and the 1:50,000 neat line was referenced. Wintering of *P. canaliculata* was confirmed in 14 out of 46 map sheet that were field surveyed. During the survey period, the largest wintering individual was identified in Goheung with a shell length of 48.94mm, and the average shell length was analyzed as 32.45 (±9.39) mm. The number of wintering individuals was analyzed to be the highest in Damyang, Jeollanam-do with 219 individuals (87.04%). The ability of the *P. caniculata* to survive in extreme conditions can be due to the effect of warm water flowing in from a *P. canaliculata* farm located nearby.

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P1-08

Identification and expression of a novel saxitoxin synthesis gene *sxtB* from the harmful marine dinoflagellate *Alexandrium catenella*

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Saxitoxin (STX) is natural neurotoxic alkaloid synthesized by several harmful dinoflagellates and cyanobacteria, and cause paralytic shellfish poisoning (PSP). It is produced by eight core enzymes, and sxtB take part in the third stage of STX synthesis. SxtB is known as a cytidine deaminase (CDA)-like enzyme, while its specific role is not well understood in toxic dinoflagellate. In the present study, we identified a novel *sxtB* from *Alexandrium catenella* (Alex03), described structural features and its evolutionary origin, and assessed the transcriptional responses under various temperatures. The gene contains a putative mitochondrial transfer peptide, and no introns was found in the genomic coding region. The gene was phylogenetically close to toxic cyanobacteria and separated from non-toxic dinoflagellates. Transcription fold of *sxtB* were up-regulated when exposed to optimal condition (16°C) and cold stress (2012°C; 1.88-fold, 2016°C; 2.07-fold), and the results showed a positive relation with cellular STX levels. These indicate that the *sxtB* also play an important role in STX synthesis. This is the first report on characterization and transcriptional regulation of *sxtB* with regard to STX production in *A. catenella.*

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P1-09

Removal property of cyanotoxin microcystin-LR in an aqueous phases by isolated bacteria from soli environment

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Harmful Algal Blooms (HABs) led by an overgrowth of harmful cyanobacterial species (*Microcystis* sp. and *Anabaena* sp.) in water resources have become one of crucial environmental events because they can discharge cyanotoxins such as microcystins (MCs) and anatoxin-a into the waterbodies. In addition, these cyanotoxins can be exposed though various routes and can cause damage to organs of humans and animals. Therefore, to protect safety of human health from HABs, the effective strategy for removal and degradation of cyanotoxins is promptly demanded. In the present study, we investigated biodegradation of cyanotoxins by microorganisms isolated from soil environment (R12 bacteria). The cultivation conditions for R12 bacteria such as pH and inoculum ratio were optimized. The microcystin-LR degradation property of the R12 bacteria was evaluated in microcystin-LR containing medium. In addition, to further confirm the cyanotoxin control mechanism of the R12 bacteria, the microcystin-LR degradation property of medium separated after R12 bacteria cultivation was compared with that of the living R12 bacteria.

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P2-01

Study of biomass and fucoxanthin productivity from *Nitzschia palea* HY1

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Microalgae, which have high growth rates and efficient biomass production, are an attractive sustainable resource for a biorefinery. In particular, diatoms are potential candidates for commercial biomass production because they can efficiently produce biomass and high value-added compounds such as fucoxanthin. Many researchers have isolated suitable strains and investigated culture techniques to produce biomass and fucoxanthin from diatoms efficiently. We isolated and identified a new freshwater diatom Nitzschia palea HY1 from the Jungnang stream (Seoul, Republic of Korea). For its seed cultivation, FDMed (Freshwater Diatom Medium) was more appropriate than DM (Diatom Medium). Additionally, we modified the concentration of sodium bicarbonate from 2 mM in FDMed to 10 mM. Using modified FDMed for its cultivation, the biomass productivity on the three days of subculture was 178±45 (mg/L/day), and the fucoxanthin productivity was 1.8±0.3 (mg/L/day), respectively. The productivity is much higher than that of Belgian domestic N. palea cultivated with the FDMed. The results indicate that N. palea HY1 could be the best candidate for commercial fucoxanthin and biomass production, supplying sufficient inorganic carbon for optimal cultivation.

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P3-01

Acrotrichis grandicollis (Mannerheim, 1844) and *Acrotrichis similaris* Sundt, 1969 new to Korea (Coleoptera: Ptiliidae)

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The family Ptiliidae is readily collected from leaf litter, fungi, mammal dung, and deadwood. They are distinguished from other coleopteran families based on feather-like hindwings, flat and minute body (usually smaller than 2 mm), as well as antenna with peculiar setae. Approximately 1,000 valid ptiliid species are distributed globally, but they are one of the unknown families of coleoptera in Korea. The genus *Acrotrichis* is the largest among ptiliid genera, it comprises a quarter of ptiliids. Until now, even though there are approximately 30 *Acrotrichis*-species recorded in nearby countries; Japan and the Russian Far East, only one species *Acrotrichis lewisii* (Matthews, 1884) has been recorded in Korea. In this study, we report two additional species, *Acrotrichis* (*Ctenopteryx*) *grandicollis* (Mannerheim, 1844) and *Acrotrichis* (*Flachiana*) *similaris* Sundt, 1969 from the Korean peninsula. Illustrations of habitus, diagnostic characters, a distribution map and a key to the Korean ptiliids are provided.

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P3-02

A new species of the genus *Trissemus* Jeannel (Staphylinidae: Pselaphinae: Goniaceritae) from Korea

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The genus *Trissemus* Jeannel is a large group in the subfamily Pselaphinae including 175 species of six subgenera (*Trissemus* Jeannel, *Trissemites* Jeannel, *Trissemellus* Jeannel, *Trissemodes* Jeannel, *Trissemosus* Jeannel, and *Trissemidius* Jeannel). Many of the species are distributed in Oriental and Afrotropical regions. Fourty-five species are found in the Palearctic region. In East Asia, *Trissemus* have been recorded in Taiwan (1 sp.), the Russian Far East (2 spp.), Japan (9 spp.), and Korea (3 spp.). This genus was first recorded in Korea in 1973 by Löbl with a report of *T. crassipes*. Among the six subgenera, only *Trissemus* has been recorded in Korea. In this study, we report a new species represented by four specimens from the Chungbuk National University Insect Collection (CBNUIC). Illustrations of the habitus and diagnostic characters, including male genitalia, are also provided. The specimens were collected by sifting clay and reed debris around a swamp.

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P3-03

Diversity of Chironomidae larvae (Diptera) in drinking water treatment plants (DWTPs)

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The Chironomidae midge (Diptera) is a benthic macroinvertebrate commonly found in freshwater ecosystem (river, lake). However, there are limited studies about species identifications of the chironomids larvae found in drinking water treatment plants (DWTPs). In the study, we investigated the distribution of chironomids larvae in five DWTPs (Boseong, Gumi, Jangseong, Jinju, Jeju) and the river near DWTPs of South Korea at April 2022. To do this, we observed the morphological characteristics of midge's mouth parts (mentum, mandible) and antenna. To confirm the molecular species identification, we analyzed cytochrome c oxidase subunit I (COI) sequences of mitochondrial DNA in chironomids larvae found in DWTPs. As a result, we identified a total 4431 individuals belonging to 43 species, 30 genera and 3 subfamilies. Dominant genus for each site were *Conchapelopia* (29.2%) in Boseong, *Stictochironomus* (36.4%) in Jangseong, *Polypedilum* (40.9%) in Gumi, *Cricotopus* (62.9%) in Jinju, *Chironomus* (39.2%) in Jeju. These results will be used as basic information for water quality management in DWTP environments.

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P3-04

Possibility of new species known as *Lourinia armata* (Claus, 1866) from Korean waters

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The genus *Lourinia* has been reported as one species, *L. armata* (Claus, 1866) before Karaytuğ et al. (2021) reported several new species. Currently, genus *Lourinia* consists of six species, *L. aculeata* (Thompson I.C. & Scott A., 1903), *L. aldabraensis* Karaytuğ, Sak, Alper & Sönmez, 2021, *L. armata* (Claus, 1866), *L. gocmeni* Karaytuğ, Sak, Alper & Sönmez, 2021, *L. nicobarica* (Sewell, 1940), and *L. wellsi* Karaytuğ, Sak, Alper & Sönmez, 2021. In addition, there are three subspecies, *L. armata major* (Sewell, 1940), *Lourinia armata minor* (Sewell, 1940), and *L. armata sulamericana* Jakobi, 1954 in the genus. Karaytuğ et al. (2021) mentioned that *L. armata* reported by Yoo & Lee (1993) has the potential of a new species. To confirm this, the *L. armata* specimens stored in the National Marine Biodiversity Institute of Korea were checked and re-described. As a result, some of specimens were almost similar to *L. wellsi* according to the following characteristics; 1) shape of sexual dimorphism in endopod of male P3; 2) endopod of female P3 has six setae/spines. In addition, considering that the leaf-shaped seta III of caudal rami in female, which is hard to find in other species, there is a possibility that these specimens are new species.

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P3-05

New record of *Pleuronema marinum* Dujardin, 1841 (Protozoa, Ciliophora) from South Korea

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During a field survey of marine Korean ciliates, we collected *Pleuronema marinum* from brackish water sample. It is characterized by the presence of a contractile vacuole in mid-body, rather than the subterminal/terminal contractile vacuole as usual in other congeners. The cells were examined in vivo and based on protargol and 'wet' silver nitrate impregnation. In addition, the nuclear 18S rRNA gene was sequenced using a single cell. The Korean population morphologically and molecularly resembles a Chinese population of *P. marinum*. Historical review of the species concludes that 1) two or more species have been assigned into *P. marinum*, 2) the position of contractile vacuole (e.g., in mid-body) is a valid character state, and 3) *P. marinum* is probably a rare species. Here we provide a monographic treatment of *P. marinum* to clarify the issue and for further studies of relevant species. Considering there are about 40 nominal species and complex nomenclatural acts in the genus *Pleuronema*, further studies should provide descriptions based on protargol and 'wet' silver impregnation with marker gene(s).

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P3-06

Creating a pond environment to induce behavior enrichment of captive bred storks, *Ciconia boyciana*

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Wild storks spend a lot of time searching for and catching prey, but captive bred storks have very little time to search for food because they are fed. To provide animal welfare to captive bred storks, a pond environment in a cage was created to induce behavior enrichment, and feeding behaviors of storks were compared. From May to September 2021, a pond environment was created with sand and/or stone, which are a hiding place for prey, loach (*Misgurnus mizolepis*). Foraging behavior of storks in a pond was compared the control and experimental group. The foraging behaviors of four storks in a separated cage were recorded for one hour a day during five days. The foraging behavior frequency of the control group was compared with that of the experimental groups. The foraging behavior of storks was divided into sweeping, visual pecking, tactile pecking, foraging success and failure. The research results are as follows. First, in the control pond environment, the foraging behavior of storks mainly depended on the visual pecking, and the foraging success time was 10-20 minutes. Second, as a result of comparing the success of foraging behavior, the foraging success by visual pecking was the control pond, the pond with sand, and the pond with sand/stone in order. However, the foraging success by tactile pecking and sweeping was found in the following order, the pond with sand, the pond with sand and stone, and the control pond environment. Third, sand and/or stone in the pond interfered with visual information and provided a hiding place for prey, so it allowed for storks to spend more time searching for prey compared to the control. In this study, it was confirmed that the more structures in the pond providing hiding places for prey, the more foraging behavior of storks such as sweeping, tactile pecking in addition to visual pecking. Therefore, creating a pond environment providing shelter for prey can induce behavioral enrichment of captive bred storks, which is positive impact in terms of animal welfare.

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P3-07

The first observation of bitterling's spawning events in a small mussel, *Corbicula fluminea* as a novel host in the Nakdong River basin from Korea

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The bitterling (Cyprinidae, Acheilongnathinae) is a temperate freshwater fish with a unique spawning symbiosis with host mussels. In Korea, there are three genera and 15 species reported so far. During a breeding season, female bitterlings use their extended ovipositors to lay the eggs onto the gills of mussels through the mussel's exhalant siphon. In recent years, freshwater mussel populations have been declining sharply, due to accelerating anthropogenic pressure, which can be large threats to the risk of bitterling extinction cascades. In the present study, we investigated spawning frequencies and patterns of four bitterling fish species with respect to host mussel species in the Nakdong River basin (Hoecheon) in April of 2020. In field surveys, a total of four bitterling species (*Acheilognathus macropterus*, *Acheilognathus yamatsute*, *Rhodeus uyekii* and *Tanakia latimarginata*) and three mussel species (*Anodonta arcaeformis*, *Corbicula fluminea* and *Nodularia douglasiae*) were identified. We observed bitterling's spawned eggs/larvae in every mussel species: *A. arcaeformis* [proportion of spawned: 45.5% (N=11)], *N. douglasiae* [45.2% (N=73)], and *C. fluminea* [12.1% (N=116)]. The number of bitterling's eggs/larvae per mussel ranged from one to 58. By using our developed restriction fragment length polymorphism (RFLP) technique, we were able to identify the number of eggs/larvae for each bitterling fish in each mussel species: *A. arcaeformis* (*A. yamatsutae*: N=19), *N. douglasiae* (*A. yamatsutae*: N=111, *R. uyekii*: N=69, *T. latimarginata*: N=423), and *C. fluminea* (*A. yamatsutae*: N=26, *T. latimarginata*: N=62). The observed bitterling's spawning events in *C. fluminea* from Korea are the first report here and its conservation importance as a new host mussel species for bitterling fishes further needs to be studied.

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P3-08

Integrative taxonomy uncovers new *Culicoides* Latreille, 1809 (Diptera: Ceratopogonidae) biting midge species from Dokdo Island South Korea

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Identification of small insects often requires integrative approach because morphological diagnostic characters are limited. In this study, both morphological characters and DNA barcoding are used to identify genetic divergence detected in biting midge *Culicoides cricumscriptus* Kieffer 1918 from Korea. Specimens were collected by sweeping, emergence trap and white light trap at Dokdo island. Collected biting midges have shown slight morphological difference from *C. circumscriptus* in shape of the paramere in males, and wing spot pattern and ratio of sensory pit width and depth of both sexes. Therefore, a formal description for this new species, *Culicoides dokdoensis* sp. nov., is provided. Mitochondrial cytochrome *c* oxidase I sequence analysis indicated this new species is different from known sequences of *C. circumscriptus* with minimum interspecific genetic divergence of 14.21%. Phylogenetic analyses revealed the new species is related to *C. circumscriptus*, as much as morphological similarity between two species does. Discovery of this cryptic species highlights the necessity of using integrated taxonomic approach for *Culicoides* Latreille 1809 taxonomy.

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P3-09

Environmental factors affecting calling activities of black-spotted pond frogs (*Pelophylax nigromaculatus*) in South Korea

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The interaction of reproductive behavior and environmental factors is very important for understanding the ecology of a species. In amphibians with reproducing in groups, the advertisement call is critical for successful breeding. This study was conducted to understand how environmental factors influence the calling activity of *Pelophylax nigromaculatus* between 2016 and 2021 in South Korea. We collected the presence or absence of the frog's calling, survey time, and environmental factors at the time of the survey (air temperature, air humidity, air pressure, water temperature, water pH, moon phase, sunset time, and cloudiness). A total of 871 cases were used to analyze the environmental factors affecting the calling activities of *P. nigromaculatus* through Binary Logistic Regression, and a regression equation was derived to estimate the likelihood of the advertisement call. The calling activity of *P. nigromaculatus* showed a positive correlation with sunset time and survey time, cloudiness, and a negative correlation with water pH and air humidity. There was no significant in air temperature, air pressure, water temperature, and moon phase. The Logistic Regression computed to explain the impact of each environmental factor on the calling activity was a good fit for the model ($P < 0.005$), explaining 72.0% of the variation (Nagelkerke test; pseudo $R^2 = 0.29$). In general, the breeding activity of summer caller amphibians among prolonged breeders is highly correlated with rain-event. As in our results, rain tends to increase cloudiness, and decrease pH. Therefore, it is thought that the breeding activity of *P. nigromaculatus* is also related to rain. To improve classification accuracy, it is necessary to study the correlation between the calling activity of *P. nigromaculatus* and rain-event.

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P3-10

A close look for the genetic and morphological differences between Kumkang fat minnow (*Rhynchocypris kumgangensis*) and a new species, Deogyu fat minnow (*Rhynchocypris deogyensis*) from Korea

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Kumkang fat minnow, *Rhynchocypris kumgangensis* (Cyprinidae, Leucisscinae) is a cold freshwater fish endemic to Korea, which only occurs in the uppermost parts of upstream rivers. This species is known to be extraordinarily sensitive to climate change and has thus been designated as a Climate-sensitive Biological Indicator Species (CBIS) since 2010. Based on genetic and morphological differences, *R. kumgangensis* inhabiting the Gucheondong Valley in the Deogyusan National Park was classified in 2017 as a new species of *Rhynchocypris deogyensis*. In this study, the genetic diversity and population structure of *R. kumgangensis* and *R. deogyensis* were investigated and the level of genetic divergence between the two species was quantitatively assessed at the whole mitochondrial genomes. A total of 275 samples [North Han River (NHR; N=2), South Han River (SHR; N=6), East-flowing river (ER; N=3), Geum River (GR; N=1)] were analyzed using our newly developed eight microsatellites as well as mtDNA markers. We found that the Pyeongchang population (SHR) had the highest microsatellite diversity (AR=3.13), while *R. deogyensis* (GR) population showed the lowest diversity (AR=1.27) with an extremely high level of inbreeding. The comparative analysis of the mitogenomes showed approximately 2.9% difference (pairwise identity = 97.1%) between *R. kumgangensis* and *R. deogyensis*, suggesting the borderline level of species boundaries in most animals (2–3%). We are now conducting detailed morphological analysis on both species to test whether they show the species-level ecological divergence.

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P3-11

Population genetic structures and demographic expansion of exotic jellyfish *Carybdea brevipedalia* in Korean coasts inferred from mitochondrial *COI* analysis

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Carybdea brevipedalia Kishinouye, 1891 is a poisonous jellyfish found only in Japanese coastal areas. However, it was recently discovered on the Korean coast, expanding its known geographic range. In this study, we analyzed the population genetics and demographic histories of 113 *C. brevipedalia* specimens from the southern and eastern coastal regions of Korea by sequencing mitochondrial DNA cytochrome c oxidase subunit I (*COI*). We identified 42 *C. brevipedalia COI* haplotypes with high genetic diversity and a significant genetic structure. Populations were highly differentiated based on geographic location and distinctly divided into A and B clades. The results of Mantel tests indicated that geographic distance influenced the genetic distance between the two clades. Moreover, demographic analyses (neutrality tests) and the star-like profile of the TCS haplotype network indicated that *C. brevipedalia* had recently expanded to the southern and eastern coastal regions of Korea. These findings suggested that *C. brevipedalia* populations along the Korean coast had significant genetic differentiation that could be influenced by geographic isolation and subsequent adaptation to regional ecological conditions.

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P4-01

The complete chloroplast genome sequences of eight *Orostachys* species: comparative analysis and assessment of phylogenetic relationships

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We analyzed the complete chloroplast genomes of eight *Orostachys* species and compared the sequences to those of published chloroplast genomes of the congeneric and closely related genera, *Meterostachys* and *Hylotelephium*. The total chloroplast genome length of thirteen species, including the eight species analyzed in this study and the five species analyzed in previous studies, ranged from 149,860 (*M. sikokianus*) to 151,707 bp (*H. verticillatum*). The overall GC contents of the genomes were almost identical (37.7 to 37.8%). The thirteen chloroplast genomes each contained 113 unique genes comprising 79 protein-coding genes, 30 tRNA genes, and four rRNA genes. Although the genome structures of all *Orostachys* and *Hylotelephium* species were identical, *Meterostachys* differed in structure due to a relatively large gene block (*trnS-GCU-trnS-GGA*) inversion. The nucleotide diversity among the subsect. *Orostachys* chloroplast genomes was extremely low in all regions, and among the subsect. *Appendiculatae*, genus *Orostachys*, and all thirteen chloroplast genomes showed high values of Pi (>0.03) in one, five, or three regions. The phylogenetic analysis showed that *Orostachys* formed polyphyly, and subsect. *Orostachys* and *Appendiculatae* were clustered with *Hylotelephium* and *Meterostachys*, respectively, supporting the conclusion that each subsection should be considered as an independent genus.

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P4-02

The complete chloroplast genome sequences of *Adenophora lamarckii* (Campanulaceae): comparative analysis with congeneric species

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The genus *Adenophora*, commonly called 'Adenophora Radix', is an important plant resource as a source of herbal medicines. The goal of this study was to assemble and annotation the chloroplast genome of *A. lamarckii* and compare it with published chloroplast genomes of six congeneric species. The total length of chloroplast genome of seven *Adenophora* species ranged from 159,759 bp (*A. stricta*) to 176,331 bp (*A. divaricate*), and each genome contains 110 unique genes (76 protein-coding genes, 30 tRNAs, and 4 rRNAs). The maximum likelihood (ML) tree showed that sect. *Remotiflorae* formed a monophyly and was the earliest diverging lineage. Additionally, two sections (*Microdiscus* and *Platyphyllae*) formed a clade, but each section did not form a clade as a monophyly. Meanwhile, *A. lamarckii* showed the closest relationship to *A. kayasanensis*. It was confirmed that many rearrangements, such as inversion, deletion and IR contraction, occurred among the chloroplast genomes of *Adenophora* species, and it is judged that these characteristics can be used as important characteristics for the classification of this genus, which is very difficult to distinguish morphologically.

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P4-03

Antioxidant activity of ten lamiaceae plant seed extracts

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In this study, the antioxidant activity of Lamiaceae plant seed extracts was evaluated for 10 species. From the seed bank of the Baekdudaegan Arboretum, the seeds of *Clinopodium micranthum* (Regel) H.Hara, *Clinopodium micranthum* (Regel) H.Hara, *Isodon excisus* (Maxim.) Kudô, *Isodon inflexus* (Thunb.) Kudô, *Isodon japonicus* (Burm.f.) H.Hara, *Isodon serra* (Maxim.) Kudô, *Leonurus japonicus* Houtt., *Mosla dianthera* (Buch.-Ham. ex Roxb.) Maxim., *Phlomis umbrosa* Turcz., and *Prunella vulgaris* L. subsp. *asiatica* (Nakai) H.Hara were received. To evaluate the quality of seeds, the percentage of filled seeds and germination percentage were investigated. Seeds with percentage of filled seeds at above 90% and germination percentage at above 50% were targeted. To evaluate the antioxidant capacity, extraction yield, total phenolic content, total flavonoid content, DPPH·ABTS radical scavenging activity, and ferric reducing antioxidant power assay were analyzed. Based on the analyzed antioxidant activity, a cluster analysis was performed and classified into three groups, from group 1 having the lowest antioxidant activity to group 3 having the highest activity. As a result, it was found that the extracts of *C. micranthum*, *M. dianthera*, and *P. vulgaris* subsp. *asiatica* had the highest antioxidant activity among the 10 analyzed species.

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P4-04

Plant virus detection using next generation sequencing (NGS) in South Korean wild plants

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Wild plants play an important role in the survival of viruses, and are potential sources of viral diseases in crop plants. In addition, wild plant hosts influence the spread of the virus because they have an extensive and intimate relationship with the life cycle of insect vectors. Nevertheless, studies on viral diseases in wild plant hosts in South Korea are very limited. In this study, the presence of plant viruses was investigated in six wild plant species (three herbaceous plants and three woody plants) showing severe mosaic, chlorosis, necrosis, and vein yellowing symptoms. To identify the causal agent(s), total RNA was extracted from collected leaf samples and subjected to next-generation sequencing (NGS). Viral contigs were detected based on NGS analysis results, and the infection of each sample was confirmed using reverse transcription polymerase chain reaction with specific primers. Among the detected plant virus contigs, two Lettuce big-vein associated virus (LBVaV) contigs were confirmed. LBVaV has been designated as a quarantine management pathogen by the Korea Animal and Plant Quarantine Agency. A virus presumed to be novel, few that have not been reported in Korea, as well as two that occurred in major crops were identified. Further studies are needed to analyze the host range, pathogenicity, and phylogeny of the virus. This study is expected to contribute to the investigation of the correlation between viruses in major crops.

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P4-05

Microbial diversity analysis of *Bupleurum latissimum* Nakai from Ulleung-do of South Korea using next generation sequencing

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Bupleurum latissimum Nakai is a rare endemic species native to Ulleung-do. This study aimed to report on the rhizosphere soil microbial diversity of *B. latissimum.* Soil samples were collected the upper part of the soil in which the plants were planted was removed by about 3-5cm, and the soil was collected up to 20cm. DNA isolation used DNeasyPowerSoil Kit (Qiagen, Hilden, Germany). Next, 16S sequencing libraries were prepared using Herculase II Fusion DNA Polymerase and Nextera XT Index Kit V2, according to Illumina's instructions, with the target region (primer set) as V3V4 (Bakt_341F-805R). The prepared library was sequenced using the Illumina MiSeq platform of Macrogen, Inc. (Korea). Results revealed 280 prokaryotic families, 815 genera, and 1845 species in approximately 22 phyla. Proteobacteria (relative abundance, 27.78%) were the most prevalent, followed by Actinobacteria (21.72%), Verrucomicrobia (15.24%), and Acidobacteria (10.12%), accounting for approximately 75% of the total population; the remaining phyla, including Bacteroidetes, accounted for 25%.

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P4-06

Chloroplast genome mapping of crop wild relatives of *Allium* using reference genome of *Allium* genus

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In order to respond to future changes in food sovereignty such as climate change, disease and insect pest, it is necessary to secure and preserve crop wild relatives (CWRs) of native plants in Korea. *Allium* is a large genus of monocotyledonous plants, including about 850 species. This genus is one of the most eaten or used genus worldwide. In this study, chloroplast genome mapping was performed on wild relatives of the *Allium* to conduct a phylogenetic study between crops and wild relatives. The low frequency of structural changes in chloroplast DNA molecules (cpDNA) and the conservative rate of sequence evolution make them ideal targets for plant phylogenetic studies. 11 species of *Allium* seeds were received from the seed bank of Baekdudaegan National Arboretum. After germination of the seeds, DNA was extracted from fresh leaves. We performed sequencing using the Illumina platform and the reads were filtered and trimmed. The trimmed reads were then used to assemble the cp genome. The cp genomes of 11 species were found to be circular molecules ranging in length from 152,443 to 154,056 bp. Annotation results indicated the presence of a minimum of 133 genes and a maximum of 139 genes, and the total GC content was in the range of 36%. This study is significant as wild relatives of *Allium* can be used as materials for future crop breeding. Also, it is a very important method to investigate the degree of variation relationship between or within species.

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P4-07

CRISPR based gene editing system for breeding of pre-harvest sprouting tolerant *Brassica napus* (L.)

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The most crucial stages in the entire life cycle of seed plants are seed germination and vegetative growth. The germination of seeds is influenced by a number of endogenous and exogenous variables, including disease, damage, water, seed vigor, temperature, oxygen, and phytohormones. Successful propagation and survival in most of the plants is determined by their seed germination and seedling establishments. Pre-harvest sprouting (PHS) is defined as the embryonic growth inside maternal tissue that nourishes and protects the embryo. In plants, PHS is the phenomenon which causes the germination of seeds while still on the parent plants due to the lack of dormancy. PHS is the result of complex genetic and environmental factors and the influence of multiple genes and the coordinated phytohormone signaling. In this study, we use RNA-Seq technology to identify and characterize the differentially expressed genes during the PHS. Further, we have attempted to found the relationship between seed fatty acid content and PHS in *Brassica napus*, *B. rapa*, and interspecific hybrid of *B. rapa* and transgenic *B. napus*. The sgRNAs were designed using online tool CRISR_P from three PHS-related genes. Three constructs for each gene were used to transform canola hypocotyl following standard procedures. Our study concluded that, the gene editing technology will help us to develop PHS tolerant canola.

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P4-08

Identification of transgenic canola (*Brassica napus* L.) and their hybrids with *B. juncea* using visible-near infrared spectroscopy

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Concerns about the safety of genetically modified (GM) crops and commodities for human health and the environment have developed as a result of GM technology's fast advancement over the years. GM agricultural gene flow could threaten the environment. As a result, it is critical to develop reliable, rapid, and low-cost technologies for detecting and monitoring the presence of GM crops and crop products. We employed visible near-infrared (Vis-NIR) spectroscopy to differentiate between GM and non-GM *Brassica napus*, *B. juncea*, and F1 hybrids (*B. juncea* X GM *B. napus*). The Vis-NIR spectra were preprocessed using various approaches, including normalization, standard normal variate, and Savitzky-Golay. For effective discrimination of GM and non-GM plants, raw and preprocessed spectra were employed in conjunction with eight different chemometric approaches. Among the several combinations, the conventional normal variate and support vector machine combination was shown to be the best accurate model in the discriminating of GM, non-GM, and hybrid plants (99.4%). Deep learning combined with Savitzky-Golay produced 99.1% classification accuracy. According to the findings, handheld Vis-NIR spectroscopy in conjunction with chemometric tests might be utilized to differentiate between GM and non-GM *B. napus*, *B. juncea*, and F1 hybrids.

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P4-09

Effect of four different environmental raster resolutions on species distribution modelling of alien plants in South Korea

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Worldclim database has been used in various studies for species distribution modeling. Worldclim database provides environmental rasters with four different resolutions, 2.5m, 5m, 10m and 30s. This study was conducted to evaluate effect of different environmental raster resolutions on Maxent modelling of five alien plants in South Korea. After removing multicollinearity, seven environmental variables from 5m and eight from 10m, 2.5m, 30s were selected. As a result, zonal averages of potential distribution from four different resolutions in *Ageratina altissima*, *Amaranthus viridis*, *Geranium carolinianum* and *Solanum carolinense* were 0.53, 0.55, 0.62, and 0.58 with 0.02 standard deviation. In *Hypochaeris radicata,* there were differences on spatial distributions and zonal averages among different raster resolutions. The zonal averages of potential distribution from *Hypochaeris radicata* were 0.40 in 10m, 0.50 in 5m, 0.40 in 2.5m, and 0.40 in 30s. This study explains selection of raster resolution is important in species distribution modelling.

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P5-01

Identification of fungal species collected from insects belonging to orders of Coleoptera, Hemiptera, and Dermaptera in Korea

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In 2022, insects belonging to orders Coleoptera, Hemiptera, and Dermaptera were collected from Gangwon-do, Chungcheongnam-do, and Gyeongsangbuk-do Provinces in Korea. A number of fungal strains were isolated from various 64 insects and 20 fungal isolates were found to belong to 11 genera based on the morphological characteristics and molecular analysis using internal transcribed spacer (ITS) regions. Among the collected fungal isolates, the most numerous were members of the genera *Cladosporium* (20%) and *Penicillium* (15%), while the identified representatives of *Alternaria*, *Ophiostoma*, *Pyrenochaeta*, *Paecilomyces*, *Mucor*, *Botryotrichum*, *Monochaetia*, and *Peroneutypa* accounted for less than 10% for each genus. Moreover, one of the strains, namely *Neocucurbitaria* sp., was identified as a novel species based on its morphological characteristics and multi-locus sequence analysis using ITS regions and large subunit of the nuclear ribosomal RNA (LSU), β-tubulin (TUB2), and RNA polymerase II genes (RPB2). The obtained results are encouraging and demonstrate the effectiveness of this approach for the evaluation of fungal diversity and identification of novel fungal species as well as to explore new opportunities for further research of insect ecology.

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P5-02

Utilization and applicable technology using biological resources isolated from costal and island area

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Sustainable use of biological resources has received attention for the Nagoya Protocol was adopted in 2010 and entered into force in 2014. Microbial resources can be useful and applicable in white-bio industry with their degrading ability and derivates. The aim of this study was exploring 1,000 microbial resources including bacteria, fungi, and microalgae from the geo-specific environments on Korean coastal and islands area from May to October 2021. Additionally, bacterial, fungal, and microalgal resources were selected through the screening platform that was operated for organic compound degradability, environmental pollutant attenuation, and contents of microalgal derivatives, respectively. Eventually, in a total of 100 microbial resources were selected including 96 bacterial, three fungal, and one microalgal strains from the individual usability tests on the screening platform. These selected microbial resources might be extensively applicable for environmental crisis remediation technology. Consequently, available bioresources will be sustainably explored and selected from the costal and islands area in long-term application.

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P5-03

Mucilaginibacter straminoryzae sp. nov., isolated from periphyton

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A rod-shaped, non-motile, Gram-negative bacterium, strain RS28^T, was isolated from periphyton. Phylogenetic analysis of the 16S rRNA gene sequence revealed that strain RS28^T was affiliated to the genus *Mucilaginibacter* and shared the highest sequence similarity with *Mucilaginibacter ginkgonis* HMF7856^T (96.47%) and *Mucilaginibacter polytrichastri* DSM 26907^T (96.12%). Strain RS28^T was found to grow at pH 5.5-8.0, temperature 17-40°C, and in the presence of 0-1.5% (w/v) NaCl. The major polar lipids were phosphatidylethanolamine, two unidentified phospholipids, two unidentified aminophospholipids, three unidentified aminolipids, and one unidentified lipid. The respiratory quinone was menaquinone 7 (MK-7). The genomic DNA G+C content was 44.7%. On the basis of the phenotypic, chemotaxonomic, and phylogenetic characteristics, strain RS28^T represents a novel species of the genus *Mucilaginibacter*, for which the name *Mucilaginibacter straminoryzae* sp. nov. is proposed. The type strain is RS28^T (=KCTC 92039^T =LMG 32424^T).

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P5-04

The inhibitory effect of biological nitrification inhibitors on the nitrification activity of three different groups of ammonia-oxidizing microorganisms in co-culture

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Nitrification is the major nitrogen (N) transformational process and the rate-limiting step in the global N cycle. Through this, ammonia (NH_3) is converted to nitrate (NO_3^-) via nitrite (NO_2^-) by soil ammonia-oxidizing microorganisms [AOMs; ammonia-oxidizing archaea (AOA), bacteria (AOB), and complete ammonia oxidizers (Comammox)] and nitrite-oxidizing bacteria. Evidence that nitrification by AOMs through overuse of N fertilizer input in the soil causes severe environmental pollution problems such as nitrous oxide (N_2O) emissions, NO_3^- leaching into groundwater, and N loss in agricultural systems. Applying biological nitrification inhibitors (BNIs), active compounds from root exudates is an efficient strategy to limit these problems by blocking two key enzymes of ammonia oxidation and disrupting the activity of AOMs to suppress N loss in soil. Previously published studies on BNIs focus mainly on evaluating the inhibitory effect on ammonia oxidation in the pure culture of nitrifiers individually; however, the environmental system is much more complex with the co-existence of a different group of nitrifiers. In this regard, we identified the specific ammonia oxidation rate and cell growth rate on various ratios of three different groups of AOM in a co-culture. Furthermore, it is also identified inhibitory nitrification effects of different plant-derived BNIs and synthetic nitrification inhibitors (SNIs) capacity in co-culture. Overall, our findings give significant insights into how we use the BNIs to control nitrification with specific AOM in the soil to reduce N_2O emissions and increase fertilizer N use efficiency for contribution to the “Net-Zero by 2030”.

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P5-05

Morphology, phylogeny, and fatty acid composition of a new useful euglenoid *Eutreptiella* sp. (KCTC 19016P) from Korean coastal waters

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Euglenoids are the primary producers of useful fatty acids that can be used in animal feed, functional foods, and biofuels. Euglenoids are mostly found in freshwater habitats. However, few of them are reported in marine ecosystems. Therefore, the isolation and identification of various marine useful euglenoids are necessary. In this study, the morphology, molecular phylogeny, and fatty acid composition were investigated to identify an unspecified euglenoid strain (KCTC 19016P) isolated off the coast of Korea. The vegetative cells were longitudinally spindle-shaped, 23.7 ± 2.9 μm in length and 7.6 ± 0.5 μm in width, and narrowed at the anterior part to a truncated apex, tail-like extension at the posterior end. Cells contained numerous chloroplasts. An eyespot was present in the anterior part of the cell. Two flagella were unequal in length. The pellicular striations of the cells, which cannot be seen with a light microscope, were easily visible in the FE-SEM. The maximum growth rate was 0.5, and the doubling time was 1.37 day^{-1} in the exponential growth phase. The phylogenetic analyses based on the nuclear SSU (nSSU) and chloroplast SSU (cpSSU) rRNA sequences revealed that *Eutreptiella* sp. (KCTC 19016P) was nested within the genus *Eutreptiella* and closely related to *E. pomquetensis* (AJ532398). The omega-3 fatty acid content in total fatty acid was 37.61 ± 1.27%, of which alpha-Linolenic acid (ALA), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) was 4.07 ± 2.01%, 19.29 ± 0.63%, and 11.5 ± 0.12%, respectively. These findings indicate that this new isolate could be a potential candidate in the field of aquaculture.

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P5-06

Distribution of sand-dwelling dinoflagellate species in Pyoseon Beach of Jeju Island during spring and summer season 2022

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Benthic dinoflagellates are one of the important components of the benthic ecosystem, and more than 200 species have been reported mainly in tropical and subtropical regions. Several previous studies of Jeju Island have reported their new and unrecorded species, however, seasonal variability and distribution have not been examined. The distribution and species diversity of benthic dinoflagellates were investigated during the spring and summer season in Jeju Island. Sand samples were collected using a 20cm core-sampler of 4cm in diameter size from 12 stations of Pyoseon Beach from March to August 2022. During the survey period, sea water temperature and salinity ranged from 13.7 to 26.9°C and from 30.9 to 34.8 psu, respectively. In March, the abundance of benthic diatoms was the highest at St. 5 of the upper part of the intertidal zone at 89 cells/cm^3, and the abundance of benthic dinoflagellates was the highest at St. 12 of lower part of the intertidal zone at 10 cells/cm^3. From March to August, the distribution ratio of benthic dinoflagellates increased from 13% to 18% on average, and in June, the benthic dinoflagellates appearance ratio of the upper part increased by 3% on average compared to March. The species diversity of benthic dinoflagellates increased in June, and toxic species *Amphidinium carterae*, *A. operculatum* and *Prorocentrum rhathymum* appeared in June.

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P5-07

Study for lactic acid bacterial diversity of environmental samples in Jeju Island

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Lactic acid bacteria (LAB) are studied more because LAB plays a beneficial role in the food, medical and health-related industries. Various microbial species, including bacteria, fungi, yeast, cyanobacteria, and algae, produce lactic acid using carbohydrates as the only primary carbon source. Jeju Island, created by volcanic activity, has diverse flora and fauna, being an ideal location for biodiversity research. In this study, we identified the LAB diversity in different environmental samples (marine water, seaweed, and forest wetted and dried soil) in Jeju Island by the culture-dependent method using LAB-specific growth media. Genus Bacillus and Lysinibacillus dominated in dried and wetted soil, respectively. In contrast, specific bacterial strains, Vibrio, Paracoccus, Yokenella, and Staphylococcus were only identified in marine water and seaweed samples. Even though we used LAB-specific media, 85% of isolated strains were pathogenic. In future studies, we will need to identify the pathogenicity and fermentation product by using the vertical distribution of these specific microbial groups.

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P5-08

Study on the physiological characterization of comammox bacterium *Nitrospira inopinata* under acidic conditions

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One of the key environmental factors affecting niche differentiation and community structure of nitrifying microbes is soil acidification, which is enhanced by agricultural production and human movement. In numerous investigations, neutral pH conditions have been found to be favorable for nitrifier N_2O generation. However, specific biological and chemical reactions connected to N_2O generation rely on the pH. This study investigated the activity of a comammox (complete ammonia oxidizer), *Nitrospira inopinata*, key member of the genus *Nitrospira* (predominant nitrite oxidizers), under acidic conditions. Our results indicated that, although the *N. inopinata* strain could grow and function over a wide pH range (5.5 to 9), it performed at its optimum at a pH of 7.5. While pH 5.5 has the lowest ammonia oxidation (20%), whereas pH 7.5 resulted in the production of elevated hydroxylamine (NH2OH), a recognized short-lived intermediary in the nitrogen cycle. Additionally, *N. inopinata* independently produced NO and N_2O at varied pH levels. This may be due to the lower N_2O production from abiotic NH_2OH breakdown at low pH levels. It has also been demonstrated that 5 μM chlorate (ClO_3^-), a nitrite-oxidizing inhibitor, completely suppressed the growth of *N. inopinata*. Hence, the results suggested that nitrite is a necessary component for *N. inopinata* growth. Overall, our findings will contribute to a better understanding of *N. inopinata's* characteristics under diverse environmental situations as well as help characterize its function in the nitrogen cycle and the generation of greenhouse gases under ecological changes like global acidification.

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P5-09

Diversity and adaptation strategies of nitrifying microorganisms in the groundwater sources of Jeju Island

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Groundwater continues to be at high risk of nitrate-nitrogen contamination from the discharge of domestic wastewater and livestock manure, and excessive use of nitrogen fertilizers. The process of nitrification, the oxidation of ammonia via nitrite to nitrate is mainly carried out by nitrifying microorganisms. Consequently, strategies to combat groundwater pollution require understanding the prevalence and ecobiochemical activity of these nitrifying microorganisms. This study examined the phenotypic traits, diversity, and abundance of nitrifying microorganisms in the groundwater through physiological, kinetic, and metagenomic sequencing analyses. Water samples were collected from the Yongcheonsu area of Jeju Island, where groundwater comes out of the ground under pressure from leaks. A link between the microbial abundance and the physico-chemical characteristics of the groundwater was observed to comprehend the environmental factors involved in the dissemination of nitrifying microorganisms. Moreover, adaptation strategies of the nitrifying microorganisms to an oligotrophic environment, such as groundwater, were also determined through physiological, and genomic characterization. This study will extend our knowledge of the microbial population and its physiological and biochemical traits in oligotrophic environments, like groundwater, and aid in the development of strategies to eliminate dissolved nitrogen from groundwater.

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P5-10

Comparative genomics and physiology of novel *Brachybacterium* sp. unveiling its metabolic potential

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The *Brachybacterium* species, which are members of the phylum Actinobacteria, have been found in a variety of biological settings. In this study, a new *Brachybacterium equifaecis JHP9* was isolated from horse feces to investigate its kinetic properties as well as its biochemical and genetic characteristics. By using 16s rRNA analysis, genome-based phylogenetic analysis, and a similarity matrix based on nucleotide and amino acid identity, the genome was delineated. Carotenoid biosynthesis, different carbohydrate metabolism under aerobic and anaerobic conditions, and lactic acid production were observed in genotypic and/or phenotypic properties of strain JHP9. This indicates the metabolic flexibility of this bacterium, which may advocate its use in a variety of industrial settings. Kinetic experiments reveal that the strain JHP9 has a high affinity for oxygen and substrate, which may point to niche differentiation. Our results increase understanding of the physiological, and genetic characteristics of the *Brachybacterium equifaecis JHP9*, indicating its carbohydrate metabolism, environmental tolerance, and growth potential.

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P5-11

Activity variations of ammonia and methane oxidizers at various copper concentrations

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Copper is an essential element involve in the enzymatic pathways of ammonia and methane oxidation. Since important enzymes like methane monooxygenase (pMMO) and ammonia monooxygenase (AMO), which are carried by methanotrophs and ammonia-oxidizing bacteria, are dependent on copper. The copper homeostasis genes that code for proteins with high copper absorption efficiency and resistance are also known to be present in comammox. Here, we investigated the changes in the activity of ammonia-oxidizing microorganisms (*Nitrosomoas europaea*, *Nitrospira inopinata*) and methaneotrophs (*Methylosinus trichosporium* OB3b) at varying copper concentrations. Additionally, strain OB3b, which produces methanobactin, is exposed to a copper-deficient environment, where the methanobactin is reabsorbed in a mixed state with copper and used by pMMO enzyme of methanotrophs. The atmosphere is lacking in copper, which inhibits the nitration reaction and prevents accessible copper from being utilized by ammonia oxidizing microbes. Eutrophication of sewage and seawater because of such suppression of ammonia oxidation lowers the effectiveness of the BNR (biological nitrogen removal) process, endangering the aquatic ecosystem. This study offers the first account of the investigation into the relationship between methane and ammonia oxidation processes, which can result in the creation of environment friendly alternatives to ineffective sewage treatment facilities.

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P5-12

Phylogenetic analysis of bacterial diversity in the marine sponge, *Callyspongia confoerderata* and *Spirastrella insignis* collected from Jeju

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In this study, two types of sponges were collected from Jeju Island (Udo), and sponge-derived bacteria were isolated and cultured to investigate the phylogenetic analysis of the bacterial community and the antibacterial activity of the bacteria-derived bacteria against fish disease bacteria. A total of 47 strains were isolated from *Callyspongia confoerderata*, and as a result of 16S rRNA sequence analysis, major taxa of bacterial community were composed of *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, and *Proteobacteria* (Alpha-, Beta-, Gamma), 6 classes, 12 orders, 15 families, 17 genera, and 30 species were identified. Bacterial community of *Spirastrella insignis* included 4 classes: *Actinobacteria*, *Firmicutes* and *Proteobacteria* (Alpha-, Gamma-). *Actinobacteria*, *Firmicutes* and *Proteobacteria* were commonly found in both sponges, but the bacterial community ratio was different in both sponges. Also, as a result of analyzing the antibacterial activity against 8 types of fish pathogens isolated from 2 species of marine sponges, a total of 12 bacterial strains showed high levels of antibacterial activity and Most of the strains were identified as genus *Bacillus*. Based on these results, additional experiments are needed to confirm the suitability and stability of the *Bacillus* sp. strain, which has antibacterial activity against fish disease bacteria, as a new feed additive. We also want to explore the potential of new probiotics.

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P5-13

Morphology and molecular phylogenetic position of three new epilithic diatom species of Han River from Korea

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Besides the assessment of the aquatic ecological health survey of the Han River, we collected and isolated epilithic diatoms. Based on morphological and molecular study, three new species were new to Korea, belonging to genus Nitzschia, Fragilaria and Encyonema. Morphological characteristics were analyzed using combined light microscopy (LM) and scanning electron microscopy (SEM), and nuclear small subunit (SSU) and ribulose-bisphosphate carboxylase (rbcL) genes to study molecular characteristics. Among the three species, Nitzschia sp. which has a small-size valve with the edge protruding and the stripes in its central part are parallel but gradually becoming radial intensively towards the poles, Fragilaria sp. which has spatulate spines tapering towards tips, Encyonema sp. showed that distance between stubs, which located on upper siliceous struts, is consistent whether near the margin or near the raphe. Through morphological and molecular studies, we can recommend these three findings as 3 new species.

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P5-14

Characterization of an extracellular protease EcpZ-1 from *Pseudoalteromonas* sp. strain SiA1

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Extracellular protease gene *ecpZ-1* from *Pseudoalteromonas* sp. strain SiA1, isolated from the Antarctic Ocean-dwelling starfish (*Pterocirrus* sp.), is 2,181 bp and coding 726 amino acids. The size of EcpZ-1 is 75.6 kDa and 24 amino acids signal peptide sequences. Thermolysin protease EcpZ-1 shows the highest activity at 60°C and self-degradation occurs over time. It was confirmed that even if self-cleavage occurred, strong activity was maintained for at least 120 min. To identify the part that affects the activity, 25-726 amino acids without signal peptides wild type and peptides removed from N-terminal mutants were overexpressed in *Escherichia coli* BL21 (DE3). It was found that propeptide residue 25-55 amino acid site had an important influence on the activity of EcpZ-1 protease.

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P6-01

Coastal warming heightens direct impacts of seawater temperature on nutrients near aquaculture farms

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The potential roles of temperature and phytoplankton in cycling of regenerated nutrients throughout the water column were investigated in Gamak Bay in the southern coastal waters of Korea, nearby aquaculture farms including oysters, mussels, and fish. Using the convergent cross mapping (CCM), which can detect causal relationships in weakly coupled nonlinear dynamic systems, we examined the relative strength of phytoplankton and temperature effects on nutrients in the surface and bottom layers of different water masses; the inner bay and outer bay. High $\delta^{15}N$ values of particulate organic matter in the inner bay (mean±sd; 7.21±0.63 ‰) were detected compared to those in the outer bay (5.31±0.15 ‰; $p<0.001$; Two-Way ANOVA). However, $\delta^{15}N$ values greater than 5 ‰ throughout the bay indicate that nitrogen influxes from the aquaculture farms are the critical nitrogen source in the study region. While dissolved inorganic nutrients were significantly different between the surface and bottom layers, NH_4^+, PO_4^{3-}, and SiO_2 were significantly different between the water masses (Permutational multivariate analysis of variance; $p<0.05$). Our CCM models revealed that water temperature positively and strongly affected the potential regeneration of nutrients, particularly associated with PO_4^{3-} while phytoplankton rapidly utilized those nutrients as soon as available. The temperature–driven nutrient regeneration was higher in the bottom layer than that in the surface layer, indicating that temperature was a more important controlling factor in nutrient fluxes from the surface sediments. While our empirical dynamic model can be a practical means of detecting the potential nutrient regeneration as a function of environmental variables, our findings highlight the substantial roles of temperature and phytoplankton in biogeochemical cycles in adjacent waters to aquaculture farms.

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P6-02

Wild hybridization between Native *Mauremys reevesii* and invasive *Mauremys sinensis* in South Korea

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Contamination of endemic genes due to crossbreeding between invasive and native species is one of the factors that disturb biodiversity. In case of endemic turtle, *Mauremys reevesii,* crossbreeding in captivity has been reported. In the wild, however, the possibility of crossbreeding was only predicted. This study aims to explore the hybridization between an endemic turtle and an invasive turtle in the wild. On Aug 2, 2022, three adult turtles (1 female, 2 male), presumed to be *M. reevesii*, were caught in a pond, Seogwipo-si, Jeju Island, South Korea. The coloration, patterns, and shape of the carapace of the turtles were close to the native turtle. However, the shape of the keel on the carapace, the pattern of the plastron, and the stripes on the side of the head were similar to the *Mauremys sinensis*, consistent with the previously known hybrid traits between the two species. In males, wounds from reproductive activity remained around the scute, but no hybrid hatchlings or subadults were observed. This is the first report of wild hybridization between a native and an invasive turtle. In future studies, it is necessary to determine how invasive turtles and even endemic turtles were introduced into Jeju Island. In addition, rapid investigation and capture of the location and surrounding areas where the hybrids were found are required.

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P6-03

Size distribution and their energy flux in belowground food web

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The size of soil organisms is a fundamental trait determining the metabolic rate and the energy status of individuals. For this reason, many studies on quantifying the energy flux of the ecosystem have been conducted based on the size distribution of the food web. However, in the belowground food web, the relationship between the size distribution and the energy flux has not been clarified because of the complexity of the terrestrial food web. In this study, we investigated the size distribution and the energy flux of the belowground food web in the gold mining area. The size of individuals was positively correlated with their trophic levels, and the energy flux was closely related to the size distribution of the food web. This result will be used as scientific data for identifying the relationship between the size distribution and the energy flux of the belowground food web.

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P6-04

Management and role of the Baekdudaegan Global Seed Vault

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IUCN(The International Union for Conservation of Nature) reports 420,000 plant species globally, of which, 369,000 flowering plants produce seeds, accounting for 87.8% of total plant species. The various benefits of plants to mankind have a huge impact on the survival and welfare of mankind. But, the climate crisis is inducing an extinction rate in plant species approximately 1,000 times faster than during the industrial revolution. Accordingly, the Convention on Biological Diversity and the Global Plant Conservation Strategy are being implemented for global biodiversity conservation through the 'Seed Vault'. The Baekdudaegan Global Seed Vault (BGSV) undertakes the prestigious challenge of storing the seeds of all wild plants on the planet. BGSV is also the first seed vault in the world to store wild plant seeds safely and permanently in preparation for global disasters, including climate crises. The goals of the BGSV are (1) to contribute to the maintenance and promotion of plant species diversity by storing plant seeds from around the world, and (2) to conserve seeds owned by arboreta, botanical gardens, institutions, and/or individuals. BGSV can conserve 2 million accessions of wild plant seeds and currently stores over 130,000 accessions of seeds from seed-related organizations, arboreta, and botanical gardens from places such as Korea, Georgia, and Kazakhstan. BGSV is a global seed repository that can be used to conserve integral plant information from and for our planet.

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P6-05

Effect of apple snail (*Pomacea canaliculata*) on aquatic invertebrates in rice fields

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Apple snails are applied for agricultural purposes to control weeds after rice seedling transplanting in rice fields. Their overwintering was observed in various habitats including channels and streams in agroecosystems. Aquatic invertebrate communities in rice fields with and without apple snails were compared. In five regions, samplings were conducted using traps in rice fields. Apple snails had a minimal effect on aquatic insects. However, the gastropod communities were significantly influenced by it. Abundances of *Hippeutis cantori* and *Gabbia kiusiuensis* were lower in the fields with apple snails than in those without apple snails. It reflects that apple snails may influence ecological functions and biodiversity of aquatic community.

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P6-06

eDNA metabarcoding analysis of compositional variation in the gut content of filter feeder *Polypedilum* (Chironomidae) in the weirs and streams

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Chironomids are among the most abundant invertebrates, widely distributed in lentic and lotic environments. Using eDNA metabarcoding, we analyzed the dietary composition of the dominant genus *Polypedilum* larvae among two contrasting habitats, river and weirs. Our approach was i) the attempt to apply eDNA-based metabarcoding to reveal the gut content of the chironomids larvae, ii) the diversity of gut contents in the two aquatic habitats, and iii) the assessment of the habitat condition with the imprints of food sources in the gut. The study's results indicated phytoplankton as the predominant food source with different distributions in the guts of midges. Chlorophyta, with 20% and 39%, was the most common food item in the guts of river and weir midges. The average ratio of fungi, protozoa, and zooplankton in river chironomids' gut was 5.9, 7.2, and 3.8%. At the same time, it was 1.2, 2.5, and 0.1% in weir chironomids. The presence of fungi was a prime factor in determining the habitat condition. The maximum ratio of fungi observed were aerobic groups in the guts of the river chironomids (3.6% - SC and 10.34% in IS), and it was in the range of 0.34 – 2.58% in the weir midges gut. The hierarchical clustering analysis showed the positive correlation and clustering pattern of the abiotic factors such as conductivity, pH, water temperature, DO, turbidity, total nitrogen, and chlorophyll-*a* in the two habitats with phytoplankton and minor groups of fungi. Our results suggest that eDNA metabarcoding is an effective tool for identifying the food sources' biodiversity and determining the habitat environmental conditions by the dietary composition, denoting regional biodiversity.

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P6-07

Discovery of exotic turtle leeches and cases of parasitism on invasive and native species in South Korea

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Parasites cause direct or indirect damage to the host by utilizing the host's resources. As well as, if parasites on the exotic species are introduced into the country with its host, they are likely to parasite on native species with similar ecological status. On July 24, 2022, several unidentified leeches were found in the carapace and breastplate of wild reeves' turtles living in the reservoir in Gurye-gun, Jeollanam-do. The leeches were morphologically different from the leeches recently found in wild reeves' turtles in Jinju, Gyeongsangnam-do, and Gyeongju, Gyeongsangbuk-do, resembling a species of leeches found in red-eared sliders in 2020. Based on its body size, eye shape, parasitism on freshwater turtles, and cub-raising behavior, the unidentified leech is presumed to be a leech included in the genus *Placobdella* living in North America. This discovery serves as an example of exotic leeches flowing into the wild in Korea with the invasive host, showing one of the problems caused by importing foreign species. Therefore, it is necessary to identify species along with determining the inflow path of exotic leeches in future studies. Furthermore, it is essential to predict the damage to native species by understanding the life history of the species and its impact on the host, and adequate measures should be taken.

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P6-08

Trend analysis of YouTube videos related to exotic amphibians and reptiles in South Korea

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As interest in exotic pets has increased recently, the frequency of import, breeding, and trade is also increasing. In addition, these activities are being shared and spread rapidly through social media such as YouTube and Instagram. This study aims to analyze changes in domestic trends related to exotic reptiles and amphibians. As a result, 1,987 videos of exotic reptiles and amphibians uploaded to YouTube Korea from 2016 to 2021 were collected. The number of videos peaked in 2018, with a total of 713, and steadily decreased until 2021. A total of 586 families and 1,573 species of exotic reptiles and amphibians were mentioned in the video during this period. Among them, reptiles were mentioned 5,133 times, about 5 times higher than 1,093 counts of amphibians. In reptiles, "*Eublepharis macularius*" had the most with 178 cases, and in amphibians, "*Litoria caerulea*" had the most with 75 cases. As for the content of the video, "trade" was the most common theme at 37.6%, followed by "caring" 26.6%, "import and export" 25.5%, "breeding" 5.7%, and "consignment" 4.4%. Looking at the transition of the theme each year, the frequency of "caring (6 cases)" was the highest in 2016, then "transaction" from 2017 to 2020, and "caring" in 2021. As for the frequency of each type of video, videos related to "import", "breeding" and "trade" were the most common in 2018, while "caring" related videos were uploaded the most in 2019, and "collecting" and "consignment" in 2021. Through this study, it is possible to examine the change in trends related to exotic reptiles and amphibians in Korea. We highlight that the strategy for managing the species is required, according to the changes in the trend of exotic reptiles and amphibians in South Korea.

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P6-09

Experiment on the food preference for invasive and native turtles in South Korea

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In this study, we investigated the preferred food resources of invasive turtles found in the wild of South Korea. In addition, the possibility of competition for food resources was confirmed through comparison with native turtles. From August to September 2021, we tested a food preference experiment using meat (pork), fish (loach), mollusk (freshwater snail), plant (lotus leaf), fruit (peach) on Red-eared sliders (*Trachemys scripta elegans*), River cooters (*Pseudemys concinna*), Chinese stripe necked turtles (*Mauremys sinensis*) and native Reeves' turtles (*M. reevesii*). To verify the results of the indoor experiment, an outdoor food source preference and attraction effect experiment was conducted from April to June 2022. As a result of the indoor experiment, *T. s. elegans* and *M. reevesii* preferred meat the most. In the case of *P. concinna* and *M. sinensis*, mollusk and fish were preferred, respectively. As a result of the field experiment using meat, 69.2% *T. s. elegans* (n=45), 29.2% *M. reevesii* (n=19), and one *P. concinna* were captured out of a total of 65 individuals. In summary, it was judged that most turtles found in the wild preferred carnivorous food than vegetable food. Moreover, *T. s. elegans* and *M. reevesii* preferred the same type of food resource. This result indicated the possibility of competition for food resources between invasive and native turtles.

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P6-10

Distributional shifts of Canopy-forming algae in Korea under climate change

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Canopy-forming algae play an important role in as primary producer coastal ecosystems and provide habitats and shelter areas for numerous marine pelagic and benthic organisms. The main species of canopy-forming algae in the coast of Korea is *Sargassum*, which consists mainly of temperate species. Recently, temperate macroalgae disappear rapidly in coastal ecosystem of Korea and tropical seaweeds and corals occupy empty space, due to rapid climate change. Despite the importance of their ecological role, studies related to the distribution changes of these species are still scarce. In this study, the distributional shift was confirmed by comparing the distribution of *Sargassum* recorded in the 20th century with the distribution studied in the last 20 years for these species. Changes in long-term distribution of *Sargassum* in Korea differed depending on the species. There was no change in the ranges of *Sargassum fusiforme*, *S. thunbergii*, *S. fulvellum*, *S. siliquastrum* and *S. piluiferum*. The distribution of *S. horneri*, *S. muticum* and *S. confusum* were relatively northward. The distributional ranges of *S. coreanum*, *S. macrocarpum*, *S. serratifolium* and *S. patens* were extended markedly to the northern part of the East Sea in South Korea. This result indicated that the northern limit of the species with a changed distribution is changing due to climate change. However, since this study only compared the presence or absence of appearance by species, there is a limitation in not being able to confirm variations in abundance by species under climate change. Therefore, it is necessary to monitor biomass fluctuations of major canopy-forming algae and predict changes in species distribution according to climate change scenarios.

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P6-11

Bemicia tabaci density prediction using machine learning algorithms in tomato greenhouses

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Bemicia tabaci is one of the serious insect pests that have more than 600 types of hosts including commercial greenhouses. Density estimation is the central part of integrated pest management of insect pests. Classical density estimation methods are based on the spatial distribution using mean and variances of target pests by laborious sampling in target crop fields. Recently, remote environmental monitoring and control systems are applied in commercial greenhouses. The remote monitoring system logged all environmental variables including temperature, RH, and so on. In this study, to predict the density of *B. tabaci*, environmental factors affecting the density fluctuation were analyzed using a machine learning model. Machine learning makes a model by learning patterns by the computer itself based on the input data. These machine learning models can predict density with environmental factors. Environmental factors affecting the density fluctuation of insect pests selected atmosphere factors (temperature and RH), soil factors (temperature, moisture, and EC), and host factors (photosynthesis potential, photosynthesis rate, and NDVI). This study aims to predict *B. tabaci* density by sampling environmental factors and applying them to the machine learning model.

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P6-12

Geostatistical analysis for *Frankliniella occidentalis* in commercial hot pepper greenhouse using variogram models

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Spatial distribution analysis of insect pest populations is the basic and essential stage for implementing integrated pest management. However, classical methods for determining spatial distribution had limitations because they focused on sample variance ignoring coordinate locations. The method introduced to overcome these problems was geostatistical analysis, in this study, three theoretical variogram model analyses were conducted using experimental variogram. The data were collected by tapping 3 flowers into a vial containing 70% ethanol (1 repetition), and this process was performed in 3 repetitions per stratum (9 flowers, 3 vials per stratum). The 62 hot pepper plants were selected for sampling in selected coordination in a commercial pepper greenhouse. *F. occidentalis* was mapped for not sampled positions in greenhouses by ordinary kriging using parameters of the theoretical variogram model whether the study area was adequately represented, the validation analysis was performed by cross-validation.

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P6-13

Monitoring the movement of native *Mauremys reevesii* and invasive *Trachemys scripta elegans* in Geumho Reservoir, South Korea, using GPS-based Telemetry

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It's important to understand the behavioral ecology of endangered species such as *Mauremys reevesii* to protect them from threats such as habitat destruction, pollution, and invasive species. We conducted a study to see the mobility and spatial behavior of native *M. reevesii* and invasive *Trachemys scripta elegans* within their habitat through GPS telemetry tracking. We attached GPS-based Telemetry Trackers (WT-450, NEWNS) on the carapace of four *M. reevesii* and three *T. s. elegans* found in Geumho Reservoir located in Jinju-si, Gyeongsangnam-do, South Korea. The individuals were released from October 2021 to August 2022. We calculated 1) the movement distance of the individuals by GPS data and analyzed 2) the home range by MCP using ArcGIS 10.8. We could also observe movement patterns such as 3) the tendency to return to the place where turtles were first captured, and 4) long-distance movement during the breeding season. From June, *M. reevesii* were tracked in nearby residential areas where some were more than 600m away from the reservoir, which is further than the known average movement distance. Turtles stayed in the breeding site for a period of time, with one individual staying there for approximately two months until its location was detected back at the reservoir on August 12. Through continuous monitoring and additional studies like this, we will be able to investigate the competitive relationship between the two species and collect detailed data useful for establishing appropriate conservation measures for *M. reevesii*.

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P6-14

Characteristic analysis of invasive turtles inhabiting Jinju Geumho reservoir according to period and habitation environment

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In this study, as part of the removal and population control of invasive turtles, the activities and habitat characteristics of invasive turtles found in the wild in Korea were identified. Monitoring was conducted once a week from June to December 2021, at 11:00, and 3 times a day (8:00, 11:00, and 14:00) from March to August 2022. The species, population, location, and habitat environment of invasive turtles found while moving to the reservoir on foot were recorded. A total of 10,698 invasive turtles were observed over a total of 54 weeks, with an average of 198.1 per week. The highest number was observed in April, with an average daily average of 349.4, followed by May and October. In the case of the native turtle *M. reevesii*, it was not observed from December to February, whereas invasive turtles were active even in winter. The time period in which the highest number of individuals was observed was 11:00, with an average of 118.8 individuals observed, followed by 14:00 and 8:00. There was no significant difference in the average number of individuals observed over time. According to the habitat, “water surface” was the highest at 36%, “natural structure (rocks and submerged tree)” 28.4%, “aquatic plant” 18.6%, “shore” 9.7%, “artificial structure” 6.2%, “lotus” 1.2%, in that order it was. The appearance of turtles showed a positive correlation between temperature and cloud amount, and a negative correlation with precipitation, humidity, and sunshine duration. In summary, the most effective period for catching and removing invasive turtles is from April to May and October to November, and the floating trap is considered to be effective.

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P6-15

Population management of American Bullfrog using calling behavior and territoriality during breeding season

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The American Bullfrog (*Lithobates catesbeianus*) is one of the world's 100 most successful invasive species. Various methods have been used to control the American Bullfrog populations, but there no effective method has been suggested to this day. The American Bullfrog is an actively chorusing anuran during the breeding season, and males remain their territory vocalizing to attract females. This research aims to suggest a new approach of population management using breeding characteristics, the calling behavior and territoriality of the American Bullfrog. All experiments were conducted during breeding season, June to August, 2022. Recordings of advertisement calls were used as acoustic lures for the calling behavior experiments. 2 call characteristics, peak frequency, and pulse rate were tested in 2 experimental sites, located in Taean, Chungcheongnam-do. For the territoriality experiment, traps without attractants were used, only differing its location within the same site. Trap locations were chosen based on micro-habitat, population density acquired through calling index. Results show that the American Bullfrogs tend to be more attracted to lower frequency calls (193Hz), especially males. For pulse rates, both sexes were more attracted to higher pulse rate calls (136pulse/s). High territoriality of males was shown, regarding all males were captured in only one of the locations within the same breeding sites, where calling indexes were high. For population control of the American Bullfrog, low frequency, and high pulse rate advertisement calls may be used as acoustic lures, and trap locations showing high population density needs to be considered. These results suggest an appropriate environment and method that needs to be used for further population management of the American Bullfrog.

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P6-16

Restored ecological role of Chilbal-do (Island) based on adaptive restoration

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This study aims to recommend scheme to restore especially natural habitats of seabirds on islands as presenting results of monitoring Chilbal-do (Is.). Costal rock sedge (*Carex boottiana* Hook. & Arn.) was planted in the island after weeding adversely affected harmful plants, Oriental chaff flower (*Achyranthes bidentata* Blume var. *japonica* Miq.) and Rape (*Brassica napus* L.), on sustaining breeding density and population size of seabirds. Restoration project including monitoring has been carried out for 13 years from 2009 to 2022 based on 'Adaptive Restoration'. Flora of the island and breeding density and population size of seabirds has been analyzed to find out any change patterns. The result shows that species diversity of plant is decreased, and dead birds with seeds sticked are rarely found. Breeding density and population size of seabirds are also stabilized. Results support that ecological role of Chilbal-do is getting restored as breeding ground of seabirds. Several valuable meanings related to adaptive restoration were obtained through the project, and it should be referenced to accomplish other similar projects.

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P6-17

Biomass and species variation of *Ulva* spp. exposed to different nutrient gradients in Jeju Island, Korea

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Green tides formed by blooms of *Ulva* species are generally linked to costal eutrophication caused by over-enrichment nutrient loads. Jeju Island is strongly affected by several nutrient sources such as groundwater, fish farm effluents and wastewater with high nitrogen concentrations. Consequently, the frequency and severity of green tides have steadily increased along the coast of Jeju Island. This study was designated to find out and elucidate effects of nutrient sources of *Ulva* blooms in Jeju Island. We investigated biomass and composition of *Ulva* species at seven stations exposed to different nutrient sources such as fish farm effluents, ground water and waste water. Water temperature, underwater light irradiance, salinity, pH and water column nutrients (NH_4^+, NO_3^-+NO_2^-, PO_4^{3-}) were also measured bimonthly from May to August 2022. As a result of the study, biomass of *Ulva* was higher in sites affected diverse nutrient sources, than other study sites which is ambient nutrient sites. *Ulva* biomass gradually increased with water temperature in March, June, and August 2022. *U. ohnoi* and *U. pertusa* were mainly observed very every sampling. Our results imply that green tide in Jeju Island may be affected by compositive environmental conditions., but a continuous investigation is needed to establish more detail information for green tides by multiple nutrient source.

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P6-18

Distribution and historical records of diatom assemblages in surface and sediment cores from the Yellow and Bohai seas

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Tidal flats in the Yellow and Bohai seas are valuable habitats attracting attention for their broad area and high ecological value. By investigating the spatiotemporal distribution of diatoms, the most important primary producer in tidal flat, we tried to understand the present and past of the Yellow and Bohai seas. Surface sediment samples (9 stations) for present conditions and sediment core samples (3 stations X 3 depths of samples) for historical conditions were analyzed. In general, pennate diatoms dominated on surface sediment, and centric diatom, *Paralia sulcata* dominated in the sediment core. Except for some stations where a specific genus dominated, most stations generally showed relatively high number of species (n = 287) and evenness (mean J = 0.77). The composition of dominant species differed by the depth of sediment core, suggesting changes in diatom community structures according to historical environmental change. The $\delta^{15}N$ concentration was the most significant factor for diatom assemblages regardless of time and region of the Yellow and Bohai seas. Total organic carbon and $\delta^{13}C$ were also revealed as major environmental factors, which revealed that the organic matter and its origins have controlled diatom diversities and several dominant species. The study area seemed to have been affected by a large influx of land-derived matters from neighboring countries (Korea and China) over several decades through many rivers. Such stress on primary producer communities could be a severe problem. Thus, constant monitoring and managing of diatoms and their controlling factors were needed.

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P6-19

First record of the invasive ascidian *Microcosmus squamiger* Michaelsen, 1927 (Ascidiacea: Pyuridae) in Jeju Island, South Korea

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Ascidians are sessile marine invertebrates with many successful invasions. In particular, *Microcosmus squamiger* has spread to temperate waters worldwide and is considered a global marine invader. This study is the first report of *M. squamiger* from Jeju Island, South Korea. We were collected specimens from Unjin and Wimi harbors on Jeju Island followed by dissection for characterization of the siphons, pharynx, and dorsal tubercle using stereomicroscopy and scanning electron microscopy. The shape of the dorsal tubercle (the peritubercular area filled with two spiral coils) and the length (15-20 μm) and shape (roof tile or fingernail) of the siphon spine were consistent with the previous studies. Additionally, molecular verification was performed by genomic DNA extraction followed by an ML-based phylogenetic tree construction, which confirmed the existence of two clades. Therefore, the presence of *M. squamiger* was verified by morphological and phylogenetic identification. Although *M. squamiger* is currently distributed in most of the continents, records from India (2006), Okinawa, and Japan (2007 and 2014) suggest that it was introduced into Asia rather recently.

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P6-20

Analysis of habitat characteristics of odonata climate-sensitive biological indicator species (CBIS) and candidate species

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Climate change is expected to affect not only the terrestrial ecosystem but also the aquatic ecosystem, resulting in a decrease in the habitat distribution of cold-water species due to the increase in water temperature. Therefore, the National Institute of Biological Resources selected climate-sensitive biological indicator species(CBIS) and candidate species to prepare an efficient monitoring and prediction method for the impact of climate change on the distribution of species. Among insects, dragonflies live in the aquatic ecosystem during the larval stage live in the terrestrial ecosystem during the adult stage, so it is considered to be a taxa vulnerable to changes in the aquatic and terrestrial system. Therefore, this study was conducted to predict the habitat characteristics and habitat changes due to climate change targeting six species of dragonflies, including the *Brachydiplax chalybea* and *Ceriagrion nipponicum*, which are CBIS and candidate species for climate change. As a result of analysis using the data of the Natural Environment Survey of the National institute of ecology to understand the distribution of odonata, which is a CBIS, six *brachydiplax chalybea*, 26 *ceriagrion nipponicum*, 94 *ischnura senegalensis*, 132 *sympetrum striolatum*, two *sympetrum fonscolombit*, 20 *ischnura elegans* were identified. As a result of checking the average annual temperature of each target species using the climate data of Worldclim, the *B. chalybea* is 13.9~15.5°C, the *C. nipponicum* is 10.9~14.8°C, *I. senegalensis* is 10.3~15.5°C, *S. striolatum* is 8.4~15.5°C, *S. fonscolombit* is 11.5~12.3°C and *I. elegans* is 10.6~12.8°C. In addition, habitat characteristics of six odonata were idenrified using spatial information, and habitat prediction analysis was performed using a species distribution model.

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P6-21

A study on habitat characteristics and food sources of brown dipper (*Cinclus pallasii*)

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This study was conducted to understand the habitat environment of brown dippers (*Cinclus pallasii*) and to prepare basic data on the conservation and management plan by identifying the food source and the stream environment in which the food source lives. Habitat characteristics were studied by examining breeding ecology, stream characteristics, surrounding environment and land use status. Food sources were investigated and studied using surber sampler and direct observation using a camera. Seventeen breeding nests showed a high recycling rate, and nest sites showed a remarkable tendency to use certain places. The clutch size was 5-6, which was higher than previously known. The type of nest is dependent on the stream environment, which is a result of reflecting various environmental factors, and detailed research is needed. The nest has a double structure composed of available materials in the area. The outside is dome-shaped nest and the inside is bowl-shaped, and the height of the nest should be higher in consideration of the fluctuation range of the stream water level, which was found to be closely related to breeding success. The brown dipper breeding activity started between 5-6 am and ended between 20-21 pm. Intervals between which adult birds visit the nest were investigated in the order of two minutes, three minutes, and one minute, indicating the abundance of food sources near the nest. As the type of food source, it was found that the EPT group was preferred. At a time when artificial changes in the stream environment are increasing, follow-up studies on the ecology and habitat of brown dippers are needed, and monitoring to identify the population is urgently needed.

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P6-22

Spatial variation of the microalgae in the Han River and its tributaries with focusing on the correlation with water quality

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The Han River system is used as an important drinking water source in Korea, requiring constant water quality monitoring. Microalgae, including diatoms, green algae, and dinoflagellates, are used worldwide for water quality assessment. In this study, the occurrence of microalgae was investigated at 30 sites in the Han River selected based on the water quality. The identifications of planktonic and benthic microalgae were done a light microscope, and detailed taxa were analyzed with a Scanning electron microscope (SEM) and metabarcoding. In the planktonic microalgae, diatoms were most broadly detected in Han River systems, and dinoflagellates and euglenoid were rare. The diatoms including *Ulnaria ulna* and *Fragilaria capucina* were common regardless of water quality. However, other microalgae such as dinoflagellates *Unruhdinium* prefer oligo-mesotrophic water. Most of the benthic algae were composed of pennate diatom, and there was no strong correlation with the water quality. This study provides fundamental data for understanding the correlation between microalgae and water quality in the Han River.

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P6-23

Prediction of habitat distribution changes of endangered conifer *Abies nepholepis* Maxim. on climate change scenarios using MaxEnt model

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Abies nephrolepis Maxim. is listed as a species of least concern (LC) in the International Union for Conservation of Nature Red List and has been designated as a climate change biomarker because it is expected to be vulnerable to climate change. The objective of this study is as follows: to predict habitat distribution changes of *A. nephrolepis* of environmental variable selection and parameter settings on the performance of the MaxEnt model under different climate change scenarios (SSP1-2.6, SSP2-4.5, SSP3-7.0, and SSP5-8.5) in 2030s and 2090s. The field survey was conducted randomly across the country, and the GPS coordinates of a total of 513 points were recorded and analyzed. The average test AUC value was calculated to be 0.985. The environmental variables that are most affected by the habitats of *A. nephrolepis* are bio01(annual average temperature), bio03 (isotherm), bio07 (annual temperature difference), bio12 (annual cumulative precipitation), bio13 (precipitation in the wettest month), bio14 (driest lunar precipitation) was finally selected. bio01 (annual average temperature) was identified as the largest environmental variable in determining the habitat of *A. nephrolepis*. In the case of 2090s, 100% of habitat distribution was exterminated. It was known through habitat prediction that *A. nephrolepis* are on the verge of extinction on the Korean Peninsula from the 2030s, the near future. It was confirmed that when the average annual temperature increased to more than 6°C, the habitat suitability of *A. nephrolepis* rapidly decreased. In accordance with this study, it is planned to establish management and conservation measures for *A. nephrolepis*. This will serve as basic data for the restoration and conservation of endangered conifers on the Korean Peninsula by predicting habitat changes due to the upcoming climate change.

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P6-24

Inhabitation status of the dominant Cyprinid fish species (*Zacco platypus* and *Zacco koreanus*) population in the Seom River

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The Seom River is a national river that originates in the area of Taegisan Mountain in Hoengseong-gun, Gangwon-do. It meets Geumgye Stream and Gye Stream and flow to Wonju-si, and joins the Namhan River. Agricultural and recreational areas are built around the river, and residential and industrial complexes are located near the area. In this study, the present inhabitation condition of *Zacco platypus* and *Zacco koreanus* populations, identified as dominant species, was confirmed when investigating the ichthyofauna of the Seom River. Analysis of the length-weight relationships and fatness index of the *Z. platypus* and *Z. koreanus* populations confirmed that both species had good growth and the state of growth. As a result of the Frequency analysis of total length, it was found that both species appeared from individuals less than one year to those more than two years, indicating that they maintained a stable life history in the Seom River. According to the analysis of the gonadosomatic index (GSI), the GSI index for males of *Z. platypus* increased from May to June and then decreased from July, and for females, the GSI index decreased from May to August, so the maximum spawning period is estimated to be between June and July. The male *Z. koreanus* showed a decreasing trend from May to August, but increased in July, and the female *Z. koreanus* showed a decreasing trend from May to August, so the maximum spawning period is estimated to be between May and August. As a result of this study, it was confirmed that the populations of *Z. platypus* and *Z. koreanus* living in the Seom River had good growth and the state of growth and maintained a stable life cycle. The spawning period was also found to be consistent with the past literature.

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P6-25

Phytoplankton community differences between lake and river sections of the Han River (Korea): Paldang Reservoir and Seongsan bridge stations

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The Han River is widely used as a water resource in Seoul and the metropolitan area, thereby continuous monitoring and management are required. This study was conducted to understand the phytoplankton community structure in the Han River in the 2000s, and to compare the community differences between the river and lake environments. Field surveys were conducted once a month from March 2019 to February 2020 at Paldang Dam (lake) and Seongsan Bridge (river), and the physicochemical data of water temperature, total phosphorus, and total nitrogen were determined, and cell number and species composition of chlorophyll *a* and phytoplankton were also determined. In terms of physicochemical changes, except for total nitrogen and total phosphorus, Paldang reservoir and Seongsan Bridge showed similar features, and in total phosphorus and total nitrogen, Seongsan Bridge was higher than Paldang reservoir. As a result of checking the phytoplanktons that exist only at Paldang reservoir and Seongsan Bridge, it was confirmed that Paldang reservoir was in a medium nutrient state and Seongsan Bridge was in a high nutrient state. This is a study on the differences of phytoplankton communities in a river and lake at Paldang reservoir and Seongsan Bridge, and the results can be used as reference data for monitoring the Han River.

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P6-26

Effect of three different environmental raster scales on species distribution modelling of alien plants in the South Korea

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This study was conducted to compare species distribution modelling results of alien plants in the South Korea according to the three different scales of environmental raster. The scales of environmental raster were World, Northeast Asia, and South Korea. Three different scale environmental rasters were used in Maxent model for five different alien plant speceis. As a result, after removing multicollinearity, selections of environmental raster were variable among the scales of environmental raster. Eight environmental factors for the World, six for Northeast Asia, and seven for South Korea were selected. The average AUC values were 0.86 in world, 0.93 in Northeast Asia, and 0.76 in South Korea. Zonal average of potential distribution and spatial distribution in South Korea also were variable among the scales of environmental raster and five plant species. The averages of zonal average for five species were 0.54 in World, 0.64 in Northeast Asia, 0.41 in South Korea. The averages of standard deviation were 0.09 in World, 0.23 in Northeast Asia, 0.24 in South Korea. These results show selection of environmental raster scale is important factor for species distribution modelling.

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P6-27

Analysis of soil seed bank in four different biotopes

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This study was conducted to provide basic data for the restoration of damaged ecosystem. The soil seed bank were analyzed among four different biotopes, artificial surface, mud flat, rural stream, and coniferous plantation. The soils were collected using a 30×30×10 cm frame with three replications. 40×60×10 cm ports were filled with 4 kg of collected soils. Irrigation was every two to three days for eight months. Every germinated seedling was identified and removed. As a result, the number of soil seeds were rural stream was 1,580, 1,408 in artificial surface, 353 in coniferous plantation, and 339 in mud flat. 25 taxa appeared in artificial surface, followed by 31% *Ambrosia tripida*, 17% *Erigeron annuus*, and 11% *Oenothera biennis*. 6 taxa appeared in the mud flat, followed by 73% *Suaida maritima*, 14% *Salicornia europa*, and 8% *Eragrostis ferruginea*. 30 taxa appeared in the rural stream, followed by 30% *Rumex obtusifolius*, 24% *Alopecurus aqualis*, and 11% *Stellaria aquatica*. 21 taxa appeared in Coniferous plantation, followed by 35% *Oplismenus undulatifolius*, 20% *Crassocephalum crepidiodides*, and 20% *American colonies*. These information about soil seed bank in biotopes show the potential of soil for a material for vegetation restoration.

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P6-28

Correlation between the occurrence of harmful cyanobacteria in the Namhan River basin and environmental factors

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The purpose of this study was to identify environmental factors that affect phytoplankton succession at three weirs (Kangcheon Weir, Yeoju Weir, and Ipo Weir) installed in the Namhan River. As a result of analyzing the status of phytoplankton occurrence and environmental factors in the three weir of the Namhan River from 2019 to 2020, the phytoplankton biomass and dominant species changed due to temperature and sufficient nutritional status (nitrogen and phosphorus concentration) of the Namhan River. At the water temperature below 20°C, the diatoms *Stephanodiscus*, *Aulacoseira*, and *Rhodomonas* were dominant, and at the temperature above 20°C, *Merismopedia*, *Aphanocapsa*, *Pseudanabaena*, and *Microcystis* were dominant. And the difference in rainfall changed the phytoplankton biomass, appearance trend, dominant species, and pollutant concentration in 2019 and 2020. These results reminded us that regular monitoring of water quality and phytoplankton fluctuations and management of non-point pollution sources are necessary to maintain stable water quality in the interpolation zone.

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P6-29

The effect of monsoon rainfall patterns on epilithic diatom communities in the stream and river, Korea

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The monsoon or Asian monsoon, also called the seasonal wind, refers to a change in wind direction in summer and winter driven by temperature differences between the land and ocean. Winds form from south to north in summer and north to south in winter. Summer winds meet with Siberian air masses and rain heavily in summer in East Asia including Korea, which is expected to have a physical and chemical impact on the Korean ecosystem. Epilithic diatom is one of the most important primary producer in the stream and river ecosystem, and show rapid responsiveness to environmental changes and are widely distributed in various environments. Therefore, water quality and health evaluation using them have been conducted for a long time.

Therefore, to evaluate the water quality environment of domestic rivers and diatom community distribution, and to investigate the changes caused by rainfall, I developed the community dynamic index (CDI) using PCA ordination and applied to performance, quantify and compare the different diatom community changes.

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P6-30

Seasonal features of benthic diatom community of the lower Han River

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We examined the seasonal variations of benthic diatom community and ecosystem health in the 12 sampling sites of the lower Han River. From April 2020 to January 2021, benthic diatom samples were studied with environmental factors including total phosphorus and total nitrogen. Statistical models such as cluster analysis and ANOVA were used to understand the characteristics of benthic diatom community, and TDI (trophic diatom index) was measured to assess ecosystem health. A 161 species of diatoms were found in the lower Han River. Differences were observed in benthic diatom species richness depending on the season($p<0.01$), especially in the summer (July), as the species richness declined. In addition, the average TDI was lowest in spring while highest in summer, both of which were the grade D, showing no significant differences. Environmental factors, especially water temperature, dissolved oxygen and electrical conductivity, also changed along with the season. In conclusion, the benthic diatom community and environmental factors showed changes according to the season, having a high correlation.

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P7-01

Gene responses in *Zacco platypus* fish as a biomarker to applications for lake environmental monitoring

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The lentic ecosystem is inhibited by artificial structure and anthropogenic pollution that flow through a variety sources continue to accumulate and have a harmful effect on habitats. *Zacco platypus* has a high dominant species in domestic freshwater, research has been conducted as an indicator of the freshwater environment. In this study, we investigated the expression of molecular marker gene (heat shock protein 70, 90, superoxide dismutase, catalase, metallothionein) using *Z. platypus* gills and livers in different lentic environments and integrated biomarker response (IBR) index observed the difference in molecular marker response between each survey location. In result, the gills observed the significantly high expression of molecular marker gene in ouflow in Singal lake. However, expression of HSP90, SOD and MT gene expression was high in Juam lake and antioxidant genes exhibit high expression in Singal lake, and differences have been observed by survey point. IBR results showed that the gills and liver had the highest IBR level in the down-stream in Singal lake and central part in Juam lake, respectively. These results suggest that potential pollution stress in lentic ecosystem may affect physiological and molecular process. Also, the comprehensive gene expression with IBR index in the *Z. platypus* give useful information to potential molecular biomarker for assessing biological health.

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P7-02

Functional diversity of the microbial community in an abandoned mine

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The release of heavy metals into the environment from mining activities can affect the soil organism's fitness and threaten the soil ecosystem. Among soil organisms, microorganisms have been known to be highly susceptible to heavy metal contamination because they have the high surface area to volume ratio. For this reason, microorganisms have been widely used as an indicator for the assessing the health of the soil ecosystem. In this study, the effect of mining activities on the soil ecosystem was evaluated by investigating the functional diversity of microbial communities using Biolog EcoPlate^{TM}. The physiological profiles were investigated through assessing the changes in the availability of microbial communities on 31 substrates measured at 24-hour intervals for a week. There was a difference in substrate use by soils sampled in mine area, and the calculated average well color development showed a high correlation with the concentration of heavy metals in the soil. Our results indicate that heavy metal contamination can affect the functional diversity of soil microbial communities and highlights the need for assessing the community-level physiological profiles of microorganisms to efficiently manage soil contaminants.

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P7-03

Short- and long-term single and combined effects of microplastics and chromium on the freshwater water flea *Daphnia magna*

Haksoo Jeong[1], Young Hwan Lee[1], Alaa El-Din H. Sayed[2], Chang-Bum Jeong[3],
Bingsheng Zhou[4], Jae-Seong Lee[c1], and Eunjin Byeon[P1]

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In this study, we investigated the individual and combined effects of microplastics (MPs) and chromium (Cr) on the freshwater water flea *Daphnia magna* by measuring mortality, bioaccumulation, antioxidative response, multixenobiotic resistance activity, and sestrin-related mitochondrial biogenesis in short-term assays and *in vivo* endpoints including reproduction and adult survival rate in long-term assays. Exposure to MPs, Cr, and their combination caused significant deleterious effects and acute toxicity in *D. magna*. Alterations in oxidative stress occurred in the groups treated with MPs and Cr alone and together. However, upon co-exposure to MPs, the Cr concentration, measured by inductively coupled plasma optical emission spectroscopy, decreased, suggesting that MPs and Cr interact with each other. Based on enzymatic activities, we found a decrease in MP egestion via inhibition of P-glycoprotein activity in the MP-exposed groups, and multidrug resistance–associated protein activity increased in some of the MP-exposed animals depending on Cr concentration. On the other hand, MP exposure seemed to lead to the mitochondrial transcription dysfunction induced by Cr via sestrin-related mitochondrial biogenesis. Overall, these results indicate that co-exposure to MPs and Cr causes acute toxicity in *D. magna* but avoid the chronic toxicity (21 days) and mitochondrial dysfunction caused by Cr exposure alone.

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P7-04

Applicability of *Brassica juncea* as bioindicator for As contamination in soil near the abandoned mine area

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Monitoring of the soil in abandoned mine area is important in the aspect of ecosystem and human health risk. Arsenic (As) is a predominant metalloid contaminant in abandoned mine area and its behavior has been affected by various soil characteristics. Eighteen soils near the mine waste dam were collected to investigate the effect of As contamination on As absorption by Brassica juncea. Bioavailability of As was assessed using Olsen method, and B. juncea was cultivated in eighteen soils for 3 weeks. To estimate a significant factor that affects the As absorption by B. juncea, principal component analysis, correlation, and multiple regression analysis were conducted. In all statistical results indicated that As bioavailability in soil is the main factor affecting As absorption in root and shoot of B. juncea. Though translocation process, the amount of As in shoot was exponentially explained by As bioavailability in soil. This result suggested that the contamination and bioavailability of As can be confirmed only by analyzing the shoot of B. juncea, which is be easily found in environmental ecosystem, and implied the applicability of B. juncea as a bioindicator for the monitoring of As contamination and its behavior in soil ecosystem.

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P7-05

Modification of arsenic contaminated *Phragmites japonica* biochar with silicon and the stabilization of arsenic

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"Waste treat waste" is a technique to remediate contaminated area with the contaminated material. Biochar from heavy metal contaminated plant can reduce the mobility of soil heavy metals and can be a case of "Waste treat waste". Even the biochar can reduce heavy metals mobility more than it has, the heavy metal leaching from contaminated biochar is still a considerable problem. Silicon in biochar can increase the resistance of chemicals and physical weathering. In this study, *Phragmites japonica* near the arsenic contaminated mine area was processed into biochar and silicon modified. The effect of silicon modification was studied with arsenic leaching in various oxidation and pH conditions. The effect of reducing arsenic dissolution from biochar according to the silicon modification with H_2O_2 was in the order of 500°C, 300°C, and 700°C. At pH 0, biochar at all temperatures showed lower arsenic leaching in the Si modified group than in the non-modified group. But the effect was not shown after the extraction solution pH over 4.

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P7-06

Qualitative status and quantitative analysis of pesticide residues of wild bird carcasses collected from islands of Marine National Park

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This paper was suggest the possibility of estimating mortality and possible effects of the accumulation of pesticide residues in the body of carcass of wild birds whose cause of death is unknown. The carcass were collected in the island area within the Marine National Park during the year of 2021, and after the autopsy, the liver was extracted and qualitative and quantitative (Etrimfos) analysis was performed by Qtrap LC/MS. The analyzed carcasses consisted of 59 individuals of 31 species, mostly collected from Heuksan Island (48 individuals of 26 species) located in Dadohaehaesang National Park. Residual pesticides accumulated in the liver consist of 12 pesticides(57%), 5 herbicides(24%), 3 fungicides(14%), and 1 plant growth inhibitor (5%). Pesticides detected over 80% of the total sample are 4 insecticides (Bioresmethrin-100%, Chlorfenvinphos-93%, Etrimfos-83%, Malaoxon-83%), 3 fungicides (Carpropamide-80%, Dodine-90%, Propamocarb) -83%) and one plant growth inhibitor (Inabenfide-100%). Etrimfos quantitative values ranged from 0 (<LOQ) to 7.55 μg/g, the mean value was 3.77 μg/g, and the median value was 4.19 μg/g. After that, residues were identified for each pesticide through comparison and statistical analysis by region, species (family), etc. The impact on the habitat environment was then inferred. The purpose of this paper is to contribute to the sustainable use and conservation of domestic wild bird habitats, and to suggest a method to block risks in advance through environmental and in vivo risk impact assessment. As a result, we intend to provide research data that will be used to establish a post-safety management system for the maintenance of wildlife health and biodiversity, and conservation of natural ecosystems.

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P8-01

Novel electrochemical PMI marker biosensor based on quantum dot dissolution using a double-label strategy

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Post-mortem interval (PMI) is the time that has elapsed since a person has died. PMI estimation is generally conducted by plain techniques, including livor, algor, and rigor mortis. However, accurate estimation of PMI is essential because it can give important evidence for the investigation of the cause and time of the death. Unfortunately, the accurate determination of PMI is very difficult, requiring many medical/scientific techniques and a long processing time. Therefore, there is an urgent need to develop a simple and rapid method for PMI detection. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) is a protein, which can be found in saliva and kidney (*Forensic Sci. Int.* 130, 127–132 (2002)), and its concentration decreases with time after death (*PLoS ONE* 11, e0160557 (2016)). This characteristic of the GAPDH protein can be utilized as a suitable protein biomarker for developing a PMI biosensor system. A novel and facile post-mortem interval (PMI) biosensor was fabricated using a double-label strategy to detect the glyceraldehyde 3-phosphate dehydrogenase (GAPDH) biomarker. A monoclonal anti-GAPDH antibody was immobilized on a surface label containing cadmium selenide quantum dots (CdSe QDs) on a cysteamine graphene oxide (Cys-GO) self-assembled monolayer. Glucose oxidase (GOx) was used as a signal label to conjugate with GAPDH. GAPDH recognition was achieved through the dissolution of the surface-attached CdSe QDs by hydrogen peroxide generated through GAPDH-conjugated GOx-catalyzed β-glucose oxidation. To enhance sensitivity, a competitive interaction was introduced between free and conjugated GAPDH to the active site of the anti-GAPDH antibody. The electrochemical response due to CdSe dissolution decreased proportionally with the concentration of free GAPDH. Differential pulsed voltammetry was conducted to determine the analytical characteristics of the immunosensor, including the limit of detection, linear dynamic range, target selectivity, system stability, and applicability toward the analysis of real samples.

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P9-01

Evaluation of drought damage by the growth stage of maize in Saemangeum reclaimed land

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Recent unexpected climate change caused the prolonged drought stress, Maize (Zea mays L.) is one of the most important major crops with variety of usages, drought stress during the growth stage has a disastrous effect on the growth of maize. This study investigated drought effect on maize at various growth stages (V5, V12, R1, R3) and salinity condition (0,3,6 dS m^{-1}) with different cultivars (Chalok4, Daehakchal, Bagsachal, Greenbaegchal) in order to evaluate response of maize to drought, an experiment was conducted in a Saemangeum green house during 2021 cropping season. Drought effect was the greatest in growth reduction at R1 and yield reduction at V5. The maize yield index of 0 dS m^{-1} treatments was significantly higher than those of 3 dS m^{-1}, 6 dS m^{-1} treatments (66.8, 49.6% respectively). Stress susceptibility index (SSI) and Tolerance index (TOL) were highest tolerance at R3 under four cultivars. These results will be useful to water management of maize and prevent drought damage in maize cultivation.

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P9-02

Characterization of three novel *CAs* related to photosynthetic reactions under different pH in the marine dinoflagellates *Prorocentrum minimum*

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Acidification of seawater is caused by an increase in atmospheric CO_2 and affects survival of dinoflagellates. However, few studies investigated the influence of pH on dinoflagellates. Carbon Concentration Mechanism (CCM) increases the level of CO_2 near RuBisCO to improve photosynthetic ability when CO_2 in seawater is limited. We cultured *Prorocentrum minimum* in the f/2 medium adjusted to pH 8 for a week, and treated different pH (pH 6, 7, 8, 9 and 10). Photosynthesis rate (Fv/Fm) was measured 0, 1, 2, 3 and 6 h, and transcriptional levels of each gene were examined at 6 h from pH treatment. In this study, we found three novel CAs (*PmCA1, 2* and *3*) from marine dinoflagellate *P. minimum* (D-127) and examined their relative expression patterns under different pH. We also identified their family based on phylogenetic analysis; PmCA1 as β-CA, PmCA2 and 3 as α-CA. Also, we predicted their locations; PmCA1 and 2 were intracellular CA (iCA), PmCA3 was extracellular CA (eCA). The expression of *PmCAs* and photosynthetic genes (*atpB* and *rbcL*) decreased at pH 6 and significantly increased at pH 9 and 10, but *Fv/Fm* was decreased at pH 10. It shows that CCM and CA were affected in high pH conditions (pH 9 and 10) although the growth of *P. minimum* was inhibited over pH 9.6. Acidification of marine environments may adversely influence photosynthesis, resulting in lowered CCM of dinoflagellates, and further research is necessary to understand effects of acid stress on other functional genes related to CCM.

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P9-03

Implementation of fuzzy logic in a system dynamics model: An application to the Korean rice production systems

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Fuzzy system dynamics (FSD) modeling, which combines fuzzy logic and a system dynamics model (SDM), has recently been spotlighted as a useful technique for simulating complex systems. However, existing methods for implementing FSD have limitations in that they require multiple modeling platforms and transform the model into a more complex form. In this study, an FSD implementation method that can overcome these limitations using only a system dynamics platform was newly developed. The main feature of the developed method was to implement the fuzzy logic in the SDM platform by temporarily converting the variables constituting the fuzzy logic into the time variables. The utility of the developed method was confirmed by case simulation studies on rice production in agricultural ecosystems. The results of the case study showed that the FSD model implemented in the SDM platform is useful for more realistic scenario simulations and control of the uncertainty in data values and interactions between components of agricultural ecosystems. The FSD implementation method developed in this study can help SDM to simulate complex ecosystems more effectively.

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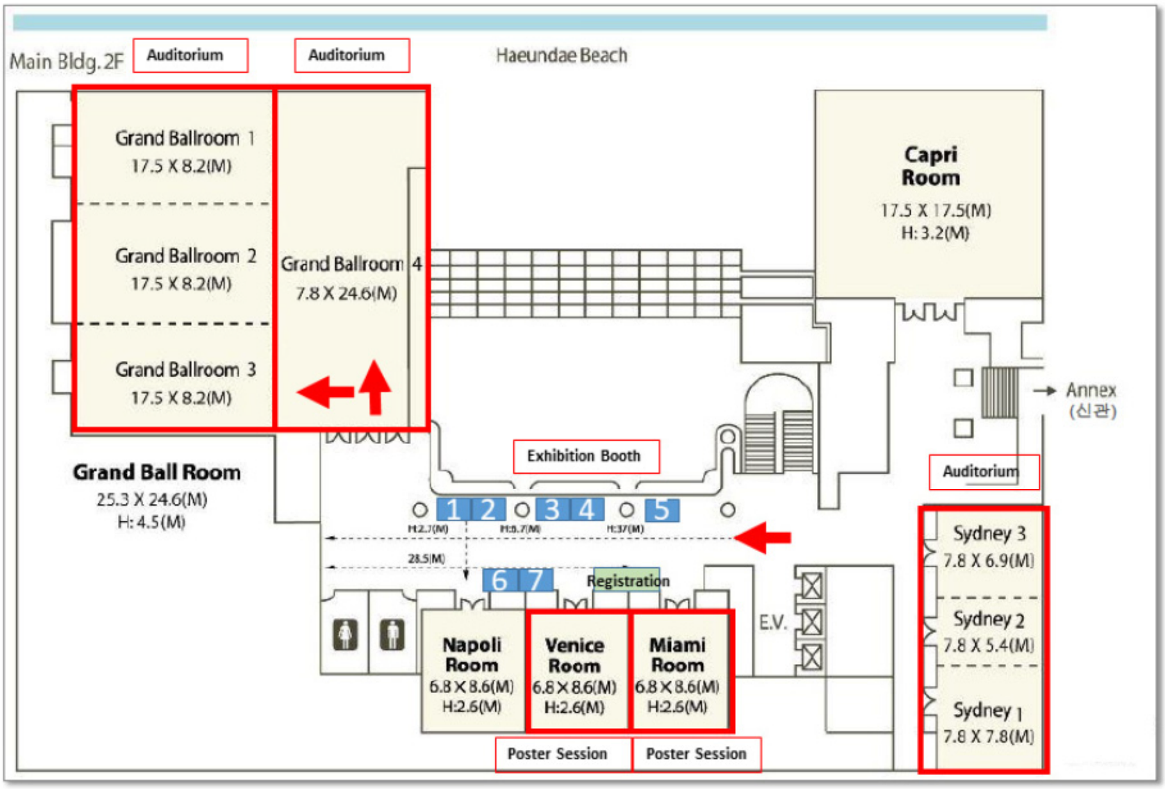
Exhibition

■ Exhibition

Date : Oct. 19 (Wed) ~ Oct. 21 (Fri)
Place: 2F Lobby, Main Bldg, Paradise Hotel, Busan, South Korea

■ Booth Layout



■ Booth No. Exhibitors

Booth No.	Exhibitors
1	한국과학기술정보연구원 (Korea Institute of Science and Technology Information)
2	한국환경연구원 (Korea Environment Institute)
3, 4	국립백두대간수목원 (Baekdudaegan National Arboretum)
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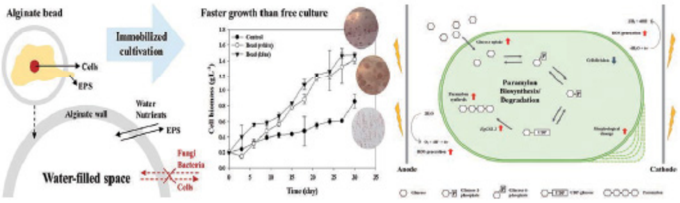
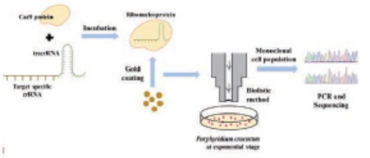
RESEARCH FIELD

Value-Added Chemical

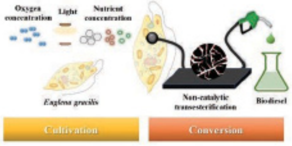
- Production induction



- Genetic engineering

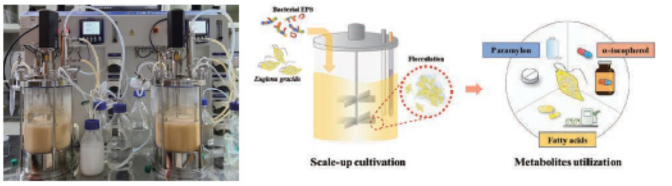


- Biodiesel

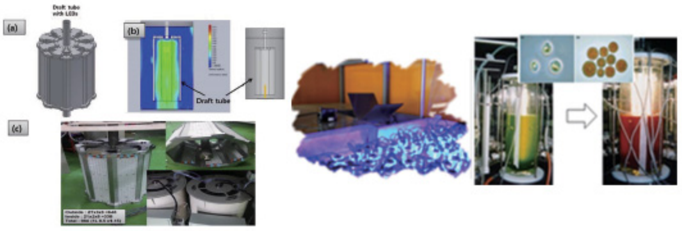


Mass Production

- Jar-fermenter

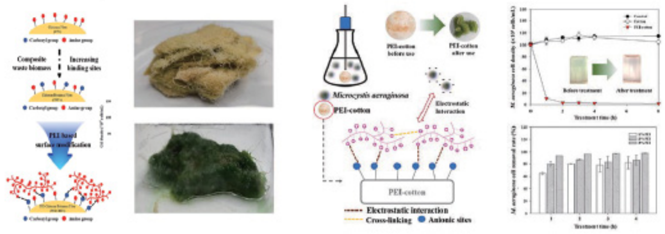


- Photo-bioreactor

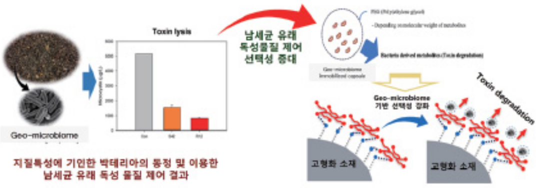


Harmful Algal Bloom

- Adsorption-based HABs control



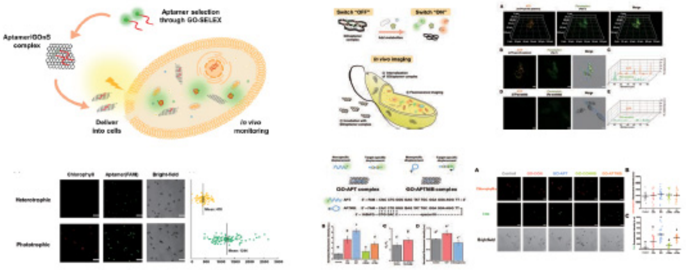
- Adsorption-based cyanotoxin removal



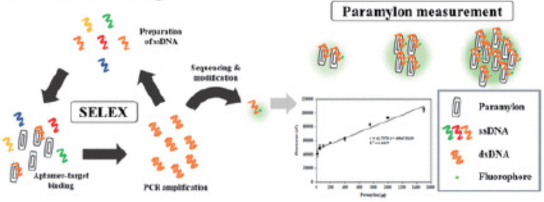
지질특성에 기인한 박테리아의 동정 및 이용한 남세균 유래 독성 물질 제어 결과

Sensor

- Intracellular sensor



- Probe screening



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